

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: GAMDEL Examiner #: 70675 Date: 7/19/01
 Art Unit: 1644 Phone Number 308 3997 Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle) PAPER DISK E-MAIL

1644 MILBOY 9012
 If more than one search is submitted, please prioritize searches in order of need. 8803

 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: OB/487203

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

SEQ + SEQ INTERVIEW IS REQUEST

- ① SEQ ID NO: 8 NA
- ② SEQ ID NO: 8 NA
- ③ SEQ ID NO: 12 NA
- ④ SEQ ID NO: 12 (1-12 NA)
- ⑤ 8-12 OF SEQ ID NO: 1 CLOSED
- ⑥ SEQ ID NO: 1 CLOSED

FRANK REQUEST JNU

STAFF USE ONLY

Searcher: Jan
 Searcher Phone #: 4498
 Searcher Location: _____
 Date Searcher Picked Up: 7/19
 Date Completed: 7/20/01
 Searcher Prep & Review Time: _____
 Clerical Prep Time: 30
 Online Time: 45

Type of Search

NA Sequence (#) 2
 AA Sequence (#) 4
 Structure (#) _____
 Bibliographic _____
 Litigation _____
 Fulltext _____
 Patent Family _____
 Other _____

Vendors and cost where applicable

STN _____
 Dialog _____
 Questel/Orbit _____
 Dr. Link _____
 Lexis/Nexis _____
 Sequence Systems ✓
 WWW/Internet _____
 Other (specify) _____

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 19, 2001, 07:47:14 : Search time 20.95 Seconds
(Without alignments)
132.621 Million cell updates/sec

Title: US-08-487-283A-1
Perfect score: 107
Sequence: 1 VIDHOGTKSKKCVKRVKSS 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 5200

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_16:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27.1	19	6	Q9TRR6	O9TRR6 oryctolagus
2	27.1	20	3	P82263	P82263 aspergillus
3	26.2	20	2	Q9R4D2	Q9R4D2 haemophilus
4	25	23.4	17	11 Q9OVAR2	Q9OVAR2 mus sp. pro
5	25	23.4	18	10 Q40499	Q40499 nicotiana t
6	25	23.4	21	14 Q93044	Q93044 maize strea
7	25	23.4	21	14 Q93046	Q93046 maize strea
8	25	23.4	21	14 Q93047	Q93047 maize strea
9	24	22.4	12	14 Q75729	Q75729 human immun
10	24	22.4	18	11 Q9WPP8	Q9WPP8 rattus norv
11	24	22.4	19	6 Q9TR05	Q9TR05 bos taurus
12	24	22.4	21	14 Q93050	Q93050 maize strea
13	23.5	22.0	13	11 Q9OVD5	Q9OVD5 rattus sp.
14	23	21.5	15	10 Q9S016	Q9S016 oryza sativ
15	23	21.5	17	10 Q9LMD7	Q9LMD7 arabidopsis
16	23	21.5	19	3 Q9P7P3	Q9P7P3 schizosacch
17	23	21.5	20	2 Q9R5P7	Q9R5P7 legionella
18	23	21.5	20	2 Q9R502	Q9R502 thermotoga
19	23	21.5	21	8 Q78339	Q78339 elmeria ten

20	23	21.5	21	14	O11816	O11816 human immun
21	23	21.5	21	14	O11836	O11836 human immun
22	22	20.6	16	4	O16350	O16350 homo sapien
23	22	20.6	16	8	O36731	O36731 homo sapien
24	22	20.6	16	10	Q9S8Y6	Q9S8Y6 lupinus arb
25	22	20.6	18	2	P72015	P72015 mycobacteri
26	22	20.6	19	10	P82245	P82245 spinactia ol
27	22	20.6	20	10	Q9S900	Q9S900 vigna sinen
28	22	20.6	20	13	Q9PRV5	Q9PRV5 xenopus lae
29	22	20.6	21	10	Q9S8Y4	Q9S8Y4 lupinus arb
30	22	20.6	21	14	O11790	O11790 human immun
31	21	19.6	8	14	O83977	O83977 influenza a
32	21	19.6	9	2	Q9JN16	Q9JN16 streptococ
33	21	19.6	10	2	Q9JNC9	Q9JNC9 streptococ
34	21	19.6	12	4	Q9UNV5	Q9UNV5 homo sapien
35	21	19.6	12	7	Q77877	Q77877 oreochromis
36	21	19.6	12	7	Q77878	Q77878 oreochromis
37	21	19.6	12	7	Q77881	Q77881 oreochromis
38	21	19.6	12	7	Q77882	Q77882 oreochromis
39	21	19.6	12	7	Q77909	Q77909 oreochromis
40	21	19.6	15	2	Q47612	Q47612 escherichia
41	21	19.6	16	2	Q9R5E4	Q9R5E4 aeromonas h
42	21	19.6	17	8	Q9T2H6	Q9T2H6 spinacia ol
43	21	19.6	18	5	Q9TWG6	Q9TWG6 trypanosoma
44	21	19.6	18	9	Q9XJ05	Q9XJ05 bacterioph
45	21	19.6	20	2	Q9R5P1	Q9R5P1 streptospo

ALIGNMENTS

RESULT	ID	Q9TRR6	PRELIMINARY;	PRT;	19 AA.
Q9TRR6	Q9TRR6	Q9TRR6	PRELIMINARY;	PRT;	19 AA.
DT	01-MAY-2000	(TREMBLrel. 13, Created)			
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)			
DT	01-OCT-2000	(TREMBLrel. 15, Last annotation update)			
DE	CALCICLIN-ASSOCIATED PROTEIN, CAP50-CA2+/PHOSPHOLIPID-BINDING PROTEIN				
DE	L-14 FRAGMENT.				
OS	Oryctolagus cuniculus (Rabbit).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.				
OX	NCBI_TaxID=9986;				
RN	[1]				
RX	MDLINE=92250478; PubMed=1533622;				
RA	Tokumitsu H., Mizutani A., Minami H., Kobayashi R., Hidaka H.:				
RT	"A calcyclin-associated protein is a newly identified member of the				
RT	Ca2+/phospholipid-binding proteins, annexin family.";				
RL	J. Biol. Chem. 267:8919-8924(1992).				
DR	HSSP: P13214; IANN.				
SO	SEQUENCE 19 AA; 2018 MW; 9A54062504B8322E CRC64;				
Query Match	27.1%;	Score 29;	DB 6;	Length 19;	
Best local Similarity	45.5%;	Pred. No. 3.9e+02;			
Matches	5;	Conservative	4;	Mismatches	2;
				Indels	0;
				Gaps	0;
QY	1 VIDHOGTKSKK 11				
	:: ::				
Db	9 IIDXLGSRSMK 19				
RESULT	2				
P82263	P82263	PRELIMINARY;	PRT;	20 AA.	
AC	P82263;				
DT	01-MAY-2000	(TREMBLrel. 13, Created)			
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)			
DT	01-MAY-2000	(TREMBLrel. 13, Last annotation update)			
DE	ALLERGEN ASP F 3 (FRAGMENT).				
OS	Aspergillus fumigatus (Sartorya fumigata).				

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OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5085;
RN [1]
RP SEQUENCE
RC STRAIN=AF-285;
RA Sarma P.O., Gupta T.M., Fairwell T.;
RL Submitted (DEC-1999) to the SWISS-PROT data bank.
CC -!- FUNCTION: BINDS TO IGG AND IGE.
KW Allergen; IgE-binding protein; IgG-binding protein.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2290 MW; 46D1CEB3AB2BF585 CRC64;

Query Match 27.1%; Score 29; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QGKSS 10
Db 12 QGKSS 17
|||||

RESULT 3
Q9R4D2 PRELIMINARY; PRT; 20 AA.
ID Q9R4D2
AC Q9R4D2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE 40.5 KDA IGA NEPHROPATHY-ASSOCIATED OUTER MEMBRANE ANTIGEN (FRAGMENT).
OS Haemophilus parainfluenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=729;
RN [1]
RP SEQUENCE.
RX MEDLINE=96215401; PubMed=8625525;
RA Suzuki S., Nakatomi Y., Odani S., Sato H., Geijo F., Arakawa M.;
RT "Circulating IgA, IgG, and IgM class antibody against Haemophilus
RT parainfluenzae antigens in patients with IgA nephropathy.";
RL Clin. Exp. Immunol. 104:306-311(1996).
SQ SEQUENCE 20 AA; 2153 MW; 4CD523E74E5639E5 CRC64;

Query Match 26.2%; Score 28; DB 2; Length 20;
Best Local Similarity 62.5%; Pred. No. 6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VIDHGTGK 8
Db 3 VYDNEGTK 10
| | : : | | | |

RESULT 4
Q9QVA2 PRELIMINARY; PRT; 17 AA.
ID Q9QVA2
AC Q9QVA2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE PROTEIN KINASE C SUBSTRATE PP80 (FRAGMENT).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE.
RX MEDLINE=93099617; PubMed=1464108;
RA Komatsu S., Hirano H.;
RT "80 kDa mouse sperm protein as a substrate of protein kinase C.";
RL Chem. Pharmacol. Bull. 40:2780-2782(1992).
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SQ SEQUENCE 17 AA; 2025 MW; B8272D8940BD0B41 CRC64;

Query Match 23.4%; Score 25; DB 11; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 8 KSKKCVQRKVEG 19
Db 4 KSEKYVFKXLEG 15
| | | | : : | |
| | | | : : | |

RESULT 5
Q40499 PRELIMINARY; PRT; 18 AA.
ID Q40499
AC Q40499;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE ELONGATION FACTOR 1-A (FRAGMENT).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
OC Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=19;
RX MEDLINE=94035181; PubMed=8220482;
RA Marty I., Brugidou C., Chartier Y.;
RT "Growth-related gene expression in Nicotiana tabacum mesophyll
RT protoplasts.";
RL Plant J. 4:265-278(1993).
DR EMBL; Z14080; CAA78458.1; -
KW Elongation factor.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 1983 MW; 5FB7282474069C97 CRC64;

Query Match 23.4%; Score 25; DB 10; Length 18;
Best Local Similarity 35.7%; Pred. No. 1.7e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 DHQGTKSSKCVROK 16
Db 3 DPTGAKVTRAAQKK 16
| | | | : : | |
| | | | : : | |

RESULT 6
O93044 PRELIMINARY; PRT; 21 AA.
ID O93044
AC O93044;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE 17.6 KDA REPB PROTEIN (FRAGMENT).
GN REPB.
OS Maize streak virus.
OC Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
OX NCBI_TaxID=10821;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SP1 FROM REUNION ISLAND;
RX MEDLINE=97049057; PubMed=8893787;
RA Peterschmitt M., Granier M., Frutos R., Reynaud B.;
RT "Infectivity and complete nucleotide sequence of the genome of a
RT genetically distinct strain of maize streak virus from Reunion
RT Island.";
RL Arch. Virol. 141:1637-1650(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SP1 FROM REUNION ISLAND;
RA Isnard M., Granier M., Frutos R., Reynaud B., Peterschmitt M.;
```

"Onaspecies nature of three related maize streak virus isolates
 RT obtained through different mode of selection."
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ224999; CAA12284.1; -
 FT NON_TER 21
 SO SEQUENCE 21 AA; 2364 MW; 267B619FB84E782B CRC64;

Query Match 23.4%; Score 25; DB 14; Length 21;
 Best Local Similarity 44.4%; Pred. No. 2e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 12 CVRQVSGS 20
 I:: III
 Db 5 CIOSSDEGS 13

RESULT 7
 093046 PRELIMINARY; PRT; 21 AA.
 AC 093046;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, last sequence update)
 DE 01-NOV-1998 (TREMBlrel. 08, last annotation update)
 DE 17.6 KDA REPB PROTEIN (FRAGMENT).
 GN REPB.
 OS Maize streak virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
 OX NCBI_TaxID=10821;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPI FROM REUNION ISLAND;
 RA MEDLINE-97049057; PubMed-8893787;
 RA Peterschmitt M., Granier M., Frutos R., Reynaud B.;
 RT "Infectivity and complete nucleotide sequence of the genome of a
 RT genetically distinct strain of maize streak virus from Reunion
 RT Island.";
 RL Arch. Virol. 141:1637-1650(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPI FROM REUNION ISLAND;
 RA Isnard M., Granier M., Frutos R., Reynaud B., Peterschmitt M.;
 RT "Quasiespecies nature of three related maize streak virus isolates
 RT obtained through different mode of selection."
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ225000; CAA12287.1; -
 FT NON_TER 21
 SO SEQUENCE 21 AA; 2364 MW; 267B619FB84E782B CRC64;

Query Match 23.4%; Score 25; DB 14; Length 21;
 Best Local Similarity 44.4%; Pred. No. 2e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 12 CVRQVSGS 20
 I:: III
 Db 5 CIOSSDEGS 13

RESULT 8
 093047 PRELIMINARY; PRT; 21 AA.
 AC 093047;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, last sequence update)
 DE 01-NOV-1998 (TREMBlrel. 08, last annotation update)
 DE 17.6 KDA REPB PROTEIN (FRAGMENT).
 GN REPB.
 OS Maize streak virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
 OX NCBI_TaxID=10821;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-SPI FROM REUNION ISLAND;
 RX MEDLINE-97049057; PubMed-8893787;
 RA Peterschmitt M., Granier M., Frutos R., Reynaud B.;
 RT "Infectivity and complete nucleotide sequence of the genome of a
 RT genetically distinct strain of maize streak virus from Reunion
 RT Island.";
 RL Arch. Virol. 141:1637-1650(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPI FROM REUNION ISLAND;
 RA Isnard M., Granier M., Frutos R., Reynaud B., Peterschmitt M.;
 RT "Quasiespecies nature of three related maize streak virus isolates
 RT obtained through different mode of selection."
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ225001; CAA12290.1; -
 FT NON_TER 21
 SO SEQUENCE 21 AA; 2364 MW; 267B619FB84E782B CRC64;

Query Match 23.4%; Score 25; DB 14; Length 21;
 Best Local Similarity 44.4%; Pred. No. 2e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 12 CVRQVSGS 20
 I:: III
 Db 5 CIOSSDEGS 13

RESULT 9
 075729 PRELIMINARY; PRT; 12 AA.
 AC 075729;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
 DE 01-MAY-2000 (TREMBlrel. 13, last annotation update)
 DE NEF (NEF).
 GN NEF.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H94FL;
 RA Mariani R., Kirchhoff F., Greenough T.C., Sullivan J.L.,
 RA Desrosiers R.C., Skowronski J.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U61801; AAB04720.1; -
 DR InterPro: IPR000583; -
 DR PROSITE: PS00443; GATASE_TYPE_II; UNKNOWN_1.
 DR PROSITE: PS00443; GATASE_TYPE_II; UNKNOWN_1.
 SO SEQUENCE 12 AA; 1238 MW; 2B921E1187B325A3 CRC64;

Query Match 22.4%; Score 24; DB 14; Length 12;
 Best Local Similarity 71.4%; Pred. No. 1.8e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 GTRSSKC 12
 I:: III
 Db 2 GTRSSKC 8

RESULT 10
 09WTP8 PRELIMINARY; PRT; 18 AA.
 ID 09WTP8
 AC 09WTP8;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, last sequence update)
 DE 01-NOV-1999 (TREMBlrel. 12, last annotation update)
 DE R-RAS GTPASE ACTIVATING PROTEIN (FRAGMENT).
 GN R-RAS GAP.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAQUE-DAWLEY;
RA Iwashita S., Kobayashi M.;
RT "NGF-mediated downregulation of R-ras GAP expression.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB020479; BAA78368.1;
FT NON_TER 18
SQ SEQUENCE 18 AA; 2104 MW; 6BC3355FDC91E28A CRC64;

Query Match 22.4%; Score 24; DB 11; Length 18;
Best Local Similarity 25.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 2 IDHQGTKSKCVROKV 17
Db : : : : :
3 VEEGLRVFOSVRIKI 18

RESULT 11
Q9TRQ5 PRELIMINARY; PRT; 19 AA.
AC Q9TRQ5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE CALCULIN-ASSOCIATED PROTEIN PEPTIDE L-II, CAP-50-ANNEXIN.
OS Bos taurus (Bovine).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=92317074; PubMed=1618851;
RA Mizutani A., Usuda N., Tokumitsu H., Minami H., Yasui K.,
RA Kobayashi R., Hidaka H.;
RT "CAP-50, a newly identified annexin, localizes in nuclei of cultured
RT fibroblast 3Y1 cells.";
RL J. Biol. Chem. 267:13498-13504(1992).
SQ SEQUENCE 19 AA; 2144 MW; F3994AFD0DE7CB05 CRC64;

Query Match 22.4%; Score 24; DB 6; Length 19;
Best Local Similarity 41.7%; Pred. No. 2.7e+03;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 6 GTKSKCVROKV 17
Db : : : : :
6 GTKDXLRDQV 17

RESULT 12
O93050 PRELIMINARY; PRT; 21 AA.
AC O93050;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE 17.6 KDA REPB PROTEIN (FRAGMENT).
GN REPB.
OS Maize streak virus.
OC Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
OX NCBI_TaxID=10821;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SP2 FROM REUNION ISLAND;
RX MEDLINE=97049057; PubMed=8893787;
RA Peterschmitt M., Granier M., Frutos R., Reynaud B.;
RT "Infectivity and complete nucleotide sequence of the genome of a
RT genetically distinct strain of maize streak virus from Reunion

RT Island.";
RL Arch. Virol. 141:1637-1650(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-SP2 FROM REUNION ISLAND;
RA Isnard M., Granier M., Frutos R., Reynaud B., Peterschmitt M.;
RT "Quasiespecies nature of three related maize streak virus isolates
RT obtained through different mode of selection.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ225005; CAA12297.1;
FT NON_TER 21
SQ SEQUENCE 21 AA; 2378 MW; 267B619FB848A32B CRC64;

Query Match 22.4%; Score 24; DB 14; Length 21;
Best Local Similarity 44.4%; Pred. No. 3e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 12 CVRQKVEGS 20
Db : : : : :
5 CIQTSDEGS 13

RESULT 13
Q9QVD5 PRELIMINARY; PRT; 13 AA.
AC Q9QVD5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE INOSITOL 1,4,5-TRISPHOSPHATE BINDING PROTEIN.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=92202192; PubMed=1313009;
RA Kanematsu T., Takeya H., Watanabe Y., Ozaki S., Yoshida M., Koga T.,
RA Iwanaga S., Hirata M.;
RT "Putative inositol 1,4,5-trisphosphate binding proteins in rat brain
RT cytosol.";
RL J. Biol. Chem. 267:6518-6525(1992).
SQ SEQUENCE 13 AA; 1537 MW; 3EA2F724AD8B85B8 CRC64;

Query Match 22.0%; Score 23.5; DB 11; Length 13;
Best Local Similarity 37.5%; Pred. No. 2.3e+03;
Matches 6; Conservative 2; Mismatches 5; Indels 3; Gaps 1;

OY 1 VIDHQGTKSKCVROK 16
Db : : : : :
1 ITHHSGMDQ---RQK 13

RESULT 14
Q9SQ16 PRELIMINARY; PRT; 15 AA.
AC Q9SQ16;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE TRANSLATION ELONGATION FACTOR (FRAGMENT).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
OC Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Li Z.-Y., Chen S.-Y.;
RT "Inducible expression of translation elongation factor 1A gene in rice
RT seedlings in response to environmental stresses.";

RL Act¹ Bot. Sin. 41:800-806(1999).
 DR EMBL; AF067195; AAC79991.1; -;
 DR InterPro; IPR001153; -;
 DR ProDom; PD004535; -; 1.
 KW Elongation factor.
 FT NON_TER 1
 SO SEQUENCE 15 AA; 1514 MW; 95E5C46F069C9775 CRC64;

Query Match 21.5%; Score 23; DB 10; Length 15;
 Best Local Similarity 35.7%; Pred. No. 3.2e+03;
 Matches 5; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 3 HQGTRKSSKCVROK 16
 | | : | : |
 Db 1 DPTGAKVTKAARK 14

RESULT 15

O9LMD7 PRELIMINARY; PRT; 17 AA.
 AC O9LMD7;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE F14D16.5.
 OS Arabidopsis thaliana (Mouse-ear cress).
 CC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 CC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 CC Brassicales; Brassicaceae; Arabidopsis.
 NX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shin P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
 Kim C., Altafi H., Bei Q., Chin C., Chou J., Choi E., Conn L.,
 Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
 Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
 Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
 Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
 Ecker J.R.;
 RA "Genomic sequence for Arabidopsis thaliana BAC F14D16 from chromosome
 1.";
 RT Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RN SEQUENCE FROM N.A.
 RP Ecker J.R.;
 RA Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RL [3]
 RN SEQUENCE FROM N.A.
 RP Cheuk R., Shin P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
 Khan S., Kim C., Altafi H., Bei B., Chin C., Chou J., Choi E.,
 Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B.,
 Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N.,
 Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
 Theologis A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
 Thaveri A., Ecker J.;
 RA Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC068602; AAF79279.1; -;
 SO SEQUENCE 17 AA; 1987 MW; 518C4C484C814D86 CRC64;

Query Match 21.5%; Score 23; DB 10; Length 17;
 Best Local Similarity 44.4%; Pred. No. 3.6e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 4 HQGTRKSSK 12
 | : | : |
 Db 8 HHLSPSRC 16

Search completed: July 19, 2001, 07:50:05
 Job time: 171 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 19, 2001, 07:46:49 ; Search time 18 Seconds
(without alignments)
70.728 Million cell updates/sec

Title: US-08-487-283A-1
Perfect score: 107
Sequence: 1 VIDHOGTKSKVCVRKVEGSS 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 163282

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_0601:*

1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
3: /SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*
4: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
5: /SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT:*
6: /SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*
7: /SIDS8/gcgdata/geneseq/geneseqp/AA1986.DAT:*
8: /SIDS8/gcgdata/geneseq/geneseqp/AA1987.DAT:*
9: /SIDS8/gcgdata/geneseq/geneseqp/AA1988.DAT:*
10: /SIDS8/gcgdata/geneseq/geneseqp/AA1989.DAT:*
11: /SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT:*
12: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:*
13: /SIDS8/gcgdata/geneseq/geneseqp/AA1992.DAT:*
14: /SIDS8/gcgdata/geneseq/geneseqp/AA1993.DAT:*
15: /SIDS8/gcgdata/geneseq/geneseqp/AA1994.DAT:*
16: /SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT:*
17: /SIDS8/gcgdata/geneseq/geneseqp/AA1996.DAT:*
18: /SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT:*
19: /SIDS8/gcgdata/geneseq/geneseqp/AA1998.DAT:*
20: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*
21: /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*
22: /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	107	100.0	21	16	AA77605
2	36	33.6	19	21	AA52695
3	32	29.9	9	16	AA67862
4	32	29.9	9	16	AA68909
5	32	29.9	11	11	AA605852
6	32	29.9	11	16	AA67860
7	32	29.9	11	16	AA68908
8	32	29.9	14	20	AA68479
9	31	29.0	9	21	AA67659
10	31	29.0	20	19	AA65855
11	31	29.0	20	19	AA65845

12	31	29.0	20	19	AA65848	HIV p17 gag protei
13	31	29.0	20	19	AA65851	HIV p17 gag protei
14	30	28.0	21	21	AA623773	Entry vector pENTR
15	29	27.1	13	14	AA635477	Phosphatidylserine
16	29	27.1	14	19	AA653864	Gravin polypeptide
17	29	27.1	14	21	AA615884	Human gravin poten
18	29	27.1	15	21	AA679915	Rhesus monkey papl
19	29	27.1	19	21	AA601692	Nuclear localisati
20	28	26.2	15	10	AA690197	Antigenic peptide
21	28	26.2	15	21	AA65517	Oestrogen receptor
22	28	26.2	18	22	AA650505	CD40-binding pepti
23	28	26.2	20	16	AA68766	Cytotoxic T lympho
24	28	26.2	20	17	AA693360	Beta-casein fragme
25	28	26.2	20	19	AA653854	HIV p17 gag protei
26	28	26.2	20	19	AA655856	HIV p17 gag protei
27	28	26.2	20	19	AA655858	HIV p17 gag protei
28	28	26.2	20	19	AA655859	HIV p17 gag protei
29	28	26.2	20	19	AA655860	HIV p17 gag protei
30	28	26.2	20	19	AA655861	HIV p17 gag protei
31	28	26.2	20	19	AA655863	HIV p17 gag protei
32	28	26.2	20	19	AA655846	HIV p17 gag protei
33	28	26.2	20	19	AA655847	HIV p17 gag protei
34	28	26.2	20	19	AA655849	HIV p17 gag protei
35	28	26.2	20	19	AA655850	HIV p17 gag protei
36	27.5	25.7	18	19	AA683057	Human Fas peptide
37	27.5	25.7	18	21	AA614765	Human Fas epitope,
38	27.5	25.7	18	21	AA690915	Human Fas extracel
39	27	25.2	10	3	AA620202	Sequence of peptid
40	27	25.2	10	3	AA620326	Decapeptide with t
41	27	25.2	11	3	AA620205	Sequence of peptid
42	27	25.2	11	22	AA672850	Human p53 S121C mu
43	27	25.2	12	19	AA686708	Synthetic peptide
44	27	25.2	13	3	AA620327	Tridecapeptide wit
45	27	25.2	14	20	AA601111	CTGF peptide fragm

ALIGNMENTS

RESULT	1
AA677605	standard; Protein: 21 AA.
AA677605:	
02-APR-1996 (first entry)	
Pro-C5 polypeptide KSSKC epitope.	
Complement C5; haemolysis; kidney; glomerulonephritis;	
monoclonal antibody; antiinflammatory; antibody engineering;	
humanised antibody; KSSKC epitope.	
Homo sapiens.	
WO9529697-A1.	
09-NOV-1995.	
01-MAY-1995; 95WO-US05688.	
02-MAY-1994; 94US-0236208.	
(ALEX-) ALEXION PHARM INC.	
Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;	
Rother RP, Springhorn J P, Squinto SP, Thomas TC;	
Wang Y, Wilkins JA;	
WPI; 1995-392923/50.	
Treating glomerulonephritis with antibody against complement C5	
component - to inhibit complement induced cell lysis	

XX Example 13; Page 81; 181pp; English.

XX The cDNA sequence of the complement C5 gene transcript predicts a

XX secreted pro-C5 precursor of 1676 amino acids (AAR77604). C5 is a

XX beta-globulin heterodimer thought to play a role in the pathogenesis

XX of glomerulonephritis (GN). Cleavage of the C5 alpha-chain

XX by a convertase enzyme generates anaphylatoxic C5a. Monoclonal

XX C and humanised recombinant antibodies that recognise the alpha-chain

XX KSSKC epitope (AAR77605) block C5a generation, thereby reducing

XX glomerular inflammation and kidney dysfunction associated with GN.

SQ Sequence 21 AA;

Query Match 100.0%; Score 107; DB 16; Length 21;

Best Local Similarity 100.0%; Pred. No. 4.6e-11;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VIDHGTGKSSKCVKQVEGSS 21

Db 1 vidhgtksskcvrkvegss 21

|||||

RESULT 2

AAY52695

ID AAY52695 standard; peptide; 19 AA.

XX AAY52695;

XX AAY52695;

DT 07-MAR-2000 (first entry)

XX Synthetic fibrinogen C-terminus peptide, peptide-07.

XX Fibrinogen; C-terminus; cell adhesion; cell binding; proliferation;

KW wound healing; diabetes mellitus; clotting; coagulation; disorder;

KW haemophilia A; factor VIII deficiency; haemophilia B;

KW factor IX deficiency; cell culture; separation; cell transplantation;

KW therapeutic structure; research tool; diagnosis.

XX Synthetic.

XX WO9961041-A1.

PN 02-DEC-1999.

XX 26-MAY-1999; 99WO-US11517.

XX 27-MAY-1998; 98US-0084371.

PR (HADA-) HADASIT MEDICAL RES SERVICES & DEV.

PA (VITE-) VI TECHNOLOGIES INC.

XX Gorodetsky R, Marx G;

PI WPI; 2000-062582/05.

XX New peptides corresponding to fibrinogen carboxy terminus, used for

PT promoting wound healing -

XX Example 1; Page 12; 46pp; English.

XX This sequence represents a synthetic peptide, peptide-07, which

XX corresponds to a fibrinogen alpha chain C-terminal sequence.

CC However, unlike the claimed peptides of the invention, this

CC peptide exhibited no cell adhesion. The invention relates

CC to novel fibrinogen C-terminal peptides, peptide-09 (AAY52600),

CC peptide-70 (AAY52693) and peptide-71 (AAY52694). These claimed

CC peptides have cell adhesive effects, with peptide-09 being the most

CC potent for cell binding, and peptide-71 being the next most potent.

CC Peptide-71 was also found to have cell proliferative effects. The

CC peptides can be used to promote healing of a wound in a patient. They

CC can also be used for diseases characterised by the absence of a

cellular product, e.g., diabetes mellitus type I, haemophilia A

(factor VIII deficiency), and haemophilia B (factor IX deficiency).

They can also be used for the growth and transport of cells in cell

culturing systems, the separation of different types of cells from

mixed cell cultures, and the transplantation of cells into tissues

or cell cultures. They can be used for producing therapeutic structures,

e.g., gels, prosthetic devices or collagen sheets. The peptides can

also be used as tools for performing analysis of other physiological

systems, and for further research and development, for example, to

identify and isolate cell receptors. The peptides can also be used in

diagnosis, e.g., of blood coagulation disorders.

XX Sequence 19 AA;

Query Match 33.6%; Score 36; DB 21; Length 19;

Best Local Similarity 66.7%; Pred. No. 22;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 DHQGTSSK 11

Db 3 dhqgthstk 11

|||||

RESULT 3

AAR67862

ID AAR67862 standard; peptide; 9 AA.

XX AAR67862;

XX AAR67862;

DT 07-SEP-1995 (first entry)

XX FVII/TF multi-protein complex inhibition test peptide FVII-4B.

XX Factor VII; Factor 7; blood clotting factor; multi-protein complex;

KW human tissue factor; FVII/TF; assay.

XX Synthetic.

XX WO9500847-A.

PN 05-JAN-1995.

XX 17-JUN-1994; 94WO-GB01314.

XX 18-JUN-1993; 93GB-0012638.

XX (HAFS-) HAFSLUND NYCOMED AS.

PA (HOLM/) HOLMES M J.

XX Oerning L, Sakariassen K, Stephens R;

PI WPI; 1995-052226/07.

XX Immunoassay for multi-protein complexes - used to detect

PT malfunction in formation of complexes in an individual, e.g. due

PT to genetic or physiological disorders

XX Example 2; Page 8; 19pp; English.

XX Synthetic peptides (AAR67858-R67865) were individually assayed as test

XX substances to ascertain their effect on the formation of the blood-

XX clotting factor VII/tissue factor multi-protein complex. Of the

XX peptides tested, the most inhibition was obtained with cyclic

XX peptides representing the ring structures present in the FVII growth

XX factor domains (i.e. AAR67861, AAR67864 and AAR67863). Peptide AAR67858,

XX a linear peptide corresp. to residues 136-146 from a region close to

XX the site of cleavage which activates FVII also had good inhibitory

XX activity.

SQ Sequence 9 AA;

Query Match 29.9%; Score 32; DB 16; Length 9;
 Best Local Similarity 75.0%; Pred. No. 3.4e+05;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 DHQGTKSS 10
 |||||
 Db 2 dhtgltkrs 9

RESULT 4

AAR68909 standard; peptide; 9 AA.

XX AAR68909;

XX 06-AUG-1995 (first entry)

XX Factor VII-derived peptide fragment FVII-4B.

XX Factor VII; blood-clotting factor; thrombosis; angina;
 XX cerebrovascular disease; pulmonary embolism; heart disease.

XX Synthetic.

XX WO9500541-A.

XX 05-JAN-1995.

XX 17-JUN-1994; 94WO-GB01315.

XX 18-JUN-1993; 93GB-0012601.

XX 10-MAY-1994; 94GB-0009335.

XX (HAFS-) HAFSLUND NYCOMED AS.

XX (HOLM/) HOLMES M J.

XX Oerling L, Sakariassen KS, Stephens RW, Sakariassen K;

XX WPI; 1995-052003/07.

XX Factor VII-derived peptide compounds - useful for

XX preventing/inhibiting binding of tissue factor to factor VII.

XX Disclosure: Page 20; 61pp; English.

XX This peptide fragment is useful for preparing pharmaceutical

XX compositions for prevention or inhibition of Factor-VII binding to

XX tissue factor. It is useful for treating or preventing blood clotting

XX disorders in humans and animals, e.g. thrombosis, angina,

XX cerebrovascular disease or pulmonary embolism.

XX Sequence 9 AA;

OY 3 DHQGTKSS 10

|||||

Db 2 dhtgltkrs 9

RESULT 5

AAR05852 standard; protein; 11 AA.

XX AAR05852;

XX 06-SEP-1990 (first entry)

XX Factor VII peptide analogue.

KW Factor VII; blood clotting; Tissue factor; TF; thrombosis.

XX Synthetic.

XX WO9003390-A.

XX 05-APR-1990.

XX 22-SEP-1989; 89WO-0004140.

XX 23-SEP-1988; 88US-0248817.

XX (CORV-) CORVAS INC.

XX Pepe MG;

XX WPI; 1990-132239/17.

XX New clotting factor VII peptide analogues -

XX useful for inhibiting blood clotting induced by tissue factor

XX complex.

XX Claim 11; Page 22; 28pp; English.

XX One or both of the two C-terminal residues may be absent, the

XX peptide is useful in inhibiting formation of active tissue factor;

XX factor VII complex and thus blood clotting.

XX Sequence 11 AA;

OY 3 DHQGTKSS 10
 |||||
 Db 3 dhtgltkrs 10

RESULT 6

AAR67860 standard; peptide; 11 AA.

XX AAR67860;

XX 07-SEP-1995 (first entry)

XX FVII/TF multi-protein complex inhibition test peptide FVII-4.

XX Factor VII; Factor 7; blood clotting factor; multi-protein complex;

XX human tissue factor; FVII/TF; assay.

XX Synthetic.

XX WO9500847-A.

XX 05-JAN-1995.

XX 17-JUN-1994; 94WO-GB01314.

XX 18-JUN-1993; 93GB-0012638.

XX (HAFS-) HAFSLUND NYCOMED AS.

XX (HOLM/) HOLMES M J.

XX Oerling L, Sakariassen K, Stephens R;

XX WPI; 1995-052226/07.

XX Immunoassay for multi-protein complexes - used to detect

XX malfunction in formation of complexes in an individual, e.g. due

XX to genetic or physiological disorders

XX Example 2; Page 8; 19pp; English.

XX Synthetic peptides (AAR67858-R67865) were individually assayed as test

CC substances to ascertain their effect on the formation of the blood-

CC clotting factor VII/tissue factor multi-protein complex. Of the

CC peptides tested, the most inhibition was obtained with cyclic

CC peptides representing the ring structures present in the FVII growth

CC factor domains (i.e. AAR67861, AAR67864 and AAR67863). Peptide AAR67858,

CC a linear peptide corresp. to residues 136-146 from a region close to

CC the site of cleavage which activates FVII also had good inhibitory

CC activity.

XX Sequence 11 AA;

SQ

Query Match 29.9%; Score 32; DB 16; Length 11;

Best Local Similarity 75.0%; Pred. No. 57;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DHQGTKSS 10

Db 2 dhtgtkrs 9

RESULT 7

AAR68908

ID AAR68908 standard; peptide; 11 AA.

XX AC AAR68908;

XX 06-AUG-1995 (first entry)

DT XX

DE XX

XX Factor-VII-derived peptide fragment FVII-4.

XX Factor-VII; blood-clotting factor; thrombosis; angina;

KW cerebrovascular disease; pulmonary embolism; heart disease.

XX Synthetic.

OS OS

XX WO9500541-A.

PN 05-JAN-1995.

XX 17-JUN-1994; 94WO-GB01315.

XX 18-JUN-1993; 93GB-0012601.

PR 10-MAY-1994; 94GB-0009335.

XX (HAFS-) HAFSLUND NYCOMED AS.

PA (HOLM/) HOLMES M J.

XX Orning L, Sakariassen KS, Stephens RW, Sakariassen K;

PI WPI; 1995-052003/07.

XX Factor VII-derived peptide compounds - useful for

PT preventing/inhibiting binding of tissue factor to factor VII.

XX Disclosure; Page 20; 61pp; English.

XX This peptide fragment is useful for preparing pharmaceutical

CC compositions for prevention or inhibition of Factor-VII binding to

CC tissue factor. It is useful for treating or preventing blood clotting

CC disorders in humans and animals, e.g. thrombosis, angina,

CC cerebrovascular disease or pulmonary embolism.

XX Sequence 11 AA;

SQ

Query Match 29.9%; Score 32; DB 16; Length 11;

Best Local Similarity 75.0%; Pred. No. 57;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DHQGTKSS 10

Db 2 dhtgtkrs 9

RESULT 8

AAW85479

ID AAW85479 standard; Peptide; 14 AA.

XX AC AAW85479;

XX 15-MAR-1999 (first entry)

DT XX

XX Mouse GP88 autocrine growth factor antigenic peptide SI4R.

DE XX

XX GP88; granulino; epithilin; mouse; growth factor; autocrine; tumour;

KW cancer; viral infection; antagonist; therapy; diagnosis; antigen;

XX antibody.

XX Mus sp.

OS OS

XX WO9852607-A1.

PN 26-NOV-1998.

XX 22-MAY-1998; 98WO-US10555.

XX 16-DEC-1997; 97US-0991862.

PR 23-MAY-1997; 97US-0863079.

XX (SERR/) SERRERO G.

PA Serrero G;

PI WPI; 1999-045276/04.

XX Composition containing antagonist of growth factor GP88 - useful for

PT treating cancer and viral diseases and also for diagnosing disease

PT from altered GP88 expression

XX Example 8; Page 45; 86pp; English.

PS This is the amino acid sequence of peptide SI4R, comprising amino

XX acid residues S562-R575 of murine GP88 (see AAW85474). GP88 is an 88

CC kDa glycoprotein autocrine growth factor that is expressed in a

CC tightly regulated manner in normal cells, is overexpressed and

CC unregulated in highly tumorigenic cells derived from normal cells,

CC and which acts as a stringently required growth stimulator for the

CC tumorigenic cells. SI4R was used to raise neutralising antibodies

CC to GP88. Antagonists to GP88, such as anti-GP88 antibodies, are

CC used to treat diseases associated with increased expression of

CC GP88, particularly cancer but also viral infections. Anti-GP88

CC antibodies can also be used as diagnostic reagents and to deliver

CC toxins or other compounds to GP88-expressing cells.

XX Sequence 14 AA;

SQ

Query Match 29.9%; Score 32; DB 20; Length 14;

Best Local Similarity 40.0%; Pred. No. 74;

Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 8 KSSKCYRQKV 17

Db 3 rgtkcirkxi 12

RESULT 9

AAW86759

ID AAY86759 standard; Peptide; 9 AA.

XX AC AAY86759;

```

XX 05-MAY-2000 (first entry)
XX Telomerase peptide #174.
XX Telomerase: antigenic peptide; cancer; therapy; human; tumour cell;
XX malignant melanoma; leukaemia; lymphoma; biliary tract carcinoma;
XX telomerase T lymphocyte.
XX Homo sapiens.
XX MO200002581-A1.
XX 20-JAN-2000.
XX 30-JUN-1999; 99WO-N000220.
XX 08-JUL-1998; 98NO-0003141.
XX (NHVD ) NORSK HYDRO AS.
XX Gaudernack G, Eriksen JA, Moller M, Gjertsen MK, Saeterdal I;
XX Saebøe-Larsen S;
XX WPI: 2000-145727/13.
XX Protein or peptide fragments useful in the treatment and prophylaxis of
XX cancer in mammals -
XX Claim 12; Page 35; 53pp; English.
XX This sequence represents a telomerase peptide of the invention, and can
XX be used in a method for the treatment or prophylaxis of cancer. The
XX sequences are useful in the treatment or prophylaxis of cancer
XX especially, breast, lung, ovarian, cervical, colorectal, prostate or
XX pancreatic cancers, malignant melanoma, leukaemia, lymphomas, or biliary
XX tract carcinomas. They are useful for generating telomerase T lymphocytes
XX capable of recognising and destroying tumour cells in a mammal,
XX comprising culturing T lymphocytes obtained from the mammal with the
XX peptides. Telomerase protein is expressed only by tumour cells, hence,
XX other body cells are not targeted or destroyed by telomerase specific T
XX cells.
XX Note: This sequence was indexed from WO200002581, which is the first
XX major country equivalent to NO9803141.
XX Sequence 9 AA:
SQ
Query Match 29.0%; Score 31; DB 21; Length 9;
Best Local Similarity 55.6%; Pred. NO. 3.4e+05;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 12 CVROKVEGS 20
   1 1 1 1 1 1
Db 1 carekpgs 9

```

RESULT 10

AAW55855

ID AAW55855 standard; peptide: 20 AA.

AC AAW55855;

XX

DT 21-JUL-1998 (first entry)

DE HIV p17 gag protein antigenic peptide HIV-1HAN.

XX

XX HIV; human immunodeficiency virus; antigen; conjugated peptide;

KW p17 gag protein; T cell specific binding peptide; TH1; TH2; AIDS;

KW Immune response; HGP-30.

XX

OS Human immunodeficiency virus type 1.

XX

```

PN MO9806416-A1.
PN 19-FEB-1998.
PD 08-AUG-1997; 97WO-US13901.
PF 09-AUG-1996; 96US-0695304.
PR (CELS-) CEL-SCI CORP.
PA Sarin PS, Zimmerman DS;
XX WPI: 1998-159280/14.
XX New conjugated peptide(s) for treating or preventing HIV infection -
XX comprise first and second T cell specific peptide(s) with one
XX peptide having a sequence derived from HIVp17gag protein
XX Disclosure; Page 10; 58pp; English.
XX The present sequence represents an HIV p17 gag protein antigenic
XX peptide species specific sequence from the present invention. The
XX present invention describes a conjugated peptide which is capable
XX of eliciting a TH1 response when administered to a human. The
XX conjugated peptide comprises a first T cell specific binding peptide
XX (SBP), and a second T cell SBP, the first and second peptides being
XX derived from different molecules and covalently linked together, where
XX the first T cell SBP binds to a specific class or subclass of T cells
XX and the second T cell SBP is an antigenic peptide capable of eliciting
XX TH1 associated antibodies and having sequence identity with the p17 gag
XX protein of HIV where the peptide has a sequence originating with an
XX amino acid residue chosen from residues 75 to 82 and ending with an
XX amino acid residue chosen from residues 106 to 111 of p17 gag protein of
XX HIV. The peptides can induce a TH1, TH2 or mixed TH1/TH2 directed immune
XX response against HIV and HIV infected cells. They can be used for
XX treating or preventing HIV infection and AIDS.
XX Sequence 20 AA:
SQ
Query Match 29.0%; Score 31; DB 19; Length 20;
Best Local Similarity 71.4%; Pred. NO. 1.6e+07;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 12 CVROKVE 18
   1 1 1 1 1 1
Db 12 cvnqkie 18

```

RESULT 11

AAW55845

ID AAW55845 standard; peptide: 20 AA.

AC AAW55845;

XX

DT 21-JUL-1998 (first entry)

DE HIV p17 gag protein antigenic peptide HIV-1TB132.

XX

XX HIV; human immunodeficiency virus; antigen; conjugated peptide;

KW p17 gag protein; T cell specific binding peptide; TH1; TH2; AIDS;

KW Immune response; HGP-30.

XX

OS Human immunodeficiency virus type 1.

XX

PN MO9806416-A1.

XX

PD 19-FEB-1998.

PF 08-AUG-1997; 97WO-US13901.

PR 09-AUG-1996; 96US-0695304.

XX

PA (CELS-) CEL-SCI CORP.
 XX Sarin PS, Zimmerman DS;
 XX WPI; 1998-159280/14.
 XX New conjugated peptide(s) for treating or preventing HIV infection -
 PT comprise first and second T cell specific peptide(s) with one
 PT peptide having a sequence derived from HIVp17gag protein
 XX Disclosure; Page 10; 58pp; English.
 XX The present sequence represents an HIV p17 gag protein antigenic
 CC peptide species specific sequence from the present invention. The
 CC present invention describes a conjugated peptide which is capable
 CC of eliciting a TH1 response when administered to a human. The
 CC conjugated peptide comprises a first T cell specific binding peptide
 CC (SBP), and a second T cell SBP, the first and second peptides being
 CC derived from different molecules and covalently linked together, where
 CC the first T cell SBP binds to a specific class or subclass of T cells
 CC and the second T cell SBP is an antigenic peptide capable of eliciting
 CC TH1 associated antibodies and having sequence identity with the p17 gag
 CC protein of HIV where the peptide has a sequence originating with an
 CC amino acid residue chosen from residues 75 to 82 and ending with an
 CC amino acid residue chosen from residues 106 to 111 of p17 gag protein of
 CC HIV. The peptides can induce a TH1, TH2 or mixed TH1/TH2 directed immune
 CC response against HIV and HIV infected cells. They can be used for
 CC treating or preventing HIV infection and AIDS.
 XX Sequence 20 AA;
 SQ Query Match 29.0%; Score 31; DB 19; Length 20;
 Best Local Similarity 71.4%; Pred. No. 1.6e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 CVRQKVE 18
 || ||:
 Db 12 cvhqkie 18

RESULT 12
 AAW55848
 ID AAW55848 standard; peptide; 20 AA.
 XX AC AAW55848;
 XX DT 21-JUL-1998 (first entry)
 XX DE HIV p17 gag protein antigenic peptide HIV-1MN.
 XX HIV; human immunodeficiency virus; antigen; conjugated peptide;
 KW p17 gag protein; T cell specific binding peptide; TH1; TH2; AIDS;
 KW immune response; HGP-30.
 XX Human immunodeficiency virus type 1.
 OS WO9806416-A1.
 PN 19-FEB-1998.
 XX PD 08-AUG-1997; 97WO-US13901.
 XX PF 09-AUG-1996; 96US-0695304.
 XX PR (CELS-) CEL-SCI CORP.
 XX Sarin PS, Zimmerman DS;
 XX WPI; 1998-159280/14.
 XX New conjugated peptide(s) for treating or preventing HIV infection -
 PT comprise first and second T cell specific peptide(s) with one
 PT peptide having a sequence derived from HIVp17gag protein
 XX Disclosure; Page 10; 58pp; English.
 XX The present sequence represents an HIV p17 gag protein antigenic
 CC peptide species specific sequence from the present invention. The
 CC present invention describes a conjugated peptide which is capable
 CC of eliciting a TH1 response when administered to a human. The
 CC conjugated peptide comprises a first T cell specific binding peptide
 CC (SBP), and a second T cell SBP, the first and second peptides being
 CC derived from different molecules and covalently linked together, where
 CC the first T cell SBP binds to a specific class or subclass of T cells
 CC and the second T cell SBP is an antigenic peptide capable of eliciting
 CC TH1 associated antibodies and having sequence identity with the p17 gag
 CC protein of HIV where the peptide has a sequence originating with an
 CC amino acid residue chosen from residues 75 to 82 and ending with an
 CC amino acid residue chosen from residues 106 to 111 of p17 gag protein of
 CC HIV. The peptides can induce a TH1, TH2 or mixed TH1/TH2 directed immune
 CC response against HIV and HIV infected cells. They can be used for
 CC treating or preventing HIV infection and AIDS.
 XX Sequence 20 AA;
 SQ Query Match 29.0%; Score 31; DB 19; Length 20;
 Best Local Similarity 71.4%; Pred. No. 1.6e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 CVRQKVE 18
 || ||:
 Db 12 cvhqkie 18

RESULT 12
 AAW55851
 ID AAW55851 standard; peptide; 20 AA.
 XX AC AAW55851;
 XX DT 21-JUL-1998 (first entry)
 XX DE HIV p17 gag protein antigenic peptide HIV-10YI.
 XX HIV; human immunodeficiency virus; antigen; conjugated peptide;
 KW p17 gag protein; T cell specific binding peptide; TH1; TH2; AIDS;
 KW immune response; HGP-30.
 XX Human immunodeficiency virus type 1.
 OS WO9806416-A1.
 PN 19-FEB-1998.
 XX PD 08-AUG-1997; 97WO-US13901.
 XX PF 09-AUG-1996; 96US-0695304.
 XX PR (CELS-) CEL-SCI CORP.
 XX Sarin PS, Zimmerman DS;
 XX WPI; 1998-159280/14.
 XX New conjugated peptide(s) for treating or preventing HIV infection -
 PT comprise first and second T cell specific peptide(s) with one
 PT peptide having a sequence derived from HIVp17gag protein
 XX Disclosure; Page 10; 58pp; English.
 XX The present sequence represents an HIV p17 gag protein antigenic
 CC peptide species specific sequence from the present invention. The
 CC present invention describes a conjugated peptide which is capable
 CC of eliciting a TH1 response when administered to a human. The

CC conjugated peptide comprises a first T cell specific binding peptide
CC (SBP), and a second T cell SBP, the first and second peptides being
CC derived from different molecules and covalently linked together, where
CC the first T cell SBP binds to a specific class or subclass of T cells
CC and the second T cell SBP is an antigenic peptide capable of eliciting
CC TH1 associated antibodies and having sequence identity with the p17 gag
CC protein of HIV where the peptide has a sequence originating with an
CC amino acid residue chosen from residues 75 to 82 and ending with an
CC amino acid residue chosen from residues 106 to 111 of p17 gag protein of
CC HIV. The peptides can induce a TH1, TH2 or mixed TH1/TH2 directed immune
CC response against HIV and HIV infected cells. They can be used for
CC treating or preventing HIV infection and AIDS.

SQ Sequence 20 AA;

Query Match 29.0%; Score 31; DB 19; Length 20;
Best Local Similarity 71.4%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 CVRQKVE 18
| | | | |
Db 12 cvnqkie 18

RESULT 14

AAB23773 AAB23773 standard; Peptide; 21 AA.

AC AAB23773;

DT 11-JAN-2001 (first entry)

DE Entry vector pENTR5 cloning site peptide sequence.

KM Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;

KW mutant; recombinational cloning; entry vector; destination vector;

XX gene product targeting; fusion tag cleavage.

OS Bacteriophage lambda.

XX Synthetic.

PN WO200052027-A1.

PD 08-SEP-2000.

PF 02-MAR-2000; 2000MO-US05432.

PR 02-MAR-1999; 99US-0122389.

PR 23-MAR-1999; 99US-0126049.

PR 28-MAY-1999; 99US-0136744.

PA (LIFE-) LIFE TECHNOLOGIES INC.

PI Hartley JL, Brasch MA, Temple GF, Cheo D;

DR MPI; 2000-543948/49.

XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,

PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the

PT recombinational cloning of polypeptides -

XX Example 4; Fig 14; 459pp; English.

CC The present invention describes isolated nucleic acid molecules (I)

CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2

CC nucleotide sequence. Also described are: (1) an isolated nucleic acid

CC molecule (II) comprising one or more att recombination sites comprising

CC at least one mutation in its core region that increases the specificity

CC of interaction between the recombination site and a second att

CC recombination site; and (2) an isolated nucleic acid molecule (III)

CC comprising one or more mutated att recombination sites comprising at

CC least one mutation in its core region that enhances the efficiency of

CC recombination between a first nucleic acid molecule comprising the
CC mutated att recombination site and a second nucleic acid molecule
CC comprising a second recombination site that interacts with the mutated
CC att recombination site. (I), (II), (III), primers, vectors and methods
CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from
CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning. (I), (II), (III), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is
CC used in the exemplification of the present invention.

SQ Sequence 21 AA;

Query Match 28.0%; Score 30; DB 21; Length 21;
Best Local Similarity 35.7%; Pred. No. 2.5e+02;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 4 HOGTKSKRCVROKV 17
| | | | | : : :
Db 8 hmgtinsvdiwryri 21

RESULT 15

AAR35477 AAR35477 standard; peptide; 13 AA.

AC AAR35477;

DT 25-AUG-1993 (first entry)

DE Phosphatidylserine recognising peptide.

KM Inhibition; activity; blood coagulation factor VIII; thrombosis;

KW treatment; artificial membrane; medicinal artificial material.

XX Synthetic.

PN JP05092993-A.

PD 16-APR-1993.

PF 30-SEP-1991; 91JP-0276138.

PR 30-SEP-1991; 91JP-0276138.

PA (TOYO) TOSOH CORP.

DR MPI; 1993-162126/20.

XX New physiologically active peptide recognising phosphatidylserine

PT and-ethanolamine - inhibits activity of blood coagulation factor VIII

PT but not factor V, used for treating thrombosis, etc.

XX Claim 2; Page 2; 6pp; Japanese.

CC The sequence is that of a peptide recognising phosphatidylserine

CC and -ethanolamine. It inhibits the activity of blood coagulation

CC factor VIII, and does not inhibit the activity of factor V. It is

CC useful in the treatment of blood coagulation disorders, e.g.

CC thrombosis, etc. It is also useful in the study of phosphatidylserine

CC which plays an important role in the cell membrane, artificial

CC membranes and medicinal artificial material.

SQ Sequence 13 AA;

Query Match 27.1%; Score 29; DB 14; Length 13;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 14 RQVVEGS 20
|| ||||
Db 2 rqnvegs 8

Search completed: July 19, 2001, 07:47:34
Job time: 45 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 19, 2001, 07:46:49 ; Search time 12.2 Seconds
(without alignments)
34.675 Million cell updates/sec

Title: US-08-487-283A-1
Perfect score: 107
Sequence: 1 VIDHGTKSKCYRQKVEGSS 21

Scoring table:
BLASTSUM62
Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 105797

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
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3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCUTS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	29.9	9	2	US-08-564-063-25
2	32	29.9	10	2	US-08-564-063-3
3	32	29.9	11	2	US-08-564-063-2
4	31	29.0	20	3	US-08-695-301A-18
5	31	29.0	20	3	US-08-695-301A-21
6	31	29.0	20	3	US-08-695-301A-24
7	31	29.0	20	3	US-08-695-301A-28
8	31	29.0	20	3	US-08-695-304C-18
9	31	29.0	20	3	US-08-695-304C-21
10	31	29.0	20	3	US-08-695-304C-24
11	31	29.0	20	3	US-08-695-304C-28
12	30	28.0	13	3	US-08-545-860D-70
13	30	28.0	13	5	PCR-US94-04486-70
14	29	27.1	14	1	US-08-769-309A-6
15	29	27.1	14	3	US-08-994-570-6
16	28	26.2	17	2	US-08-248-839C-66
17	28	26.2	20	3	US-08-695-301A-16
18	28	26.2	20	3	US-08-695-301A-19
19	28	26.2	20	3	US-08-695-301A-20
20	28	26.2	20	3	US-08-695-301A-22
21	28	26.2	20	3	US-08-695-301A-23
22	28	26.2	20	3	US-08-695-301A-26
23	28	26.2	20	3	US-08-695-301A-27
24	28	26.2	20	3	US-08-695-301A-29
25	28	26.2	20	3	US-08-695-301A-31
26	28	26.2	20	3	US-08-695-301A-32
27	28	26.2	20	3	US-08-695-301A-33

28	28	26.2	20	3	US-08-695-301A-34	Sequence 34, Appl
29	28	26.2	20	3	US-08-695-304C-16	Sequence 16, Appl
30	28	26.2	20	3	US-08-695-304C-19	Sequence 19, Appl
31	28	26.2	20	3	US-08-695-304C-20	Sequence 20, Appl
32	28	26.2	20	3	US-08-695-304C-22	Sequence 22, Appl
33	28	26.2	20	3	US-08-695-304C-23	Sequence 23, Appl
34	28	26.2	20	3	US-08-695-304C-27	Sequence 27, Appl
35	28	26.2	20	3	US-08-695-304C-29	Sequence 29, Appl
36	28	26.2	20	3	US-08-695-304C-31	Sequence 31, Appl
37	28	26.2	20	3	US-08-695-304C-32	Sequence 32, Appl
38	28	26.2	20	3	US-08-695-304C-33	Sequence 33, Appl
39	28	26.2	20	3	US-08-695-304C-34	Sequence 34, Appl
40	27	25.2	14	2	US-08-908-526-5	Sequence 5, Appl
41	27	25.2	15	2	US-08-429-964-75	Sequence 75, Appl
42	27	25.2	19	2	US-08-637-759B-290	Sequence 290, App
43	27	25.2	19	3	US-08-871-355A-290	Sequence 290, App
44	27	25.2	20	4	US-08-840-006-4	Sequence 4, Appl
45	27	25.2	21	4	US-09-179-558-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-564-063-25
; Sequence 25, Application US/08564063
; Patent No. 5962418
; GENERAL INFORMATION:
; APPLICANT: SAKARIASSEN, Kjell S
; APPLICANT: STEPHENS, Ross W
; APPLICANT: ORNING, Lars
; TITLE OF INVENTION: FACTOR VII-DERIVED PEPTIDES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Testa, Hurwitz & Thibault, LLP
; STREET: 125 High Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/564,063
; FILING DATE: 28-MAY-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, Paula A
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: FRD-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-564-063-25

Query Match 29.9%; Score 32; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 DHGCTKSS 10
|||
Db 2 DHTGTRKS 9

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/564,063
; FILING DATE: 28-MAY-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, Paula A
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: FRD-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-564-063-2

Query Match 29.9%; Score 32; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 2; Indels

QY 3 DHOGTKSS 10
   || |||||
Db 2 DHTGTRK 9

RESULT 4
US-08-695-301A-18
; Sequence 18, Application US/08695301A
; Patent No. 6093400
; GENERAL INFORMATION:
; APPLICANT: DANIEL H. ZIMMERMAN, PREM S. SARIN
; TITLE OF INVENTION: Modified HGP-30 peptides, Conjugates,
; TITLE OF INVENTION: Compositions and Methods of Use
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Office of Sherman and Shalloway
; STREET: 413 N. Washington Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 1.2 mb storage
; MEDIUM TYPE: 3.5 inch, 1.44 mb storage
; COMPUTER: Dell System 210; Intel 80 286 Microprocessor
; OPERATING SYSTEM: MS DOS 6.22
; SOFTWARE: Word Perfect, Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,301A
; FILING DATE: August 9, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard A. Steinberg
; REGISTRATION NUMBER: 26,588
; REFERENCE/DOCKET NUMBER: CELL-101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 549-2282
; TELEFAX: (703) 836-0106
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: Internal fragment
; FEATURE:

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NAME/KEY:
LOCATION: 75 to 94
OTHER INFORMATION: fragment of p-17 gag protein of
OTHER INFORMATION: HIV-1TBJ32
US-08-695-301A-18

Query Match 29.0%; Score 31; DB 3; Length 20;
Best Local Similarity 71.4%; Pred. No. 69;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 CVRQKVE 18
|||11:1
Db 12 CVHOKIE 18

RESULT 5
US-08-695-301A-21
Sequence 21, Application US/08695301A
Patent No. 6093400

GENERAL INFORMATION:
APPLICANT: DANIEL H. ZIMMERMAN, PREM S. SARIN
TITLE OF INVENTION: Modified HGP-30 Peptides, Conjugates,
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESS: Law Office of Sherman and Shalloway
STREET: 413 N. Washington Street
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 1.2 mb storage
MEDIUM TYPE: 3.5 inch, 1.44 mb storage
COMPUTER: Dell System 210; Intel 80 286 Microprocessor
OPERATING SYSTEM: MS DOS 6.22
SOFTWARE: Word Perfect, Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/695,301A
FILING DATE: August 9, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Richard A. Steinberg
REGISTRATION NUMBER: 26,588
REFERENCE/DOCKET NUMBER: CELL-101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 549-2282
TELEFAX: (703) 836-0106
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
FEATURE:
NAME/KEY:
LOCATION: 75 to 94
OTHER INFORMATION: fragment of p-17 gag protein of
OTHER INFORMATION: HIV-1MN
US-08-695-301A-21

Query Match 29.0%; Score 31; DB 3; Length 20;
Best Local Similarity 71.4%; Pred. No. 69;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 CVRQKVE 18
|||11:1
Db 12 CVHOKIE 18

RESULT 6

US-08-695-301A-24
Sequence 24, Application US/08695301A
Patent No. 6093400

GENERAL INFORMATION:
APPLICANT: DANIEL H. ZIMMERMAN, PREM S. SARIN
TITLE OF INVENTION: Modified HGP-30 Peptides, Conjugates,
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESS: Law Office of Sherman and Shalloway
STREET: 413 N. Washington Street
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 1.2 mb storage
MEDIUM TYPE: 3.5 inch, 1.44 mb storage
COMPUTER: Dell System 210; Intel 80 286 Microprocessor
OPERATING SYSTEM: MS DOS 6.22
SOFTWARE: Word Perfect, Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/695,301A
FILING DATE: August 9, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Richard A. Steinberg
REGISTRATION NUMBER: 26,588
REFERENCE/DOCKET NUMBER: CELL-101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 549-2282
TELEFAX: (703) 836-0106
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
FEATURE:
NAME/KEY:
LOCATION: 75 to 94
OTHER INFORMATION: fragment of p-17 gag protein of
OTHER INFORMATION: HIV-1DY1
US-08-695-301A-24

Query Match 29.0%; Score 31; DB 3; Length 20;
Best Local Similarity 71.4%; Pred. No. 69;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 CVRQKVE 18
|||11:1
Db 12 CVHOKIE 18

RESULT 7
US-08-695-301A-28
Sequence 28, Application US/08695301A
Patent No. 6093400

GENERAL INFORMATION:
APPLICANT: DANIEL H. ZIMMERMAN, PREM S. SARIN
TITLE OF INVENTION: Modified HGP-30 Peptides, Conjugates,
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESS: Law Office of Sherman and Shalloway
STREET: 413 N. Washington Street
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 1.2 mb storage

;; MEDIUM TYPE: 3.5 inch, 1.44 mb storage
;; COMPUTER: Dell System 210; Intel 80 286 Microprocessor
;; OPERATING SYSTEM: MS DOS 6.22
;; SOFTWARE: Word Perfect, Version 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/695,301A
;; FILING DATE: August 9, 1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Richard A. Steinberg
;; REGISTRATION NUMBER: 26,588
;; REFERENCE/DOCKET NUMBER: CELL-101
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 549-2282
;; TELEFAX: (703) 836-0106
;; INFORMATION FOR SEQ ID NO: 28:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FRAGMENT TYPE: internal fragment
;; FEATURE:
;; NAME/KEY:
;; LOCATION: 75 to 94
;; OTHER INFORMATION: fragment of p-17 gag protein of
;; HIV-1HAN
US-08-695-301A-28

Query Match 29.0%; Score 31; DB 3; Length 20;
Best Local Similarity 71.4%; Pred. No. 69;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 12 CVRQKVE 18
|||
Db 12 CVHQKIE 18

RESULT 8
US-08-695-304C-18
;; Sequence 18, Application US/08695304C
;; Patent No. 6103239
;; GENERAL INFORMATION:
;; APPLICANT: DANIEL H. ZIMMERMAN, PREM S. SARIN
;; TITLE OF INVENTION: Modified HGP-30 Heteroconjugates,
;; TITLE OF INVENTION: Compositions and Methods of Use
;; NUMBER OF SEQUENCES: 56
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Law Office of Sherman and Shalloway
;; STREET: 413 N. Washington Street
;; CITY: Alexandria
;; STATE: Virginia
;; COUNTRY: USA
;; ZIP: 22314
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 5.25 inch, 1.2 mb storage
;; MEDIUM TYPE: 3.5 inch, 1.44 mb storage
;; COMPUTER: Dell System 210; Intel 80 286 Microprocessor
;; OPERATING SYSTEM: MS DOS 6.22
;; SOFTWARE: Word Perfect, Version 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/695,304C
;; FILING DATE: August 9, 1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Richard A. Steinberg
;; REGISTRATION NUMBER: 26,588
;; REFERENCE/DOCKET NUMBER: CELL-102
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 549-2282
;; TELEFAX: (703) 836-0106
;; INFORMATION FOR SEQ ID NO: 18:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids

;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FRAGMENT TYPE: internal fragment
;; FEATURE:
;; NAME/KEY:
;; LOCATION: 75 to 94
;; OTHER INFORMATION: fragment of p-17 gag protein of
;; HIV-ITB132
US-08-695-304C-18

Query Match 29.0%; Score 31; DB 3; Length 20;
Best Local Similarity 71.4%; Pred. No. 69;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 12 CVRQKVE 18
|||
Db 12 CVHQKIE 18

RESULT 9
US-08-695-304C-21
;; Sequence 21, Application US/08695304C
;; Patent No. 6103239
;; GENERAL INFORMATION:
;; APPLICANT: DANIEL H. ZIMMERMAN, PREM S. SARIN
;; TITLE OF INVENTION: Modified HGP-30 Heteroconjugates,
;; TITLE OF INVENTION: Compositions and Methods of Use
;; NUMBER OF SEQUENCES: 56
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Law Office of Sherman and Shalloway
;; STREET: 413 N. Washington Street
;; CITY: Alexandria
;; STATE: Virginia
;; COUNTRY: USA
;; ZIP: 22314
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 5.25 inch, 1.2 mb storage
;; MEDIUM TYPE: 3.5 inch, 1.44 mb storage
;; COMPUTER: Dell System 210; Intel 80 286 Microprocessor
;; OPERATING SYSTEM: MS DOS 6.22
;; SOFTWARE: Word Perfect, Version 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/695,304C
;; FILING DATE: August 9, 1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Richard A. Steinberg
;; REGISTRATION NUMBER: 26,588
;; REFERENCE/DOCKET NUMBER: CELL-102
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 549-2282
;; TELEFAX: (703) 836-0106
;; INFORMATION FOR SEQ ID NO: 21:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FRAGMENT TYPE: internal fragment
;; FEATURE:
;; NAME/KEY:
;; LOCATION: 75 to 94
;; OTHER INFORMATION: fragment of p-17 gag protein of
;; HIV-1MN
US-08-695-304C-21

Query Match 29.0%; Score 31; DB 3; Length 20;
Best Local Similarity 71.4%; Pred. No. 69;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 12 CVRQKVE 18

Db 12 CVHOKIE 18

RESULT 10
US-08-695-304C-24
Sequence 24, Application US/08695304C
Patent No. 6103239

GENERAL INFORMATION:
APPLICANT: DANIEL H. ZIMMERMAN, PREM S. SARIN
TITLE OF INVENTION: Modified HGP-30 Heteroconjugates,
TITLE OF INVENTION: Compositions and Methods of Use
NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Office of Sherman and Shalloway
STREET: 413 N. Washington Street
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 1.2 mb storage
MEDIUM TYPE: 3.5 inch, 1.44 mb storage
COMPUTER: Dell System 210; Intel 80 286 Microprocessor
OPERATING SYSTEM: MS DOS 6.22
SOFTWARE: Word Perfect, Version 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/695,304C
FILING DATE: August 9, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Richard A. Steinberg
REGISTRATION NUMBER: 26,588
REFERENCE/DOCKET NUMBER: CELL-102

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 549-2282
TELEFAX: (703) 836-0106
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal fragment
FEATURE:

NAME/KEY:
LOCATION: 75 to 94
OTHER INFORMATION: fragment of p-17 gag protein of
OTHER INFORMATION: HIV-1DVI
US-08-695-304C-24

Query Match 29.0%; Score 31; DB 3; Length 20;
Best Local Similarity 71.4%; Pred. No. 69;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 CVROKVE 18
Db 12 CVHOKIE 18

RESULT 11
US-08-695-304C-28
Sequence 28, Application US/08695304C
Patent No. 6103239

GENERAL INFORMATION:
APPLICANT: DANIEL H. ZIMMERMAN, PREM S. SARIN
TITLE OF INVENTION: Modified HGP-30 Heteroconjugates,
TITLE OF INVENTION: Compositions and Methods of Use
NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Office of Sherman and Shalloway
STREET: 413 N. Washington Street
CITY: Alexandria

STATE: Virginia
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 1.2 mb storage
MEDIUM TYPE: 3.5 inch, 1.44 mb storage
COMPUTER: Dell System 210; Intel 80 286 Microprocessor
OPERATING SYSTEM: MS DOS 6.22
SOFTWARE: Word Perfect, Version 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/695,304C
FILING DATE: August 9, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Richard A. Steinberg
REGISTRATION NUMBER: 26,588
REFERENCE/DOCKET NUMBER: CELL-102

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 549-2282
TELEFAX: (703) 836-0106
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal fragment
FEATURE:

NAME/KEY:
LOCATION: 75 to 94
OTHER INFORMATION: fragment of p-17 gag protein of
OTHER INFORMATION: HIV-1HAN
US-08-695-304C-28

Query Match 29.0%; Score 31; DB 3; Length 20;
Best Local Similarity 71.4%; Pred. No. 69;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 CVROKVE 18
Db 12 CVHOKIE 18

RESULT 12
US-08-545-860D-70
Sequence 70, Application US/08545860D
Patent No. 6040140

GENERAL INFORMATION:
APPLICANT: Croce, Carlo
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the ALL-1 Region
NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Macklewitz &
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,860D
FILING DATE: 07-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04496

;
; FILING DATE: 22-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10930
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/327,392
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/320,559
; FILING DATE: 11-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/062,443
; FILING DATE: 14-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/971,094
; FILING DATE: 30-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/888,839
; FILING DATE: 27-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/805,093
; FILING DATE: 11-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca Esq., Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1262
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-545-860D-70

Query Match 28.0%; Score 30; DB 3; Length 13;
Best Local Similarity 63.6%; Pred. No. 62;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 SKCVRQKVEGS 20
:|||||
Db 3 TKCVRCCKSGS 13

RESULT 13
PCT-US94-04496-70
; Sequence 70, Application PC/TUS9404496
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Canaani, Eli
; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
; TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
; ADDRESSEE: Norris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04496
; FILING DATE:

;
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca Esq., Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1242
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-04496-70

Query Match 28.0%; Score 30; DB 5; Length 13;
Best Local Similarity 63.6%; Pred. No. 62;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 SKCVRQKVEGS 20
:|||||
Db 3 TKCVRCCKSGS 13

RESULT 14
US-08-769-309A-6
; Sequence 6, Application US/08769309A
; Patent No. 5741890
; GENERAL INFORMATION:
; APPLICANT: Scott, John D.,
; APPLICANT: Nauert, Brian J.,
; APPLICANT: Klauk, Theresa M.
; TITLE OF INVENTION: Protein Binding Domains of Gravin
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/769,309A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5741890and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33451
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-769-309A-6

Query Match 27.1%; Score 29; DB 1; Length 14;
Best Local Similarity 50.0%; Pred. No. 98;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 7 TKSSKCVROKVE 18
 ||||| : : :
 Db 3 TKSSKLVONIIQ 14

RESULT 15

US-08-994-570-6
 ; Sequence 6, Application US/08994570
 ; Patent No. 6090929
 ; GENERAL INFORMATION:
 ; APPLICANT: Scott, John D.,
 ; APPLICANT: Nauert, Brian J.,
 ; APPLICANT: Knauck, Theresa M.
 ; TITLE OF INVENTION: Protein Binding Domains of Gravin
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower/233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/994,570
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 6090929and, Greta E.
 ; REGISTRATION NUMBER: 35,302
 ; REFERENCE/DOCKET NUMBER: 27866/33451
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-474-6300
 ; TELEFAX: 312-474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 14 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-994-570-6

Query Match 27.1%; Score 29; DB 3; Length 14;
 Best Local Similarity 50.0%; Pred. No. 98;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 7 TKSSKCVROKVE 18
 ||||| : : :
 Db 3 TKSSKLVONIIQ 14

Search completed: July 19, 2001, 07:47:09
 Job time: 20 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 19, 2001, 07:49:39 ; Search time 12.68 Seconds

(without alignments)
30.037 Million cell updates/sec

Title: US-08-487-283A-1_COPY_8_12

Perfect score: 27

Sequence: 1 KSKC 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 205

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	37.0	4	2	PT0534
2	10	37.0	4	2	S55238
3	10	37.0	5	2	A33882
4	10	37.0	5	2	B45525
5	10	37.0	5	2	S65726
6	10	37.0	5	2	PT0577
7	10	37.0	5	2	PT0565
8	10	37.0	5	2	PT0700
9	10	37.0	5	2	A22565
10	9	33.3	4	2	I40505
11	9	33.3	4	2	I51049
12	9	33.3	4	2	S43959
13	9	33.3	5	2	D60274
14	9	33.3	5	2	B22565
15	9	33.3	5	2	F22565
16	9	33.3	5	2	S11127
17	9	33.3	5	2	PT0295
18	9	33.3	5	2	PT0308
19	9	33.3	5	2	PT0610
20	9	33.3	5	2	PT0660
21	9	33.3	5	2	PT0535
22	9	33.3	5	2	PT0684
23	8	29.6	3	2	PT0622
24	8	29.6	4	2	PT0696
25	8	29.6	4	2	PT0645
26	8	29.6	4	2	PT0712
27	8	29.6	4	2	PT0698
28	8	29.6	4	2	PT0551
29	8	29.6	4	2	A40135

30	8	29.6	5	2	I40698	biotin B - Citroba
31	8	29.6	5	2	A37114	hypoxanthine phosph
32	8	29.6	5	2	PT0536	T-cell receptor be
33	8	29.6	5	2	PT0597	T-cell receptor be
34	8	29.6	5	2	PT0644	T-cell receptor be
35	8	29.6	5	2	PT0600	T-cell receptor be
36	8	29.6	5	2	PT0729	T-cell receptor be
37	8	29.6	5	2	PT0624	T-cell receptor be
38	8	29.6	5	2	PT0686	T-cell receptor be
39	8	29.6	5	2	PT0601	T-cell receptor be
40	8	29.6	5	2	PT0625	T-cell receptor be
41	8	29.6	5	2	PT0672	T-cell receptor be
42	8	29.6	5	2	PT0656	T-cell receptor be
43	8	29.6	5	2	PT0659	T-cell receptor be
44	8	29.6	5	2	PT0699	T-cell receptor be
45	8	29.6	5	2	PT0561	T-cell receptor be

ALIGNMENTS

RESULT 1
PT0534
T-cell receptor beta chain V-D-J region (126-1Ac) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0534
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601
A:Accession: PT0534
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-4 <REP>
A:Experimental source: adult thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 37.0%: Score 10; DB 2; Length 4;
Best Local Similarity 66.7%: Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSK 4
DB 1 ASK 3

RESULT 2
S55238
pallidipin - assassin bug (fragment)
C:Species: Triatoma pallidipennis (assassin bug)
C:Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 19-May-2000
C:Accession: S55238
R:Haendler, B.; Becker, A.; Noeske-Jungblut, C.; Kraetzschmar, J.; Donner, P.; Schlen
Biochem. J. 307, 465-470, 1995
A:Title: Expression of active recombinant pallidipin, a novel platelet aggregation in
A:Reference number: S55238; MUID:95251610
A:Accession: S55238
A:Molecule type: protein
A:Residues: 1-4 <HAE>

Query Match 37.0%: Score 10; DB 2; Length 4;
Best Local Similarity 50.0%: Pred. No. 2.2e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KC 5
DB 2 EC 3

RESULT 3

A33882
 cadmium-binding pentapeptide - downy thornapple
 C:Species: Datura innoxia (downy thornapple)
 C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 18-Jun-1993
 C:Accession: A33882
 R:Jackson, P.J.; Unkefer, C.J.; Doolen, J.A.; Watt, K.; Robinson, N.J.
 Proc. Natl. Acad. Sci. U.S.A. 84, 6619-6623, 1987
 A:Title: Poly(gamma-glutamylcysteinyl)glycine: its role in cadmium resistance in plant
 A:Reference number: A94182; MUID:88016144
 A:Accession: A33882
 A:Molecule type: protein
 A:Residues: 1-5 <JAC>

Query Match 37.0%; Score 10; DB 2; Length 5;
 Best Local Similarity 50.0%; Pred. No. 2.2e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KC 5
 :|
 Db 1 EC 2

RESULT 4
 B45525
 actin I - malaria parasite (Plasmodium falciparum) (fragments)
 C:Species: Plasmodium falciparum
 C:Date: 03-Jun-1993 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
 C:Accession: B45525
 R:Wesseling, J.G.; Snijders, P.J.F.; van Someren, P.; Jansen, J.; Smits, M.A.; Schoenmak
 Mol. Biochem. Parasitol. 35, 167-176, 1989
 A:Title: Stage-specific expression and genomic organization of the actin genes of the ma
 A:Reference number: A45525; MUID:89364996
 A:Accession: B45525
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-5 <WES>
 A:Cross-references: GB:J03988
 A:Note: The authors translated the codon GAA for residue 3 as Gly
 C:Comment: The actin I gene contains no introns.

Query Match 37.0%; Score 10; DB 2; Length 5;
 Best Local Similarity 50.0%; Pred. No. 2.2e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KC 5
 :|
 Db 3 EC 4

RESULT 5
 S65726
 hemoglobin, extracellular, chain b - earthworm (Lumbricus terrestris) (fragment)
 C:Species: Lumbricus terrestris (Common earthworm)
 C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
 C:Accession: S65726
 R:Fushitani, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.
 Biochim. Biophys. Acta 1292, 273-280, 1996
 A:Title: Characterization of the constituent polypeptides of the extracellular hemoglobi
 A:Reference number: S65721; MUID:96176855
 A:Accession: S65726
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-5 <FUS>

Query Match 37.0%; Score 10; DB 2; Length 5;
 Best Local Similarity 50.0%; Pred. No. 2.2e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KC 5
 :|
 Db 3 EC 4

Db 3 QC 4
 RESULT 6
 PT0577
 T-cell receptor beta chain V-D-J region (141-1BC) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0577; PT0574
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
 A:Reference number: PT0509; MUID:91277601
 A:Accession: PT0577
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-5 <FEE>
 A:Experimental source: day 19 fetal thymus, strain BALB/c, clone 141-1BC
 A:Accession: PT0574
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-5 <FE2>
 A:Experimental source: day 19 fetal thymus, strain BALB/c, clone 141-1Q
 C:Keywords: T-cell receptor

Query Match 37.0%; Score 10; DB 2; Length 5;
 Best Local Similarity 66.7%; Pred. No. 2.2e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSK 4
 :|
 Db 2 SSR 4

RESULT 7
 PT0565
 T-cell receptor beta chain V-D-J region (141-1CF) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0565
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
 A:Reference number: PT0509; MUID:91277601
 A:Accession: PT0565
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-5 <FEE>
 A:Experimental source: day 19 fetal thymus, strain BALB/c
 C:Keywords: T-cell receptor

Query Match 37.0%; Score 10; DB 2; Length 5;
 Best Local Similarity 66.7%; Pred. No. 2.2e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSK 4
 :|
 Db 2 SSR 4

RESULT 8
 PT0700
 T-cell receptor beta chain V-D-J region (161-2A) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0700
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
 A:Reference number: PT0509; MUID:91277601
 A:Accession: PT0700

A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-5 <FE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 37.0%; Score 10; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 SSK 4
DB 2 SSR 4

RESULT 9
A22565
R-phycoerythrin alpha-1 chain - red alga (Gastrocloonium coulteri) (fragment)
C:Species: Gastrocloonium coulteri
C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C:Accession: A22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85182601
A:Accession: A22565
A:Molecule type: protein
A:Residues: 1-3 <KLO>

Query Match 33.3%; Score 9; DB 2; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 C 5
DB 1 C 1

RESULT 10
I40505
Hypothetical protein 3 (4 aa) - Bacillus stearothermophilus
C:Species: Bacillus stearothermophilus
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 15-Oct-1999
C:Accession: I40505
R:Waye, M.M.; Winter, G.
Eur. J. Biochem. 158, 505-510, 1986
A:Title: A transcription terminator in the 5' non-coding region of the tyrosyl tRNA synthetase gene of Bacillus stearothermophilus.
A:Reference number: I40503; MUID:86274732
A:Accession: I40505
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <RES>
A:Cross-references: EMBL:X04193; NID:g40233; PIDN:CAA27783.1; PID:g580944

Query Match 33.3%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 SK 4
DB 3 SK 4

RESULT 11
I51049
Metallothionein-A - rainbow trout (fragment)
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I51049
R:Olsson, P.E.; Kling, P.; Erkell, L.J.; Kille, P.

Eur. J. Biochem. 230, 344-349, 1995
A:Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss) metallothionein-A.
A:Reference number: I51049; MUID:95324545
A:Accession: I51049
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <OLS>
A:Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1; PID:g4379328

Query Match 33.3%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 C 5
DB 4 C 4

RESULT 12
S43959
Ig mu chain V region (clone 13) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 20-Oct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C:Accession: S43959
R:Wagner, S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, Nucleic Acids Res. 22, 1389-1393, 1994
A:Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.
A:Reference number: S43956; MUID:94248036
A:Accession: S43959
A:Molecule type: DNA
A:Residues: 1-4 <WAG>
C:Keywords: immunoglobulin

Query Match 33.3%; Score 9; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 C 5
DB 2 C 2

RESULT 13
D60274
Major protein antigen MP946 - Mycobacterium tuberculosis (fragment)
C:Species: Mycobacterium tuberculosis
C:Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C:Accession: D60274
R:Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991
A:Title: Isolation and partial characterization of major protein antigens in the culture filtrate of Mycobacterium tuberculosis.
A:Reference number: A60274; MUID:91099989
A:Accession: D60274
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <NAG>

Query Match 33.3%; Score 9; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.2e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 SSK 4
DB 3 SSK 5

RESULT 14
B22565
R-phycoerythrin alpha-2 chain - red alga (Gastrocloonium coulteri) (fragment)
C:Species: Gastrocloonium coulteri

C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C;Accession: B22565
R;Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A;Reference number: A22565; MUID:85182601
A;Accession: B22565
A;Molecule type: protein
A;Residues: 1-5 <KLO>

Query Match 33.3%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 C 5
|
Db 2 C 2

RESULT 15
F22565
R-phycoerythrin gamma-A chain - red alga (Gastroclonium coulteri) (fragment)
C;Species: Gastroclonium coulteri
C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C;Accession: F22565
R;Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A;Reference number: A22565; MUID:85182601
A;Accession: F22565
A;Molecule type: protein
A;Residues: 1-5 <KLO>

Query Match 33.3%; Score 9; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.2e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 C 5
|
Db 3 C 3

Search completed: July 19, 2001, 07:51:23
Job time: 104 sec

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OM protein - protein search, using sw model

Run on: July 19, 2001, 07:51:09 ; Search time 9.96 Seconds
(without alignments)
17.197 Million cell updates/sec

Title: US-08-487-283a-1_COPY_8_12

Perfect score: 27
Sequence: 1 KSKC 5

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 28

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	29.6	5	1	BIOB_CITFR
2	7	25.9	5	1	TRM3_ECOLI
3	6	22.2	4	1	DCMS_PSECH
4	6	22.2	4	1	TOFT_HUMAN
5	5	18.5	3	1	GRWA_HUMAN
6	5	18.5	3	1	LUXE_VIBFI
7	5	18.5	4	1	POST_HUMAN
8	5	18.5	5	1	BPP7_BOTIN
9	4	14.8	4	1	RM01_YEAST
10	4	14.8	5	1	AL14_CARMA
11	4	14.8	5	1	UXA4_CHLTR
12	3	11.1	5	1	BIOB_SALTY
13	3	7.4	4	1	PAR3_HIRME
14	2	7.4	4	1	PAR4_HIRME
15	2	7.4	4	1	FLRF_HIRME
16	2	7.4	4	1	FMRF_MACNI
17	2	7.4	5	1	BIOA_CITFR
18	2	7.4	5	1	BIOA_SALTY
19	2	7.4	5	1	PARP_ARTTR
20	2	7.4	5	1	PROCT_PPRAM
21	2	7.4	5	1	SUGA_ACHDO
22	2	7.4	5	1	TPIS_CANFA
23	2	7.4	5	1	UP01_MOUSE
24	1	3.7	3	1	THYL_PIG
25	1	3.7	4	1	ACH1_ACHFU
26	1	3.7	4	1	UC22_MAIZE
27	0	0.0	4	1	DCML_PSECH
28	0	0.0	5	1	PAP2_PARMA

ALIGNMENTS

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RESULT 1
ID BIOB_CITFR STANDARD: PRT: 5 AA.
AC P12997:
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE) (FRAGMENT).
GN BIOB.
OS Citrobacter freundli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP MEDLINE=89006280; PubMed=2971595;
RA Shivan D., Campbell A.;
RT "Transcriptional regulation and gene arrangement of Escherichia coli,
RT Citrobacter freundli and Salmonella typhimurium biotin operons.";
RL Gene 67:203-211(1988).
CC -1- CATALYTIC ACTIVITY: DETHIOBIOTIN + (S) - BIOTIN.
CC -1- PATHWAY: LAST STEP IN BIOTIN BIOSYNTHESIS PATHWAY.
CC -1- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
CC FAMILY.
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CC
DR EMBL: M21922; ; NOT ANNOTATED_CDS.
KW Biotin biosynthesis; Iron-sulfur; Transferase.
FT NON_TER 5 AA; 532 MW; 75A5B1EDD6F0000 CRC64;
SQ SEQUENCE 5 AA; 532 MW; 75A5B1EDD6F0000 CRC64;

Query Match 29.6%; Score 8; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SS 3
   11
DB 4 SS 5

RESULT 2
ID TRM3_ECOLI STANDARD: PRT: 5 AA.
AC P13973:
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE TRAM PROTEIN (FRAGMENT).
GN TRAM.
OS Escherichia coli.
OG Plasmid IncFII R100.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP MEDLINE=88227859; PubMed=2836369;
RA Inamoto S., Yoshioaka Y., Ohtsubo E.;
RT "Identification and characterization of the products from the tram
RT and tram genes of plasmid R100.";
RL J. Bacteriol. 170:2749-2757(1988).
CC -1- FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONUGATION
CC PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: TO TRAM PROTEIN OF OTHER PLASMIDS.

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CC -----
DR EMBL: M20941; ; NOT_ANNOTATED_CDS.
DR PIR: A32014; A32014.
KW Conjugation; Plasmid; DNA-binding.
FT NON_TER 1
SQ SEQUENCE 5 AA; 634 MW; 681B1AA443500000 CRC64;

Query Match 25.98; Score 7; DB 1; Length 5;
Best Local Similarity 25.08; Pred. No. 9.3e+04;
Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSK 4
DB 1 KNDE 4

RESULT 3
DCMS_PSECH STANDARD; PRT; 4 AA.
AC P19918;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE CARBON MONOXIDE DEHYDROGENASE SMALL CHAIN (EC 1.2.99.2) (FRAGMENT).
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=290;
RN [1]
RP SEQUENCE.
RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
RL Arch. Microbiol. 152:335-341(1989).
CC -1- CATALYTIC ACTIVITY: CO + H(2)O + ACCEPTOR -> CO(2) + REDUCED
CC ACCEPTOR.
CC -1- COFACTOR: MOLYBDENUM.
CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
CC SMALL.
DR PIR: PLO146; PLO146.
KW Oxidoreductase; Molybdenum.
FT NON_TER 4
SQ SEQUENCE 4 AA; 420 MW; 6DD33DD6F0000000 CRC64;

Query Match 22.28; Score 6; DB 1; Length 4;
Best Local Similarity 50.08; Pred. No. 9.3e+04;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SK 4
DB 2 AK 3

RESULT 4
TUFT_HUMAN STANDARD; PRT; 4 AA.
ID TUFT_HUMAN
AC P01858;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PHAGOCYTOSIS-STIMULATING PEPTIDE (TUFTSIN).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72187087; PubMed=4112769;
RA Nishioka K., Constantopoulos A., Satoh P.S., Najjar V.A.;
RT "The characteristics, isolation and synthesis of the phagocytosis
RT stimulating peptide tuftsin."
RL Biochem. Biophys. Res. Commun. 47:172-179(1972).
RN [2]
RP IMMUNOGLOBULIN CLASS.
RX MEDLINE=68091045; PubMed=4169272;
RA Fidalgo B.V., Najjar V.A.;
RT "The physiological role of the lymphoid system. VI. The stimulatory
RT effect of leucophilic gamma globulin (leucokinin) on the phagocytic
RT activity of human polymorphonuclear leucocyte."
RL Biochemistry 6:3386-3392(1967).
CC -1- MISCELLANEOUS: AN IGG (CALLED LEUCOKININ) BINDS REVERSIBLY TO THE
CC CELL MEMBRANE OF NEUTROPHILS IN THE BLOOD. LEUCOKININASE ON THE
CC MEMBRANE RELEASES THE ACTIVE PEPTIDE TUFTSIN FROM THE GAMMA CHAIN.
CC TUFTSIN IS ESSENTIAL FOR MAXIMUM STIMULATION OF THE PHAGOCYTIC
CC ACTIVITY OF NEUTROPHILS.
DR PIR: A02147; A02147.
DR MIM; 191150; -.
SQ SEQUENCE 4 AA; 501 MW; 74176321C0000000 CRC64;

Query Match 22.28; Score 6; DB 1; Length 4;
Best Local Similarity 50.08; Pred. No. 9.3e+04;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SK 4
DB 1 TK 2

RESULT 5
GRWM_HUMAN STANDARD; PRT; 3 AA.
ID GRWM_HUMAN
AC P01157;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE GROWTH-MODULATING PEPTIDE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77162369; PubMed=858356;
RA Schlesinger D.H., Pickart L., Thaler M.M.;
RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine."
RL Experientia 33:324-325(1977).
CC -1- MISCELLANEOUS: THIS SERUM TRIPEPTIDE HAS BEEN FOUND TO STIMULATE
CC GROWTH OF SOME CELL TYPES AND TO INHIBIT OTHER TYPES IN VITRO.
DR PIR: A01421; GKHU.
SQ SEQUENCE 3 AA; 340 MW; 6331E81000000000 CRC64;

Query Match 18.58; Score 5; DB 1; Length 3;
Best Local Similarity 100.08; Pred. No. 9.3e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 K 1
DB 3 K 3

RESULT 6
LUXE_VIBFI STANDARD; PRT; 3 AA.
ID LUXE_VIBFI
AC P24272;

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DR 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DE 01-OCT-1996 (Rel. 34, Last annotation update)
DE LONG-CHAIN-FATTY-ACID-LUCIFERIN-COMPONENT LIGASE (EC 6.2.1.19)
DE (ACYL-PROTEIN SYNTHETASE) (FRAGMENT).
GN LUXE.
OS Vibrio fischeri.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=668;
RN [1]
RP MEDLINE-91072226; PubMed-2254256;
RA Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;
RT "A new Vibrio fischeri lux gene precedes a bidirectional termination
RT site for the lux operon."
RL J. Bacteriol. 172:6797-6802(1990).
CC -1- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.
CC IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE
CC FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS
CC SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.
CC -1- CATALYTIC ACTIVITY: ATP + AN ACID + PROTEIN -> AMP + PYROPHOSPHATE
CC + AN ACYL-PROTEIN THIOLESTER.
CC -1- PATHWAY: SECOND STEP IN THE BIOLUMINESCENT FATTY ACID REDUCTASE
CC COMPLEX.
CC -----
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CC -----
DR EMBL: M62812; ? NOT ANNOTATED_CDS.
KW Luminescence; Ligase.
FT NON_TER 1
SQ SEQUENCE 3 AA; 374 MW; 6AA3303000000000 CRC64;

Query Match 18.5%; Score 5; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 9.3e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 K 1
DB 2 K 2

RESULT 7
BOSI_HUMAN STANDARD; PRT; 4 AA.
ID ESI_HUMAN
AC P02731;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE EOSINOPHILOTOXIC PEPTIDES.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE-76078412; PubMed-106093;
RA Goetzl E.J., Austen K.F.;
RT "Purification and synthesis of eosinophilotoxic tetrapeptides of
RT human lung tissue: identification as eosinophil chemotactic factor of
RT anaphylaxis."
RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).
CC -1- MISCELLANEOUS: THESE PEPTIDES ARE RELEASED FROM MAST CELLS IN LUNG
CC (AND OTHER TISSUES) DURING HYPERSENSITIVITY REACTIONS
CC (ANAPHYLAXIS). THEIR ACTIVITIES, PREFERENTIALLY AFFECTING
CC EOSINOPHILS, INCLUDE CHEMOTAXIS, CHEMOTACTIC DEACTIVATION, RELEASE
CC OF ENZYMES, AND STIMULATION OF THE HEXOSE MONOPHOSPHATE SHUNT.

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DR PIR: A03190; ETHUL. 1 V -> A (IN OTHER PEPTIDE).
FT VARIANT 1
SQ SEQUENCE 4 AA; 390 MW; 6B05B862A0000000 CRC64;

Query Match 18.5%; Score 5; DB 1; Length 4;
Best Local Similarity 50.0%; Pred. No. 9.3e+04;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SK 4
DB 3 SE 4

RESULT 8
BPP_BOTIN STANDARD; PRT; 5 AA.
ID BPP7_BOTIN
AC P30425;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE BRADYKININ-POTENTIATING PEPTIDE S5,2 (5A) (ANGIOTENSIN-CONVERTING
DE ENZYME INHIBITOR).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE-Venom;
RA MEDLINE-90351557; PubMed-2386615;
RA Cifra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom."
RL J. Protein Chem. 9:221-227(1990).
CC -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
DR PIR: G37196; G37196.
KW Hypotensive agent; Venom.
FT MOD_RES 1
SQ SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;

Query Match 18.5%; Score 5; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 K 1
DB 2 K 2

RESULT 9
RM01_YEAST STANDARD; PRT; 4 AA.
ID RM01_YEAST
AC P36515;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L1 (YML1) (FRAGMENT).
GN MRPL1.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE.
RX MEDLINE-91285106; PubMed-2060626;
RA Grohmann L., Graack H.-R., Kruff V., Choli T., Goldschmidt-Reisin S.,

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RA Kitakawa M.;
RT "Extended N-terminal sequencing of proteins of the large ribosomal
RL subunit from yeast mitochondria";
RL FEBS Lett. 284:51-56(1991).
DR PIR: S17255; S17255.
DR SGD: L0002681; MRPL1.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 4
SQ SEQUENCE 4 AA; 402 MW; 7771B2D5D0000000 CRC64;

Query Match 14.8%; Score 4; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 9.3e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 S 2
DB 1 S 1

RESULT 10
AL14_CARMA STANDARD; PRT; 5 AA.
ID AL14_CARMA
AC P1817;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CARCINUSSTATIN 14.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- SIMILARITY: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 5
SQ SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;

Query Match 14.8%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 S 2
DB 2 S 2

RESULT 11
UXA4_CHLTR STANDARD; PRT; 5 AA.
ID UXA4_CHLTR
AC P38005;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE FROM ELEMENTARY BODY (FRAGMENT).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE.
RC STRAIN=L2/434/BU;
RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,

RA Comanducci M., Christianen G., Birkelund S., Vretou E., Ratti G.,
RA Pallini V.;
RL Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.5, ITS MW IS: 28 KDA.
FT NON_TER 5
SQ SEQUENCE 5 AA; 474 MW; 75BAA865AA800000 CRC64;

Query Match 14.8%; Score 4; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 S 2
DB 2 S 2

RESULT 12
BIOB_SALTY STANDARD; PRT; 5 AA.
ID BIOB_SALTY
AC P12678;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE) (FRAGMENT).
GN BIOB.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89006280; PubMed=2971595;
RA Shiuan D., Campbell A.;
RT "transcriptional regulation and gene arrangement of Escherichia coli,
RT Citrobacter freundii and Salmonella typhimurium biotin operons";
RL Gene 67:203-211(1988).
CC -!- CATALYTIC ACTIVITY: DETHIOBIOTIN + (S) = BIOTIN.
CC -!- PATHWAY: LAST STEP IN BIOTIN BIOSYNTHESIS PATHWAY.
CC -!- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M21923; -; NOT_ANNOTATED_CDS.
DR StyGene; SGI0027; bioB.
KW Biotin biosynthesis; Iron-sulfur; Transferase.
FT NON_TER 5
SQ SEQUENCE 5 AA; 611 MW; 7761F40DD6F00000 CRC64;

Query Match 11.1%; Score 3; DB 1; Length 5;
Best Local Similarity 0.0%; Pred. No. 9.3e+04;
Matches 0; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SK 4
DB 2 AR 3

RESULT 13
FAR3_HIRME STANDARD; PRT; 4 AA.
ID FAR3_HIRME
AC P42562;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)

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DT 01-NOV-1995 (Rel. 32, last annotation update)
DE FMRFAMIDE-LIKE NEUROPEPTIDE YLRP-AMIDE.
OS Hirudo medicinalis (medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea;
OX Arynchobdellida; Hirudiniformes; Hirudindae; Hirudo.
RN NCB1_TaxID=6421;
RP SEQUENCE.
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rfamid neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
CC -! SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 4 AA; 598 MW; 69D4073B300000000 CRC64;
SQ SEQUENCE 4 AA; 598 MW; 69D4073B300000000 CRC64;

Query Match 7.4%; Score 2; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 9.3e+04;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 K 1
DB 3 R 3

RESULT 14
FAR4_HIRME STANDARD; PRT; 4 AA.
AC P42563;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, last sequence update)
DE FMRFAMIDE-LIKE NEUROPEPTIDE YMRP-AMIDE.
OS Hirudo medicinalis (medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea;
OX Arynchobdellida; Hirudiniformes; Hirudindae; Hirudo.
RN NCB1_TaxID=6421;
RP SEQUENCE.
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rfamid neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
CC -! SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 4 AA; 616 MW; 69D4068B300000000 CRC64;
SQ SEQUENCE 4 AA; 616 MW; 69D4068B300000000 CRC64;

Query Match 7.4%; Score 2; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 9.3e+04;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 K 1
DB 3 R 3

RESULT 15
FLRF_HIRME STANDARD; PRT; 4 AA.
AC P42561;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, last sequence update)
DE FLRFAMIDE.
OS Hirudo medicinalis (medicinal leech), and Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea;
OX Arynchobdellida; Hirudiniformes; Hirudindae; Hirudo.

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OX NCB1_TaxID=6421, 27815;
RN [1]
RP SEQUENCE.
RC SPECIES=H.medicalinalis;
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rfamid neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
RN [2]
RP SEQUENCE.
RC SPECIES=H.trivolvis; TISSUE=Kidney;
RX MEDLINE=94286417; PubMed=7912428;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRFamide-related peptides from the kidney of the snail, Helisoma
trivolvis.";
RL Peptides 15:31-36(1994).
CC -! SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 4 AA; 582 MW; 69D40729A00000000 CRC64;
SQ SEQUENCE 4 AA; 582 MW; 69D40729A00000000 CRC64;

Query Match 7.4%; Score 2; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 9.3e+04;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 K 1
DB 3 R 3

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Search completed: July 19, 2001, 07:53:50
 Job time: 161 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 19, 2001, 07:50:49 ; Search time 20.81 Seconds
(without alignments)
31.789 Million cell updates/sec

Title: US-08-487-283A-1_COPY_8_12
Perfect score: 27
Sequence: 1 KSKC 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues
Total number of hits satisfying chosen parameters: 8

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mnc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-unclassified:*
13: SP-vertebrate:*
14: SP-virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	25.9	5	099007	Q09007 hordeum vul
2	5	18.5	4	11 008433	Q08433 rattus norv
3	1	3.7	5	13 P82070	P82070 ittoria rub
4	1	3.7	5	13 P82071	P82071 ittoria rub
5	1	3.7	5	13 P82072	P82072 ittoria rub
6	1	3.7	5	13 P82073	P82073 ittoria rub
7	1	3.7	5	13 P82100	P82100 ittoria rub
8	0	0.0	5	13 P82099	P82099 ittoria rub

ALIGNMENTS

RESULT 1
ID 099007 PRELIMINARY; PRT: 5 AA.
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)

DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE ALPHA-AMYLASE (EC 3.2.1.1) (FRAGMENT).
GN AMY1.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae;
OC Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HIMALAYA; TISSUE-ALEURONE LAYER;
RX MEDLINE=91329704; PubMed=1831055;
RA Jacobsen J.V., Close T.J.,
RT "Control of transient expression of chimeric genes by gibberellic
RT acid and abscisic acid in protoplasts prepared from mature barley
RT aleurone layers.";
RL Plant Mol. Biol. 16:713-721(1991).
CC -|- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
CC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
CC -|- COFACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -|- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
CC BARLEY.
DR EMBL: X54643; CAA38455.1; -;
KW Hydrolase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
KW Calcium; Multigene family.
FT NON_TER 5
SQ SEQUENCE 5 AA; 600 MW; 61E3344DD6F00000 CRC64;

Query Match 25.9%; Score 7; DB 10; Length 5;
Best Local Similarity 33.3%; Pred. No. 4.2e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSK 4
Db 2 ANK 4

RESULT 2
ID 008433 PRELIMINARY; PRT: 4 AA.
AC 008433;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JAN-1999 (TREMblrel. 09, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE, MICROSMAL (EC 2.4.1.17) (UDPCT)
DB (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-GUNN;
RX MEDLINE=91282758; PubMed=1840486;
RA Sato H., Aono S., Kashiwamata S., Koizumi O.;
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
RT hyperbilirubinemic Gunn rat.";
RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
CC -|- FUNCTION: UDPCT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC ENDOGENOUS COMPOUNDS.
CC -|- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR -> UDP + ACCEPTOR
CC BETA-D-GLUCURONOSIDE.
CC -|- SUBCELLULAR LOCATION: MICROsome.
DR EMBL: S38636; AAB19259.1; -;
KW Transferase; Glycosyltransferase; Microsome; Multigene family.
FT NON_TER 1
SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 18.5%; Score 5; DB 11; Length 4;

Best Local Similarity 100.0%; Pred. No. 4.2e+05; Mismatches 0; Indels 0; Gaps 0;

QY 1 K 1

Db 4 K 4

RESULT 3

P82070
ID P82070 PRELIMINARY; PRT; 5 AA.
AC P82070;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE RUBELLIDIN 1.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-SKIN SECRETION;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
'Litoria rubella', the skin peptide profile as a probe for the study
of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
ANTIBIOTIC ACTIVITY.
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -!- MASS SPECTROMETRY: MW=598; METHOD=FAB.
KW Amphibian skin.
SQ SEQUENCE 5 AA; 598 MW; 6DD9C9CAB2A00000 CRC64;

Query Match

Best Local Similarity 3.7%; Score 1; DB 13; Length 5;

Mismatches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 S 2

Db 5 A 5

RESULT 4

P82071
ID P82071 PRELIMINARY; PRT; 5 AA.
AC P82071;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE RUBELLIDIN 2.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-SKIN SECRETION;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
'Litoria rubella', the skin peptide profile as a probe for the study
of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
ANTIBIOTIC ACTIVITY.
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -!- MASS SPECTROMETRY: MW=626; METHOD=FAB.

KW Amphibian skin.
SQ SEQUENCE 5 AA; 626 MW; 6DD9C9CB10300000 CRC64;

Query Match 3.7%; Score 1; DB 13; Length 5;

Best Local Similarity 0.0%; Pred. No. 4.2e+05;

Mismatches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 K 1

Db 2 E 2

RESULT 5

P82072
ID P82072 PRELIMINARY; PRT; 5 AA.
AC P82072;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE RUBELLIDIN 3.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-SKIN SECRETION;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
'Litoria rubella', the skin peptide profile as a probe for the study
of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
ANTIBIOTIC ACTIVITY.
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -!- MASS SPECTROMETRY: MW=655; METHOD=FAB.
KW Amphibian skin; Amidation.
FT MOD_RES 5 5 AMIDATION.
SQ SEQUENCE 5 AA; 656 MW; 71A9C9CB10300000 CRC64;

Query Match 3.7%; Score 1; DB 13; Length 5;

Best Local Similarity 0.0%; Pred. No. 4.2e+05;

Mismatches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 K 1

Db 2 E 2

RESULT 6

P82073
ID P82073 PRELIMINARY; PRT; 5 AA.
AC P82073;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE RUBELLIDIN 3.2.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE-SKIN SECRETION;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
Litoria electrica. Comparison with the skin peptides from Litoria
rubella.";

RL Aust. J. Chem. 52:0-0(1999).
 CC -1- FUNCTION: CARBIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
 CC ANTIBIOTIC ACTIVITY.
 CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 KW Amphibian skin.
 SQ SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;

Query Match 3.7%; Score 1; DB 13; Length 5;
 Best Local Similarity 0.0%; Pred. No. 4.2e+05;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 S 2
 DB 5 T 5

RESULT 7
 P82100 PRELIMINARY; PRT; 5 AA.
 ID P82100;
 AC P82100;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
 DE 01-MAY-2000 (TREMBlrel. 13, last annotation update)
 DE ELECTRIN 4
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 OC Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=SKIN SECRETION;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 RT Litoria electrica. Comparison with the skin peptides from Litoria
 RT rubella".
 RL Aust. J. Chem. 52:0-0(1999).
 KW Amphibian skin; Amidation.
 FT MOD_RES 5
 SQ SEQUENCE 5 AA; 616 MW; 61F2D1A059A00000 CRC64;

Query Match 3.7%; Score 1; DB 13; Length 5;
 Best Local Similarity 0.0%; Pred. No. 4.2e+05;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 S 2
 DB 3 T 3

RESULT 8
 P82099 PRELIMINARY; PRT; 5 AA.
 ID P82099;
 AC P82099;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
 DE 01-MAY-2000 (TREMBlrel. 13, last annotation update)
 DE ELECTRIN 3
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 OC Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=SKIN SECRETION;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 RT Litoria electrica. Comparison with the skin peptides from Litoria
 RT rubella".
 RL Aust. J. Chem. 52:0-0(1999).

KW Amphibian skin; Amidation.
 FT MOD_RES 5
 SQ SEQUENCE 5 AA; 630 MW; 666761F2C9A00000 CRC64;

Query Match 0.0%; Score 0; DB 13; Length 5;
 Best Local Similarity 0.0%; Pred. No. 4.2e+05;
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 K 1
 DB 1 F 1

Search completed: July 19, 2001, 07:53:34
 Job time: 165 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 19, 2001, 07:47:59 ; Search time 17.33 Seconds
(without alignments)
17.491 Million cell updates/sec

Title: US-08-487-283A-1_COPY_8_12

Perfect score: 27

Sequence: 1 KSKC 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 18613

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq_0601.*
1: /SID8/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID8/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID8/gcgdata/geneseq/geneseq/AA1982.DAT.*
4: /SID8/gcgdata/geneseq/geneseq/AA1983.DAT.*
5: /SID8/gcgdata/geneseq/geneseq/AA1984.DAT.*
6: /SID8/gcgdata/geneseq/geneseq/AA1985.DAT.*
7: /SID8/gcgdata/geneseq/geneseq/AA1986.DAT.*
8: /SID8/gcgdata/geneseq/geneseq/AA1987.DAT.*
9: /SID8/gcgdata/geneseq/geneseq/AA1988.DAT.*
10: /SID8/gcgdata/geneseq/geneseq/AA1989.DAT.*
11: /SID8/gcgdata/geneseq/geneseq/AA1990.DAT.*
12: /SID8/gcgdata/geneseq/geneseq/AA1991.DAT.*
13: /SID8/gcgdata/geneseq/geneseq/AA1992.DAT.*
14: /SID8/gcgdata/geneseq/geneseq/AA1993.DAT.*
15: /SID8/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SID8/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SID8/gcgdata/geneseq/geneseq/AA1996.DAT.*
18: /SID8/gcgdata/geneseq/geneseq/AA1997.DAT.*
19: /SID8/gcgdata/geneseq/geneseq/AA1998.DAT.*
20: /SID8/gcgdata/geneseq/geneseq/AA1999.DAT.*
21: /SID8/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	81.5	5	20	AAV14283
2	22	81.5	5	20	AAV14251
3	22	81.5	5	21	AAI15838
4	22	81.5	5	21	AAI15855
5	22	81.5	5	22	AAI15855
6	18	66.7	5	21	AAI17208
7	17	63.0	5	21	AAV83309
8	16	59.3	5	21	AAV63087
9	16	59.3	5	22	AAI72577
10	16	59.3	5	22	AAI72592
11	16	59.3	5	22	AAI37555

12	15	55.6	4	21	AAI12055
13	15	55.6	5	11	AAV07335
14	15	55.6	5	11	AAV07336
15	15	55.6	5	16	AAI77331
16	15	55.6	5	19	AAI77359
17	15	55.6	5	19	AAI67231
18	15	55.6	5	19	AAI65315
19	15	55.6	5	21	AAI65614
20	15	55.6	5	21	AAI64348
21	14	51.9	3	21	AAI51896
22	14	51.9	4	14	AAI36615
23	14	51.9	4	14	AAI36658
24	14	51.9	4	16	AAI85513
25	14	51.9	4	17	AAI20407
26	14	51.9	4	19	AAI61298
27	14	51.9	4	19	AAI61298
28	14	51.9	4	19	AAI61134
29	14	51.9	4	19	AAI3267
30	14	51.9	4	19	AAI3268
31	14	51.9	4	19	AAI3269
32	14	51.9	4	19	AAI3270
33	14	51.9	4	19	AAI3271
34	14	51.9	4	19	AAI3272
35	14	51.9	4	19	AAI3273
36	14	51.9	4	19	AAI3274
37	14	51.9	4	19	AAI3275
38	14	51.9	4	19	AAI3276
39	14	51.9	4	19	AAI3277
40	14	51.9	4	19	AAI3278
41	14	51.9	4	19	AAI3279
42	14	51.9	4	19	AAI3284
43	14	51.9	4	20	AAI30280
44	14	51.9	4	20	AAI88038
45	14	51.9	4	20	AAI88040

ALIGNMENTS

RESULT 1		
ID	AAI14283	standard: peptide: 5 AA.
XX	AAI14283:	
XX	29-JUL-1999	(first entry)
DE	Chemokine peptide, LFL peptide(6-10)[MCP-1].	
XX		
KW	Chemokine; Immune response; monocyte chemoattractant protein-1; MCP-1;	
KW	chemokine-induced activity; inflammatory response; vascular induction;	
KW	haematopoietic cell-associated activity; tumour; coronary artery disease;	
KW	myocardial infarction; unstable angina pectoris; atherosclerosis; asthma;	
KW	vasculitis; lentiviral infection; low bone mineral density; suppressor;	
KW	parasitic infection; autoimmune disease; psoriasis; wound healing;	
KW	organ transplant rejection; rheumatoid arthritis; allergy; therapy;	
KW	arachidonic acid pathway.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
PN	W09912968-A2.	
XX		
PD	18-MAR-1999.	
XX		
PR	11-SEP-1998;	98WO-US19052.
XX		
PR	11-SEP-1997;	97US-0927939.
XX		
PA	(NEOR-) NEORX CORP.	
XX		
PI	Gralinger DJ, Kanaly ST, Tatalick LM;	
XX		

G4 GTPase motif fr
Matrix metallopro
Matrix metallopro
Human apolipoprote
ML-10 C-terminal
apL immunoreactive
Peptide #7. Synth
Desmoglein cell ad
Cadherin-related n
Biosartin T7232 sy
Group I synthetic
Group III syntheti
Antimicrobial tetr
Chelating moiety f
Human microtubule
Peptide 13 used to
Peptide 13 used to
Peptide #44 having
Peptide #45 having
Peptide #46 having
Peptide #47 having
Peptide #48 having
Peptide #49 having
Peptide #50 having
Peptide #51 having
Peptide #52 having
Peptide #53 having
Peptide #54 having
Peptide #55 having
Peptide #56 having
Peptide #11 having
Integrin alpha-v-b
Peptide used in th

DR WPI; 1999-347124/29.
 XX New chemokine peptides and mimetics
 XX
 XX Disclosure; Fig 14; 208pp; English.
 XX
 CC This sequence represents a fragment of the chemokine MCP-1.
 CC The invention relates to chemokine peptides and mimetics, particularly
 CC derived from monocyte chemoattractant protein-1 (MCP-1). The chemokine
 CC peptides and variants and derivatives can inhibit or reduce or increase,
 CC or enhance chemokine-induced activity. They can be used for increasing or
 CC enhancing an inflammatory response, an immune response or haematopoietic
 CC cell-associated activity at a tumour site. They can also be used for
 CC preventing or inhibiting an indication associated with haematopoietic
 CC cell recruitment or histamine release from basophils or mast cells. They
 CC can also be used to modulate the chemokine-induced activity of
 CC haematopoietic cells at a preselected physiological site, to treat a
 CC vascular indication, e.g. coronary artery disease, myocardial infarction,
 CC unstable angina pectoris, atherosclerosis, or vasculitis, lentiviral
 CC infection or replication in a vertebrate animal (e.g. malaria), an autoimmune
 CC disease, to suppress tumour growth in a vertebrate animal, to prevent or
 CC treat psoriasis in a mammal, to enhance wound healing, to prevent or
 CC treat asthma, organ transplant rejection, rheumatoid arthritis or
 CC allergy. They can also be used to inhibit a product or intermediate in
 CC the arachidonic acid pathway and where leukotriene, thromboxane and/or
 CC prostaglandin are inhibited and to prevent or inhibit an indication
 CC associated with elevated TNF-alpha.
 XX
 XX Sequence 5 AA;
 SQ

Query Match 81.5%; Score 22; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSKC 5
 Db ||||
 2 sskc 5

RESULT 2
 AAY14251
 ID AAY14251 standard; peptide; 5 AA.
 XX
 XX AAY14251;
 XX
 DT 29-JUL-1999 (first entry)
 XX
 XX Chemokine peptide, Peptide2(1-5)[MCP-1].
 XX
 KW Chemokine; immune response; monocyte chemoattractant protein-1; MCP-1;
 KW chemokine-induced activity; inflammatory response; vascular indication;
 KW haematopoietic cell-associated activity; tumour; coronary artery disease;
 KW myocardial infarction; unstable angina pectoris; atherosclerosis; asthma;
 KW vasculitis; lentiviral infection; low bone mineral density; suppressor;
 KW parasitic infection; autoimmune disease; psoriasis; wound healing;
 KW organ transplant rejection; rheumatoid arthritis; allergy; therapy;
 KW arachidonic acid pathway.
 XX
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX WO9912968-A2.
 XX
 XX 18-MAR-1999.
 XX
 XX 11-SEP-1998; 98WO-US19052.
 XX
 XX 11-SEP-1997; 97US-0927939.
 XX
 XX (NEOR-); NEORX CORP.
 PA
 XX

PI Grainger DJ, Kanaly ST, Tatalick LM;
 XX WPI; 1999-347124/29.
 XX
 XX New chemokine peptides and mimetics
 XX
 XX Disclosure; Page 10; 208pp; English.
 XX
 CC This sequence represents a fragment of the chemokine hMCP-1.
 CC The invention relates to chemokine peptides and mimetics, particularly
 CC derived from monocyte chemoattractant protein-1 (MCP-1). The chemokine
 CC peptides and variants and derivatives can inhibit or reduce or increase,
 CC or enhance chemokine-induced activity. They can be used for increasing or
 CC enhancing an inflammatory response, an immune response or haematopoietic
 CC cell-associated activity at a tumour site. They can also be used for
 CC preventing or inhibiting an indication associated with haematopoietic
 CC cell recruitment or histamine release from basophils or mast cells. They
 CC can also be used to modulate the chemokine-induced activity of
 CC haematopoietic cells at a preselected physiological site, to treat a
 CC vascular indication, e.g. coronary artery disease, myocardial infarction,
 CC unstable angina pectoris, atherosclerosis, or vasculitis, lentiviral
 CC infection or replication in a vertebrate animal (e.g. malaria), an autoimmune
 CC disease, to suppress tumour growth in a vertebrate animal, to prevent or
 CC treat psoriasis in a mammal, to enhance wound healing, to prevent or
 CC treat asthma, organ transplant rejection, rheumatoid arthritis or
 CC allergy. They can also be used to inhibit a product or intermediate in
 CC the arachidonic acid pathway and where leukotriene, thromboxane and/or
 CC prostaglandin are inhibited and to prevent or inhibit an indication
 CC associated with elevated TNF-alpha.
 XX
 XX Sequence 5 AA;
 SQ

Query Match 81.5%; Score 22; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSKC 5
 Db ||||
 2 sskc 5

RESULT 3
 AAB15838
 ID AAB15838 standard; Peptide; 5 AA.
 XX
 XX AAB15838;
 XX
 DT 17-JAN-2001 (first entry)
 XX
 XX Human chemokine PF-4 SEQ ID NO: 90.
 XX
 KW Macrophage recruitment; chemokine derivative; MCP-1; osteoporosis;
 KW monocyte chemoattractant protein-1; inflammation; atherosclerosis; HIV;
 KW AIDS; stroke; psoriasis; autoimmune disease; hypertension; endotoxaemia;
 KW basophil-mediated disease; myocardial infarction; acute ischaemia;
 KW rheumatoid arthritis; contraception.
 XX
 XX Homo sapiens.
 OS
 XX WO200042071-A2.
 XX
 XX 20-JUL-2000.
 XX
 XX 12-JAN-2000; 2000WO-US00821.
 XX
 XX 12-JAN-1999; 99US-0229071.
 XX
 XX 17-MAR-1999; 99US-0271192.
 XX
 XX 01-DEC-1999; 99US-0452406.
 XX
 XX (NEOR-) NEORX CORP.
 PA
 XX

PI Granger DJ, Tatalick LM;
XX WPI: 2000-499101/44.
XX New peptide 3, amide and heterocyclic compounds and saccharide
PT conjugates used for inhibiting chemokine induced activity and for
PT treating e.g. stroke, vascular diseases, autoimmune diseases and tumour
PT growth
XX
XX Disclosure; Page 384; 387pp; English.
XX
XX The present invention concerns the identification of a number of
CC chemokines which can be used to produce derivatives, agonists and
CC antagonists which are then useful in disease treatment. The chemokines
CC include sequences AAB15785-B15794, AAB15803-B15813 and AAB15831-B15848.
CC These chemokine derivatives can be used to treat diseases such as
CC autoimmune diseases, atherosclerosis, osteoporosis, HIV infection and
CC AIDS, psoriasis, inflammatory diseases, hypertension, basophil-mediated
CC diseases, endotoxaemia, myocardial infarction, acute ischaemia and
CC rheumatoid arthritis, and can be used to prevent strokes and as
CC contraceptives. The coding sequences for the chemokines can be used in
CC gene therapy for the same diseases, as well as in the production of
CC animal models.
XX
XX Sequence 5 AA;
SQ

Query Match 81.5%; Score 22; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSKC 5
Db 2 sskc 5

RESULT 4
AAB15855
ID AAB15855 standard; peptide; 5 AA.
XX
XX AAB15855;
XX
XX 17-JAN-2001 (first entry)
XX
XX Human chemokine derived peptide #7.
XX
XX Macrophage recruitment; chemokine derivative; MCP-1; osteoporosis;
KW monocyte chemoattractant protein-1; inflammation; atherosclerosis; HIV;
KW AIDS; stroke; psoriasis; autoimmune disease; hypertension; endotoxaemia;
KW basophil-mediated disease; myocardial infarction; acute ischaemia;
KW rheumatoid arthritis; contraception.
XX
XX Synthetic.
XX
XX WO200042071-A2.
XX
XX 20-JUL-2000.
XX
XX 12-JAN-2000; 2000WO-US00821.
XX
XX 12-JAN-1999; 99US-0229071.
XX 17-MAR-1999; 99US-0271192.
XX 01-DEC-1999; 99US-0452406.
XX
XX (NEOR-) NEORX CORP.
XX
XX Granger DJ, Tatalick LM;
XX WPI: 2000-499101/44.
XX
XX New peptide 3, amide and heterocyclic compounds and saccharide
PT conjugates used for inhibiting chemokine induced activity and for
PT treating e.g. stroke, vascular diseases, autoimmune diseases and tumour

PT growth
XX
XX Disclosure; Fig 18; 387pp; English.
XX
XX The present invention concerns the identification of a number of
CC chemokines which can be used to produce derivatives, agonists and
CC antagonists which are then useful in disease treatment. The chemokines
CC include sequences AAB15785-B15794, AAB15803-B15813 and AAB15831-B15848.
CC These chemokine derivatives can be used to treat diseases such as
CC autoimmune diseases, atherosclerosis, osteoporosis, HIV infection and
CC AIDS, psoriasis, inflammatory diseases, hypertension, basophil-mediated
CC diseases, endotoxaemia, myocardial infarction, acute ischaemia and
CC rheumatoid arthritis, and can be used to prevent strokes and as
CC contraceptives. The coding sequences for the chemokines can be used in
CC gene therapy for the same diseases, as well as in the production of
CC animal models.
XX
XX Sequence 5 AA;
SQ

Query Match 81.5%; Score 22; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SSKC 5
Db 2 sskc 5

RESULT 5
AAB37548
ID AAB37548 standard; peptide; 5 AA.
XX
XX AAB37548;
XX
XX 01-MAR-2001 (first entry)
XX
XX CD8 activation complex SSK ridge analogue SC8-17.
XX
XX CD8 activation complex; cytotoxic T lymphocyte response; analogue;
KW surface feature; gene therapy; diabetes; tissue transplantation.
XX
XX Unidentified.
XX
XX WO200066146-A1.
XX
XX 09-NOV-2000.
XX
XX 02-MAY-2000; 2000WO-US11902.
XX
XX 04-MAY-1999; 99US-0132361.
XX 20-AUG-1999; 99US-0150150.
XX 01-NOV-1999; 99US-0162632.
XX
XX (PHIL-) PHILADELPHIA HEALTH & EDUCATION CORP.
XX
XX Jameson BA, Tretiakova A;
XX WPI: 2001-015912/02.
XX
XX Composition for inhibition of detrimental cytotoxic T lymphocyte
PT responses comprising a compound that mimics or interacts with a surface
PT feature of the CD8/MHC I complex
XX
XX Disclosure; Page 33; 40pp; English.
XX
XX The present invention provides compositions which can be used to inhibit
CC detrimental cytotoxic T lymphocyte responses. These compounds mimic or
CC interact with a surface feature (such as SHN, KIT, SSK, DEK and RPT) of
CC the CD8/MHC I complex. This is useful in gene therapy, in the treatment of
CC diabetes and in tissue transplantation.
XX
XX Sequence 5 AA;
SQ

Query Match 81.5%; Score 22; DB 22; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SSKC 5
 ||||
 Db 2 sskc 5

RESULT 6
 AAB17208
 ID AAB17208 standard; Peptide; 5 AA.
 XX
 AC AAB17208;
 XX
 DT 31-OCT-2000 (first entry)
 XX
 DE IL-1 antagonist peptide sequence SEQ ID NO:264.
 XX
 KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
 KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase;
 KW asthma; thrombosis; pharmaceutical.
 XX
 OS Synthetic.
 XX
 PN WO200024782-A2.
 XX
 PD 04-MAY-2000.
 XX
 PF 25-OCT-1999; 99WO-US25044.
 XX
 PR 23-OCT-1998; 98US-0105371.
 PR 22-OCT-1999; 99US-0428082.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Feige U, Liu C, Cheetham J, Boone TC;
 XX
 DR WPI; 2000-350702/30.
 XX
 PT Novel composition of matter comprising an Fc domain and
 PT pharmacologically active peptides, useful for treating cancer and
 PT autoimmune diseases -
 XX
 PS Claim 10; Page 289; 608pp; English.
 XX
 CC The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)-a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,
 CC -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4
 CC where P1, P2, P3, and P4 = are each independently sequences of
 CC pharmacologically active peptides; L1, L2, L3, and L4 = are each
 CC independently linkers; and a, b, c, d, e, and f = are each independently
 CC 0 or 1, provided that at least 1 of a and b is 1. The composition can
 CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive
 CC activities. DNAs, vectors and host cells from the present invention can
 CC be used for producing pharmaceutical compositions. The compositions are
 CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.
 CC The use of an Fc domain (rather than a Fab domain) can provide a longer
 CC half-life or incorporate functions such as Fc receptor binding, protein
 CC A binding, complement fixation, and possibly placental transfer. AAA69443
 CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid
 CC sequences used in the exemplification of the present invention.

Sequence 5 AA;

Query Match 66.7%; Score 18; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSKK 4
 ||||
 Db 2 kskk 5

RESULT 7
 AAY83309
 ID AAY83309 standard; Peptide; 5 AA.
 XX
 AC AAY83309;
 XX
 DT 16-AUG-2000 (first entry)
 XX
 DE Peptide motif of SDDL subtilisin-like serine protease.
 XX
 KW SDDL; serine protease; subtilisin; transgenic plants; dry weight;
 KW stomata; sugar; water; protein; CO₂; H₂O; CO₂; H₂O;
 KW crop protection; feed; foodstuffs.
 XX
 OS Synthetic.
 OS Arabidopsis thaliana.
 XX
 PN WO200022144-A2.
 XX
 PD 20-APR-2000.
 XX
 PF 12-OCT-1999; 99WO-EP07633.
 XX
 PR 12-OCT-1998; 98EP-0119244.
 XX
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 PA (PLAN-) PLANTTEC BIOTECHNOLOGIE GMBH.
 XX
 PI Berger D, Altmann T;
 XX
 DR WPI; 2000-317995/27.
 XX
 PT Novel recombinant DNA molecules encoding subtilisin-like serine
 PT protease, useful for producing transgenic plants with altered stomata,
 PT lower water consumption and enhanced diseased resistance
 XX
 PS Disclosure; Page 9; 101pp; English.
 XX
 CC Sequences encoding SDDL, a subtilisin-like serine protease, can be
 CC used to produce transgenic plants with altered stomata
 CC characteristics. These plants exhibit improved freshness,
 CC increased dry weight, reduced leaf temperatures, reduced water loss
 CC and lower water consumption and for enhancing the sugar and/or
 CC protein content of plant leaves, modulating CO₂ uptake into and H₂O
 CC release from leaves, for sustained photosynthesis under high
 CC intensity conditions or for the improvement of disease resistance
 CC of plants. The transgenic plants and cells of such plants are useful
 CC in the preparation of feed, food or additives.

Sequence 5 AA;

Query Match 63.0%; Score 17; DB 21; Length 5;
 Best Local Similarity 75.0%; Pred. No. 3.4e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SSKC 5
 ||||
 Db 1 sskc 4

RESULT 8
 AAY63087

ID AAY63087 standard; Peptide: 5 AA.
AC AAY63087;
XX
DT 02-MAR-2000 (first entry)
XX
DE LI-cadherin cell adhesion recognition cyclic peptide SEQ ID NO:2629.
XX
KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;
KW inhibition; cadherin extracellular domain; cell adhesion recognition;
KW 08-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8;
KW cadherin-12; cadherin-14; cadherin-15; T-cadherin; PR-cadherin;
KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
KW neurological disease; cyclic.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1..5
XX
PN WO957149-A2.
XX
PD 11-NOV-1999.
XX
PE 05-MAY-1999; 99WO-CA00363.
XX
PR 05-MAY-1998; 98US-0073040.
PR 06-NOV-1998; 980S-0187859.
PR 20-JAN-1999; 99US-0234395.
PR 08-MAR-1999; 99US-0264516.
XX
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
PI Blaschuk OW, Gour BJ, Byers S;
XX
DR WPI: 2000-038791/03.
XX
PT New cadherin modulating agents, used for modulating nonclassical
PT cadherin-mediated functions for treating e.g. cancers, obesity,
PT rheumatoid arthritis, multiple sclerosis, diabetes or a neurological
PT disease
XX
PS Claim 78; Page 198; 252pp; English.
XX
CC The present invention describes cadherin modulating agents (MA)
CC comprising peptides which comprise a nonclassical cadherin cell adhesion
CC recognition (CAR) sequence. The MAs can be used for modulating
CC nonclassical cadherin-mediated functions. They can be used for e.g.
CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
CC mammal, enhancing delivery of a drug through the skin of a mammal,
CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
CC expressing cell, preventing or treating obesity in a mammal, stimulating
CC blood vessel regression in a mammal, enhancing drug delivery to the
CC central nervous system, treating a demyelinating neurological disease,
CC increasing vasopermeability in a mammal, enhancing adhesion of
CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
CC a mammal, or preventing pregnancy in a mammal. They can also be used for
CC e.g. enhancing or directing neurite outgrowth, facilitating wound
CC healing or reducing scar tissue, or enhancing adhesion of foreign tissue
CC in a mammal. They can also be used for treating e.g. psoriasis,
CC arthritis, age-related macular degeneration, multiple sclerosis and
CC diabetes. The products can also be used for detection and diagnosis and
CC in bioreactors. AAY60592 to AAY64572 represent specifically claimed
CC peptides, and AAY64573 to AAY64643 and AA233183 to AA333186 represent
CC sequences used in the exemplification of the present invention.
XX
SQ Sequence 5 AA;

Query Match 59.3%; Score 16; DB 21; Length 5;
Best Local Similarity 50.0%; Pred. No. 3.4e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0;
OY 2 SSRC 5
Db 2 nkc 5
RESULT 9
AAB72577
ID AAB72577 standard; Peptide: 5 AA.
XX
AC AAB72577;
XX
DT 09-MAY-2001 (first entry)
XX
DE Thrombin-induced platelet activator antagonist #16.
XX
KW Platelet aggregation inhibitor; thrombin activation inhibitor;
KW protease activated receptor 1; PAR1; platelet activation inhibitor;
KW thrombosis; acute coronary syndrome.
XX
OS Unidentified.
XX
PN WO200112656-A1.
XX
PD 22-FEB-2001.
XX
PE 17-AUG-2000; 2000WO-US40669.
XX
PR 17-AUG-1999; 99US-0375808.
XX
PA (THRO-) THROMGEN INC.
PI Schmaier AH, Hasan AAK;
XX
DR WPI: 2001-226546/23.
XX
PT Inhibiting thrombin activation in human cell expressing protease
PT activated receptor 1 (PAR1), comprises contacting mixtures of thrombin
PT and human cell expressing PAR1, with a peptide that inhibits platelet
PT activation
XX
PS Claim 7; Page 25; 49pp; English.
XX
CC The present invention relates to a method for inhibiting thrombin
CC activation in a human cell expressing protease activated receptor 1
CC (PAR1). The method involves using peptides (e.g. the present peptide)
CC that inhibit platelet activation. The method is useful for preventing
CC thrombosis and platelet aggregation. The method can be used for patients
CC with acute coronary syndromes (e.g. crescendo angina, myocardial
CC infarction) and for individuals who have acute coronary syndromes and
CC receive percutaneous transluminal coronary angioplasty with an artificial
CC stent placement.
XX
SQ Sequence 5 AA:
Query Match 59.3%; Score 16; DB 22; Length 5;
Best Local Similarity 40.0%; Pred. No. 3.4e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 KSKC 5
Db 1 rpkc 5
RESULT 10
AAB72592
ID AAB72592 standard; Peptide: 5 AA.
XX

AC	AAB72592;
XX	
DT	09-MAY-2001 (first entry)
XX	
DE	Thrombin-induced platelet activator antagonist #31.
XX	
KW	Platelet aggregation inhibitor; thrombin activation inhibitor;
KW	protease activated receptor 1; PAR1; platelet activation inhibitor;
KW	thrombosis; acute coronary syndrome.
XX	
OS	Unidentified.
XX	
PN	WO200112656-A1.
XX	
PD	22-FEB-2001.
XX	
PF	17-AUG-2000; 2000WO-US40669.
XX	
PR	17-AUG-1999; 99US-0375808.
XX	
PA	(THRO-) THROMGEN INC.
XX	
PI	Schmaier AH, Hasan AAK;
XX	
DR	WPI; 2001-226546/23.
XX	
PT	Inhibiting thrombin activation in human cell expressing protease
PT	activated receptor 1 (PAR1), comprises contacting mixtures of thrombin
PT	and human cell expressing PAR1, with a peptide that inhibits platelet
PT	activation
XX	
PS	Claim 5; Page 25; 49pp; English.
XX	
CC	The present invention relates to a method for inhibiting thrombin
CC	activation in a human cell expressing protease activated receptor 1
CC	(PAR1). The method involves using peptides (e.g. the present peptide)
CC	that inhibit platelet activation. The method is useful for preventing
CC	thrombosis and platelet aggregation. The method can be used for patients
CC	with acute coronary syndromes (e.g. crescendo angina, myocardial
CC	infarction) and for individuals who have acute coronary syndromes and
CC	receive percutaneous transluminal coronary angioplasty with an article
CC	stent placement.
XX	
SQ	Sequence 5 AA;
Query Match	59.3%; Score 16; DB 22; Length 5;
Best Local Similarity	40.0%; Pred. No. 3.4e+05;
Matches	2; Conservative 1; Mismatches 2; Indels 0; Gaps 0
Qy	1 KSSKC 5
	:
Db	1 rgdkc 5
RESULT 11	
AAB37555	
ID	AAB37555 standard; peptide; 5 AA.
XX	
AC	AAB37555;
XX	
DT	01-MAR-2001 (first entry)
XX	
DE	CD8 activation complex RDT ridge analogue SC8-21.
XX	
KW	CD8 activation complex; cytotoxic T lymphocyte response; analogue;
KW	surface feature; gene therapy; diabetes; tissue transplantation.
XX	
OS	Unidentified.
XX	
PN	WO2000066146-A1.
XX	
PD	09-NOV-2000.

XX	02-MAY-2000; 2000WO-US11902.
PF	
XX	
PR	04-MAY-1999; 99US-0132361.
PR	20-AUG-1999; 99US-0150150.
PR	01-NOV-1999; 99US-0162632.
XX	
PA	(PHIL-) PHILADELPHIA HEALTH & EDUCATION CORP.
XX	
PI	Jameson BA, Tretiakova A;
XX	
DR	WPI; 2001-015912/02.
XX	
PT	Composition for inhibition of detrimental cytotoxic T lymphocyte
PT	responses comprising a compound that mimics or interacts with a surface
PT	feature of the CD8/MHC I complex
XX	
PS	Disclosure; Page 35; 40pp; English.
XX	
CC	The present invention provides compositions which can be used to inhibit
CC	detrimental cytotoxic T lymphocyte responses. These compounds mimic or
CC	interact with a surface feature (such as SHN, KIT, SSK, DEK and RDT) of
CC	the CD8/MHCI complex. This is useful in gene therapy, in the treatment of
CC	diabetes and in tissue transplantation.
XX	
SQ	Sequence 5 AA;
	Query Match 59.3%; Score 16; DB 22; Length 5;
	Best Local Similarity 50.0%; Pred. No. 3.4e+05;
	Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Oy	2 SSKC 5
	::::
Db	2 mnkc 5
RESULT 12	
AAB12055	
ID	AAB12055 standard; Peptide; 4 AA.
XX	
AC	AAB12055;
XX	
DT	17-JAN-2001 (first entry)
XX	
DE	G4 GTPase motif from EF-Tu/ Ha-RAS.
XX	
KW	Rb-interacting zinc finger; R12; retinoblastoma; heart disease;
KW	cell proliferation; cell differentiation; tissue repair;
KW	transcription regulator; breast cancer; gene therapy; melanoma;
KW	neuroblastoma; leukaemia; Parkinson's disease; Huntington's disease;
KW	Alzheimer's disease; paralysis; motor neurone disorder;
KW	G4 GTPase motif; EF-Tu/ Ha-RAS.
XX	
OS	Unidentified.
XX	
PN	US6069231-A.
XX	
PD	30-MAY-2000.
XX	
PF	18-AUG-1995; 99US-0516859.
XX	
PR	18-AUG-1994; 94US-0292683.
PR	06-MAR-1995; 95US-0399411.
XX	
PA	(LJOL-) LA JOLLA CANCER RES FOUND.
XX	
PI	Huang S;
XX	
DR	WPI; 2000-410879/35.
XX	
PT	New PR domain peptides comprising amino acid sequences from, for
PT	example retinoblastoma-interacting zinc finger, or egl-43 proteins, for

Db 1 rkpkc 5

RESULT 15

AAR77331

ID AAR77331 standard; Peptide; 5 AA.

XX AC AAR77331;

XX DT 06-FEB-1996 (first entry)

XX DE Human apolipoprotein (a) (apo(a)) antigenic peptide.

XX KW Human; old world monkey; apolipoprotein (a); apo(a); primer; probe;

XX KW antigenic peptide; immunoassay; detection; quantification.

XX OS Homo sapiens.

XX PN EP659765-A2.

XX PD 28-JUN-1995.

XX PF 16-DEC-1994; 94EP-0203653.

XX PR 27-JUN-1994; 94US-0266407.

XX PR 21-DEC-1993; 93US-0172461.

XX PA (ALKU) AKZO NOBEL NV.

XX PI Butler SM, Taddei-peters WC;

XX DR WPI; 1995-226203/30.

XX DR N-PSDB; AAQ91625.

XX PT New immuno:reactive peptide(s) of apo:lipoprotein - used for prodn.

XX PT of antibodies and development of immunoassays, for the detection and

XX PT quantification of apo(a)

XX PS Claim 3; Page 26; 44pp; English.

XX CC AAQ91625 encodes AAR77331 a human/old world monkey apolipoprotein (a)

XX CC (apo(a)) antigenic peptide. The peptide can be used to raise anti-

XX CC apo(a) antibodies, for use in immunoassays for the detection of

XX CC apo(a). The DNA sequence can be used as a primer and/or probe for

XX CC the detection, and quantification of apo(a) DNA.

XX SQ Sequence 5 AA;

Query Match 55.6%; Score 15; DB 16; Length 5;
Best Local Similarity 75.0%; Pred. No. 3.4e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSSK 4

Db 1 kssr 4

Search completed: July 19, 2001, 07:50:45
Job time: 166 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 19, 2001, 07:48:49 : Search time 12.12 Seconds
(without alignments)
8.310 Million cell updates/sec

Title: US-08-487-283A-1_COPY_8_12

Perfect score: 27

Sequence: 1 KSKK 5

Scoring table: BLOSOM62

Gapop 10.0 , Gapext 0.5

Searched: 193259 seqs, 20144635 residues

Total number of hits satisfying chosen parameters: 15047

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, AA:*

1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
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3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCUTS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	66.7	4	1	US-07-694-983-2
2	18	66.7	4	1	US-08-243-082-23
3	15	55.6	4	2	US-08-459-568-41
4	15	55.6	4	2	US-08-399-411-41
5	15	55.6	4	3	US-08-516-859A-41
6	15	55.6	5	1	US-08-363-475-13
7	15	55.6	5	1	US-08-456-840-34
8	15	55.6	5	1	US-08-329-820-102
9	15	55.6	5	1	US-08-329-820-103
10	15	55.6	5	1	US-08-329-820-108
11	15	55.6	5	1	US-08-266-407A-34
12	15	55.6	5	2	US-08-892-544-34
13	15	55.6	5	2	US-08-814-567A-6
14	15	55.6	5	3	US-08-915-189-90
15	15	55.6	5	3	US-08-894-173-36
16	15	55.6	5	4	US-09-398-193-36
17	15	55.6	5	4	US-08-660-092-192
18	14	51.9	3	1	US-07-789-913-26
19	14	51.9	3	1	US-08-049-794-26
20	14	51.9	3	1	US-08-496-847-26
21	14	51.9	3	2	US-08-742-774-26
22	14	51.9	3	2	US-08-675-354-26
23	14	51.9	3	2	US-08-965-918-26
24	14	51.9	3	2	US-09-138-439-26
25	14	51.9	3	3	US-08-613-400A-26
26	14	51.9	3	3	US-09-298-017-26
27	14	51.9	4	4	US-09-392-979A-26

28	14	51.9	4	1	US-07-694-983-3	Sequence 3, Appl1
29	14	51.9	4	1	US-07-694-983-4	Sequence 4, Appl1
30	14	51.9	4	1	US-08-234-602-7	Sequence 7, Appl1
31	14	51.9	4	2	US-08-244-496-5	Sequence 5, Appl1
32	14	51.9	4	2	US-08-244-496-47	Sequence 47, Appl1
33	14	51.9	4	6	5168050-9	Patent No. 5168050
34	14	51.9	5	1	US-08-234-602-8	Sequence 8, Appl1
35	14	51.9	5	1	US-08-199-778-5	Sequence 5, Appl1
36	14	51.9	5	1	US-08-483-434A-35	Sequence 35, Appl1
37	14	51.9	5	2	US-08-244-496-48	Sequence 48, Appl1
38	14	51.9	5	2	US-08-531-525-2	Sequence 2, Appl1
39	14	51.9	5	2	US-08-928-958-22	Sequence 22, Appl1
40	14	51.9	5	2	US-08-718-270A-2	Sequence 2, Appl1
41	14	51.9	5	2	US-08-747-137-168	Sequence 168, App
42	14	51.9	5	2	US-09-072-429-22	Sequence 22, Appl1
43	14	51.9	5	3	US-08-760-903-5	Sequence 5, Appl1
44	14	51.9	5	3	US-08-722-258-71	Sequence 71, Appl1
45	14	51.9	5	4	US-08-882-046-107	Sequence 107, App

ALIGNMENTS

RESULT 1
US-07-694-983-2
; Sequence 2, Application US/07694983
; Patent No. 5432260
; GENERAL INFORMATION:
; APPLICANT: Stahl, Phillip D.
; TITLE OF INVENTION: HIGH AFFINITY MANNOSE RECEPTOR
; NUMBER OF INVENTION: 19
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Irell & Manella
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/694,983
; FILING DATE: 19910503
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 9500-0039.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-694-983-2

Query Match 66.7%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
QY 1 KSKK 4
IIII
Db 1 KSKK 4

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/399,411
; FILING DATE: 06-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1264
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-459-568-41

Query Match 55.6%; Score 15; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SKC 5
DB 1.NKC 3

RESULT 4
US-08-399-411-41
; Sequence 41, Application US/08399411
; Patent No. 5831008
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/399,411
; FILING DATE: 06-MAR-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1264
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-243-082-23

Query Match 66.7%; Score 18; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSK 4
DB 1 KSK 4

RESULT 3
US-08-459-568-41
; Sequence 41, Application US/08459568
; Patent No. 5811304
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 05-JUN-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/853,754
; FILING DATE: 05-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Schneller, John W.
; REGISTRATION NUMBER: 26,031
; REFERENCE/DOCKET NUMBER: KUWAT 0010
; TELEPHONE: (202) 828-8000
; TELEFAX: (202) 828-8038
; TELEX: SPENCER 64267
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-243-082-23
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US-08-399-411-41

Query Match 55.6%; Score 15; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SKC 5
:11
Db 1 NKC 3

RESULT 5

US-08-516-859A-41
; Sequence 41, Application US/08516859A
; Patent No. 6069231
; GENERAL INFORMATION:
; APPLICANT: Huang, Shi
; TITLE OF INVENTION: Retinoblastoma Protein - Interacting
; TITLE OF INVENTION: Zinc Finger Proteins
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/516,859A
; FILING DATE: 18-AUG-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/399,411
; FILING DATE: 06-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/292,683
; FILING DATE: 18-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1776
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-516-859A-41

Query Match 55.6%; Score 15; DB 3; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SKC 5
:11
Db 1 NKC 3

RESULT 6

US-08-363-475-13
; Sequence 13, Application US/08363475
; Patent No. 551679
; GENERAL INFORMATION:
; APPLICANT: Chiang, Shu-Jen

APPLICANT: Burnett Jr., William V.
; APPLICANT: Tonzi, Sean M.
; TITLE OF INVENTION: PENICILLIN V AMIDOHYDROLASE GENE FROM
; TITLE OF INVENTION: FUSARIUM OXYSPORUM
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thomas R. Savitsky
; STREET: P.O. Box 4000
; CITY: Princeton
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 08543

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,475
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitsky, Thomas R.
; REGISTRATION NUMBER: 31,661
; REFERENCE/DOCKET NUMBER: ON-0134
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 252 4956
; TELEFAX: (609) 252 4526
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-363-475-13

Query Match 55.6%; Score 15; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SKC 5
:11
Db 2 AKC 4

RESULT 7

US-08-456-840-34
; Sequence 34, Application US/08456840
; Patent No. 5597908
; GENERAL INFORMATION:
; APPLICANT: Taddel-Peters, W. C.
; APPLICANT: Butler, Sandra M.
; TITLE OF INVENTION: Immunoreactive Peptides of Apo(a)
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akzo No. 5597908el
; STREET: 1330 Piccard Drive
; CITY: Rockville
; STATE: Maryland
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,840
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/266,407
FILING DATE: 27-JUN-1994
APPLICATION NUMBER: US 08/172,461
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Gormley, Mary E.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-258-5200
TELEFAX: 301-977-0847
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-456-840-34

Query Match 55.6%; Score 15; DB 1; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0;

QY 1 KSSK 4
Db 1 KSSR 4

RESULT 8
US-08-329-820-102
Sequence 102, Application US/08329820
Patent No. 5747457
GENERAL INFORMATION:
APPLICANT: JONCZYK, ALFRED
APPLICANT: FELDING-HABERMANN, BRUNHILDE
APPLICANT: DIEFENBACH, BEATE
APPLICANT: RIPPMANN, FRIEDRICH
TITLE OF INVENTION: Linear Adhesion Inhibitors
NUMBER OF SEQUENCES: 228
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/329,820
FILING DATE: 27-OCT-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4336758.5
FILING DATE: 28-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hamlet-King, Diana
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1635
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: /product= "Cys-trityl"
OTHER INFORMATION: /note= "S-trityl"

FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /product= "Lys(BOC)"
OTHER INFORMATION: /note= "N-terminal: FMOC"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2
OTHER INFORMATION: /product= "Thr(But)"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /product= "Asp(OBut)"
US-08-329-820-102

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Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSSK 5
Db 1 KTADC 5

RESULT 9
US-08-329-820-103
Sequence 103, Application US/08329820
Patent No. 5747457
GENERAL INFORMATION:
APPLICANT: JONCZYK, ALFRED
APPLICANT: FELDING-HABERMANN, BRUNHILDE
APPLICANT: DIEFENBACH, BEATE
APPLICANT: RIPPMANN, FRIEDRICH
TITLE OF INVENTION: Linear Adhesion Inhibitors
NUMBER OF SEQUENCES: 228
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/329,820
FILING DATE: 27-OCT-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4336758.5
FILING DATE: 28-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hamlet-King, Diana
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1635
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: /product= "Cys-trityl"
OTHER INFORMATION: /note= "S-trityl"
US-08-329-820-103

Query Match 55.6%; Score 15; DB 1; Length 5;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSSKC 5
DB 1 KTADC 5

RESULT 10

US-08-329-820-108
Sequence 108, Application US/08329820
Patent No. 5747457

GENERAL INFORMATION:

APPLICANT: JONCZYK, ALFRED
APPLICANT: FELDING-HABERMANN, BRUNHILDE
APPLICANT: DIEFENBACH, BEATE
APPLICANT: RIPPMANN, FRIEDRICH
TITLE OF INVENTION: Linear Adhesion Inhibitors
NUMBER OF SEQUENCES: 228

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/329,820
FILING DATE: 27-OCT-1994
CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 4336758.5
FILING DATE: 28-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: Hamlet-King, Diana
REGISTRATION NUMBER: 33,302

TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333

TELEFAX: 703-243-6410

INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids
TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear
MOLECULE TYPE: peptide

HYPOTHETICAL: YES
ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal
FEATURE:

NAME/KEY: Modified-site
LOCATION: 1

OTHER INFORMATION: /product- "Boc-Lys(Boc)"
FEATURE:

NAME/KEY: Modified-site
LOCATION: 2

OTHER INFORMATION: /product- "Thr(But)"
FEATURE:

NAME/KEY: Modified-site
LOCATION: 4

OTHER INFORMATION: /product- "asp(Obut)"
FEATURE:

NAME/KEY: Modified-site
LOCATION: 5

OTHER INFORMATION: /product- "Cys(Trt)"
US-08-329-820-108

Query Match 55.6%; Score 15; DB 1; Length 5;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSSKC 5

DB 1 KTADC 5

RESULT 11

US-08-266-407A-34
Sequence 34, Application US/08266407A
Patent No. 5786156

GENERAL INFORMATION:

APPLICANT: Taddel-Peters, W. C.
APPLICANT: Butler, Sandra M.

TITLE OF INVENTION: Immunoreactive Peptides of Apo(a)
NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESSES:
ADDRESSEE: AKZO No. 5786156el

STREET: 1330 Piccard Drive
CITY: Rockville

STATE: Maryland
COUNTRY: US

ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/266,407A
FILING DATE: 27-JUN-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/172,461

FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:

NAME: Gornley, Mary E.
REGISTRATION NUMBER: 34,409

TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-258-5200

TELEFAX: 301-977-0847

INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:

LENGTH: 5 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-266-407A-34

Query Match 55.6%; Score 15; DB 1; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KSSK 4
DB 1 KSSR 4

RESULT 12

US-08-892-544-34
Sequence 34, Application US/08892544
Patent No. 5874544

GENERAL INFORMATION:
APPLICANT: Taddel-Peters, W. C.

APPLICANT: Butler, Sandra M.
TITLE OF INVENTION: Immunoreactive Peptides of Apo(a)

NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESSES:
ADDRESSEE: AKZO No. 5874544el

STREET: 1330 Piccard Drive
CITY: Rockville

STATE: Maryland
COUNTRY: US

ZIP: 20850

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/892,544
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/266,407
; FILING DATE: 27-JUN-1994
; APPLICATION NUMBER: US 08/172,461
; FILING DATE: 21-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Gormley, Mary E.
; REGISTRATION NUMBER: 34,409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-258-5200
; TELEFAX: 301-977-0847
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-892-544-34

Query Match 55.6%; Score 15; DB 2; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSR 4
Db 1 KSSR 4

RESULT 13
US-08-814-567A-6
; Sequence 6, Application US/08814567A
; Patent No. 5998598
; GENERAL INFORMATION:
; APPLICANT: CSARY, KARL G.
; APPLICANT: ANGLADE, EDDY
; APPLICANT: SULLIVAN, DANIEL M.
; APPLICANT: LAROCHELLE, WILLIAM
; TITLE OF INVENTION: IMMUNOADHESINS AND METHODS OF PRODUCTION
; TITLE OF INVENTION: AND USE THEREOF
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: 127 PEACHTREE STREET, NE
; CITY: ATLANTA
; STATE: GEORGIA
; COUNTRY: USA
; ZIP: 30303-1811
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,567A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: SELBY, ELIZABETH
; REGISTRATION NUMBER: 38,298
; REFERENCE/DOCKET NUMBER: 14014.0214
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 688-0770
; TELEFAX: (404) 688-9880
; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-814-567A-6

Query Match 55.6%; Score 15; DB 2; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSSK 4
Db 2 KSSR 5

RESULT 14
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; Sequence 90, Application US/08915189
; Patent No. 6001965
; Patent No. 6001965 6001955
; GENERAL INFORMATION:
; APPLICANT: Livant, Donna L.
; TITLE OF INVENTION: Anticancer Compounds and Methods
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/915,189
; FILING DATE: 20-AUG-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Carroll, Peter G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: UM-02877
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; US-08-915-189-90

Query Match 55.6%; Score 15; DB 3; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SKC 5
Db 3 SRC 5

RESULT 15
US-08-894-173-36
; Sequence 36, Application US/08894173A
; Patent No. 6090612

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: GENERAL INFORMATION:
: APPLICANT: Medical Research Council
: TITLE OF INVENTION: Adenylylate cyclase and uses therefor
: FILE REFERENCE: P14716C
: CURRENT APPLICATION NUMBER: US/08/894,173A
: CURRENT FILING DATE: 1997-08-13
: NUMBER OF SEQ ID NOS: 97
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO: 36
: LENGTH: 5
: TYPE: PRT
: ORGANISM: Mouse
: FEATURE:
: OTHER INFORMATION: STRANDEDNESS : Single
: FEATURE:
: OTHER INFORMATION: TOPOLOGY : Linear
: FEATURE:
: OTHER INFORMATION: MOLECULE TYPE : Peptide
: FEATURE:
: OTHER INFORMATION: HYPOTHETICAL : NO
: FEATURE:
: OTHER INFORMATION: ANTI-SENSE : NO
US-08-894-173-36

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Query Match          55.6%; Score 15; DB 3; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 3 SKC 5
: 11
Db 1 TKC 3

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Search completed: July 19, 2001, 07:51:04
Job time: 135 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2001, 00:49:32 ; Search time 2123.9 Seconds
(without alignments)
5440.185 Million cell updates/sec

Title: US-08-487-283A-8

Perfect score: 747
Sequence: 1 ATGCCCATATCCAGATGAC.....TGGTCACTGTCTCGAGCTGA 747

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 segs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

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96: gb_in4:*
97: gb_pr10:*
98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	314.8	42.1	1612	9	AX057943	AX057943 Sequence
2	310.6	41.6	840	56	AF329458	AF329458 Synthetic
3	294	39.4	819	9	A18692	A18692 Synthetic n
4	290.4	38.9	1637	9	AX006750	AX006750 Sequence
5	283.4	37.9	723	9	AR003797	AR003797 Sequence
6	283.4	37.9	723	9	AR010133	AR010133 Sequence
7	283.4	37.9	723	9	AR055339	AR055339 Sequence
8	283.4	37.9	723	10	II1980	II1980 Sequence 92

9	283.4	37.9	723	10	I40550	I40550 Sequence 89
10	266	35.6	2871	9	AX023363	AX023363 Sequence
11	262	35.1	888	56	AF132308	Synthetic
12	259	34.7	1630	9	AX023365	AX023365 Sequence
13	259	34.7	1630	9	AX023367	AX023367 Sequence
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15	250	33.5	729	9	AR027053	AR027053 Sequence
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17	250	33.5	729	45	E10362	E10362 cDNA encodi
18	249.2	33.4	780	56	SYNN198SCF	L43067 Synthetic s
19	247.2	33.1	916	10	I45604	I45604 Sequence 29
20	245.6	32.9	828	94	MMZ95478	Z95478 Mus musculu
21	245.2	32.8	1371	9	AX023359	AX023359 Sequence
22	245.2	32.8	1389	9	AX023361	AX023361 Sequence
23	242	32.4	1611	9	AX014270	AX014270 Sequence
24	241.6	32.3	877	10	E31225	E31225 Device for
25	241.6	32.3	925	10	E30616	E30616 Antibody an
26	239.6	32.1	1149	9	A63778	A63778 Sequence 42
27	239.6	32.1	1212	9	A63772	A63772 Sequence 36
28	239.6	32.1	1422	9	A63768	A63768 Sequence 32
29	239.6	32.1	1545	9	A63770	A63770 Sequence 34
30	239.6	32.1	1956	9	A63774	A63774 Sequence 38
31	239.6	32.1	2079	9	A63776	A63776 Sequence 40
32	239.4	32.0	801	56	AF027160	AF027160 Synthetic
33	238.6	31.9	1239	9	AX057945	AX057945 Sequence
34	236.6	31.7	733	9	AR027763	AR027763 Sequence
35	236.6	31.7	733	9	AR088764	AR088764 Sequence
36	234.4	31.4	721	9	AR027762	AR027762 Sequence
37	234.4	31.4	721	9	AR088763	AR088763 Sequence
38	232.8	31.2	720	10	E13599	E13599 DNA encodin
39	232.4	31.1	2178	9	AR048108	AR048108 Sequence
40	232.4	31.1	2178	9	AR054190	AR054190 Sequence
41	232.2	31.1	822	94	MMZ95477	Z95477 Mus musculu
42	231	30.9	6727	9	AR060673	AR060673 Sequence
43	231	30.9	6727	9	AR074430	AR074430 Sequence
44	230.6	30.9	1299	9	AR060677	AR060677 Sequence
45	230.6	30.9	1299	9	AR074434	AR074434 Sequence

ALIGNMENTS

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LOCUS		Sequence 3 from Patent WO0075333.				
DEFINITION		AX057943				
ACCESSION		AX057943.1	GI:12310570			
VERSION						
KEYWORDS		Streptomyces avidinii.				
SOURCE		Streptomyces avidinii.				
ORGANISM		Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.				
REFERENCE		1 (bases 1 to 1612)				
AUTHORS		Goshorn,S.C., Graves,S.S., Schultz,J.E., Lin,Y., Sanderson,J.A. and Reno,J.M.				
TITLE		Streptavidin expressed gene fusions and methods of use thereof				
JOURNAL		Patent: WO 0075333-A 3 14-DEC-2000;				
FEATURES		NEORA CORPORATION (US)				
source		Location/Qualifiers				
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		Best Local Similarity	56.1%;	Pred. No. 7.8e-80;		
		Matches 489;	Conservative 0;	Mismatches 242;	Indels 9;	Gaps 2;
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Db	371	ATGGGTGACATCCAGATGACTCAGTCTCCATCGTCTCTTGTCTGCCCTCTGTGGGAGACAGA	430
Qy	61	GTCAACATCACCTGGCGGCCAGCAAAACATCTATGGCGCGCTGAACCTGGTATCAACGT	120
Db	431	GTCAACATCACCTGGCGGCCAGTCTAGGCGCATAGAGGTAATTTAGACTGGTATCAGCAG	490
Qy	121	AAACCTGGGAAAGCTCCAGAGTCTTGATTTACGGTGGGACGAACCTGGCAGATGAGGTC	180
Db	491	AAACCTGGTAAAGGACCGAAATCCCTAATCTACTCCACATCCAAATTTAAATTTCTGGTGC	550
Qy	181	CTTCTCGCTTCTCTGGATCCGGCTCCGGAACGGATTTCACTCTGACCATCAGCAGTCG	240
Db	551	CCATCAAGGTCTCAGTGGGCTGGTCTGGTCTGAGATATATCTCTCACCATCAGACGCTT	610
Qy	241	CAGCTGGAAGCTTCGCTACGTATTACTGTCAAGCTTTTAAATCTCCGTTGACTTTC	300
Db	611	CAGCTGGAAGTTCGCAACGTATTACTGTCTACACCGTAATCCGTATCCGTACACGTTTC	670
Qy	301	GGACAGGTGTACCAAGTGGAAATAAACACTACTGGCGGTGGTGTCTGGTGGCGGTGA	360
Db	671	GGACAAGGACCAAGCTGGAGATCAAGATCTCTGGTGGCGGTGGCTCGGCGGTGGTGGG	730
Qy	361	TCGTGGTGGCGGTTC---TCAAGTCCAACTGGTGCATCCGGCCCGGAGGTCAAGAAG	417
Db	731	TCGGGTGGCGGAGGCTCGAGCCAGGTTCCAGTGTCCAGTCTGGGCGAGGTGAAAAG	790
Qy	418	CCAGGCGCTCAGTCAAGTGTCTCTGTAAGCTAGCGGTATATTTTCTTAATTTATTGG	477
Db	791	CCAGGCGCTCAGTCAAGTGTCTCTGTAAGCTAGCGGTATATTTTCTTAATTTATTGG	850
Qy	478	ATCAATGGGTGCGTCAGCGCCCGGCGGCTGGAGCTGGATGGATGGGTGAGATCTTACCG	537
Db	851	ATGCACTGGTGGCGGAGGACCTCGGACAGGCGCTCAGTGGATGGGAGGATGATCTCT	910
Qy	538	GGCTCTGGTAGCAGCAATATATCCGAAATTTAAAGACCGTCTTACTATGACGCGTGAC	597
Db	911	GGCAATGGTAATTAATTAATCCGACCTGTCTCTCCAGGCGAGGTGACTATAACAGCAGAC	970
Qy	598	ACTTCGACTAGTACATATACATGAGCTCTCCAGCTCGCATCGGAGGACGAGCGCGTC	657
Db	971	AGTTCATCAACACACCTACATGGAATCAGCAGCGCTGAGGTCTGACGACATCGCGTC	1030
Qy	658	TATTATTCGCGGTATTTTGTGTTCTAGCCCGAATTTGTTGATTTGATTTGTTGGGT	717
Db	1031	TATTACTGTTAGAGAGGTCTCTCTCTCCAGGCGGTGCTTTGGACTACTGGGT	1084
Qy	718	CAAGAACCTGGTCACTGT 737	
Db	1085	CAAGAACCTTAGTCACCGT 1104	

RESULT 2

LOCUS	AF329458	840 bp	mRNA	SYN	17-FEB-2001
DEFINITION		Synthetic construct SP-8C5 recombinant single chain Fv antibody			
ACCESSION		AF329458			
VERSION		AF329458.1	GI:12957383		
KEYWORDS					
SOURCE		synthetic construct.			
ORGANISM		synthetic construct			
REFERENCE		1 (bases 1 to 840)			
AUTHORS		Paul,S., Zhou,Y., Planque,S., Bangale,Y., Nishiyama,Y., Luo,J. and O'Connor-McCourt,M.			
TITLE		Binding of Native EGFR and Interference with EGFR Function by Antibodies to a Linear EGFR Peptide			
JOURNAL		Unpublished			
REFERENCE		2 (bases 1 to 840)			
AUTHORS		Paul,S., Zhou,Y., Planque,S., Bangale,Y., Nishiyama,Y., Luo,J. and O'Connor-McCourt,M.			
TITLE		Direct Submission			
JOURNAL		Submitted (18-DEC-2000) Pathology and Laboratory Medicine,			

University of Texas-Houston Medical School, 6431 Fannin, Houston,
TX 77030, USA

FEATURES
Location/Qualifiers

CDS

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/db_xref="taxon:32630"
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/transl_table=11
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BASE COUNT 203 a 221 c 234 g 182 t
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Query Match 41.6%; Score 310.6; DB 56; Length 840;
Best Local Similarity 66.9%; Pred. No. 1.3e-78;
Matches 493: Conservative 0; Mismatches 229; Indels 15; Gaps 3;

QY 7 GATATCCAGATGACCCAGTCCCTCCCTGTCGCGCTGTGGCGATAGGCTACC 66
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DB 61 ATCAGCTGGGGGCGGCGGAAACATCTATGGGCGCTGAACGTATCAACGTAACCT 120
QY 127 GGGAAAGCTCCGAGCTGTGATTTACGGTGCAGCAACCTGCGAGATGAGTCCCTCT 186
DB 121 GGGAAAGCTCCGAGCTGTGATTTACGGTGCAGCAACCTGCGAGATGAGTCCCTCT 180
QY 187 CGCTTCCTGATCCGCGCTCCGGAACGATTTCACTCTGACATCAGACCTTGCACCT 246
DB 181 AGCTTCAGTGGGAGTGAATCTGGGACAGATTTCACTCTGACATCAGACCTTGCACCT 240
QY 247 GAAAGACTTCGCTACGATTTACTGTCAGAACGTTTAAATCTCCGTTGACTTTCGACAG 306
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DB 298 GGGACCAAGTGAATTAACG---TACGCGGGTGGTGTCTGTCGCGGGTGGATCT 357
QY 364 GGTGCTGGGCTTCTCACTGTCGAATTCGCGGCGCGGAGGTCAAGAACCCAGGG 423
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LOCUS A18692 819 bp DNA PAT 06-JUL-1995
DEFINITION Synthetic nucleotide B72.3 single chain Fv hinge.
ACCESSION A18692
VERSION A18692.1 GI:513358
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 819)
AUTHORS
TITLE MULTIVALENT ANTIGEN-BINDING PROTEINS
JOURNAL Patent: WO 91/9739-A 26-26-DEC-1991;
FEATURES
Location/Qualifiers

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Best Local Similarity 66.3%; Pred. No. 7.9e-74;
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QY	7	GATATCCGATGAGACCAGGATCCCGGCTCCCTCCCTGTCGCGCTCTGTGGGCGATATAGGCTAC	66
Db	1	GACATCCAGATGACTCAGCTCAGTCTCCATCTCCCTGTCTCATCTGTAGGAGACAGAGTACT	60
QY	67	ATCACCTCGCGCGCCAGCAGGAAMAACATATATGCGCGCTGACACTGATGATATCAACGAATACCT	126
Db	61	ATCACTTTCGCGGGGAGTCAAGGACATTAATATAGCATATTTAAGTGGTTCACAGCAAMAACA	120
QY	127	GGGAAAGCTCCGAAGCTTCTGTATTTACGCTGCAGCAACCTGGCAGATGAGTCCCTTCT	186
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QY	187	CGCTCTCTGGATCCGGCTCGGAGAGGATTTTCACTCTGACCAATACACACTGCGACACT	246
Db	181	AGCTTCACTGGCACTGATCTCGGAGCAGATTAATACCTCAACCAATCAGCACTCTCAATAT	240
QY	247	GAAGACTCTCGTACGATATATCTGTGCAGACAGTTTAAATACTCCGTGTACCTTTCGCAG	306
Db	241	GAAGATTTTGAATTTATATATGTTCACACAGATATATGATCTCCGTGAGAGTTTCGGTGA	300
QY	307	GGTACCAAGGTGGAAATPAAACGTACTGCGGGGTGGTCTGTGTTGGCGGTGATCTGTT	366
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QY	487	GTCGCTCAGGCCCCCGGGCAGGCGCTGGAATGATGGGTAGATCTTACCGGGGCTCTGTT	546
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QY	547	AGCAACCGAATPACCGGAAATTTTAAAGACCGGTGTCTATNGACCGCTGACACTTCGACT	606
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QY	607	AGTACAGTATACATGAGAGCTCTCCAGCGCTGAGATCGAGAGACAGCGCGCTATATTATTCG	666
Db	595	AACACTGCTATTTACAGATCAACAGGCTCAGACCCGAGGACACAGCGCTGTGTATTTCTGT	654
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QY	727	CTGGTCACTGTCTGAGACTGA 747	
Db	703	ACGGTCAACGTTCTCTCATGA 723	

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DEFINITION	Sequence 89 from patent US 5756699.				
ACCESSION	AR010133				
VERSION	AR010133.1	GI:3968938			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 723)				
TITLE	Better,M.D., Carroll,S.F. and Studnicka,G.M.				
JOURNAL	Immunotoxins comprising ribosome-inactivating proteins				
FEATURES	Patent: US 5756699-A 89 26-MAY-1998;				
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BASE COUNT	178 a 162 c 207 g 176 t				
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Query Match	37.9%;	Score 283.4;	DB 9;	Length 723;
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QY	367	GGTGGCGGTGTCAAGTCCCACTGGTGCATTCGGGCGCGAGTGTCAAGAACCCAGGGGCC	426
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Db	703	ACGGTACCGTCTCCTATGA 723	

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DEFINITION	Sequence 89	from patent	US 5837491.	
ACCESSION	AR055339			
VERSION	AR055339.1	GI:5980916		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
ATTORNS	1 (bases 1 to 723)			
TITLE	Better M.D., Carroll, S.F. and Studnicka, G.M.			
JOURNAL	Polynucleotides encoding gelatin sequences			
	Patent: US 5837491-A 89 17-NOV-1998;			

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Best Local Similarity 63.7%; Pred. No. 9.1e-71;
Matches 472; Conservative 0; Mismatches 251; Indels 18; Gaps 2;
QY 7 GATATCCAGATGACCCAGTCCCTCCCTGTCGCGCTCTGTGGCGATAGGTACACC 66
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LOCUS 723 bp DNA PAT 26-JUL-1995
DEFINITION Sequence 92 from Patent US 5416202.
ACCESSION 111980
VERSION 111980.1 GI:909423
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
1 (bases 1 to 723)
Bernhard,S.L., Better,M.D., Carroll,S.F., Lane,J.A. and Lei,S.
Materials comprising and methods of preparation and use for
ribosome-inactivating proteins
Patent: US 5416202-A 92 16-MAY-1995;
Location/Qualifiers
1. .723
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BASE COUNT 178 a 162 c 207 g 176 t
ORIGIN
Query Match 37.9%; Score 283.4; DB 10; Length 723;
Best Local Similarity 63.7%; Pred. No. 9.1e-71;
Matches 472; Conservative 0; Mismatches 251; Indels 18; Gaps 2;
QY 7 GATATCCAGATGACCCAGTCCCTCCCTGTCGCGCTCTGTGGCGATAGGTACACC 66
Db 1 GACATCCAGATGACTCAGTCTCCATCTCCCTGTCGATCTAGGAGACAGATCACT 60
QY 67 ATCACTGCGCGCCAGCGAAACATCTATGGCGCTGAACCTGGTATCAACGTAACCT 126
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LOCUS 723 bp DNA PAT 13-MAY-1997
140550

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DEFINITION Sequence 89 from patent US 5621083.
ACCESSION I40550
VERSION I40550.1 GI:2082842
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 723)
AUTHORS Better,M.D., Carroll,S.F. and Studnicka,G.M.
TITLE Immunotoxins comprising ribosome-inactivating proteins
JOURNAL Patent: US 5621083-A 89 15-Apr-1997;
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Query Match      37.9%; Score 283.4; DB 10; Length 723;
Best Local Similarity 63.7%; Pred. No. 9,1e-71;
Matches 472; Conservative 0; Mismatches 251; Indels 18; Gaps 2;
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RESULT 10
LOCUS AX023363
DEFINITION Sequence 34 from Patent W0006605.
ACCESSION AX023363
VERSION AX023363.1 GI:10183775
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2871)
AUTHORS Kufer,P., Zettl,F., Dreier,T., Baeuerle,P.A. and Borschert,K.
TITLE Heteromibodies
JOURNAL Patent: WO 0006605-A 34 10-FEB-2000;
KUFER PETER (DE) ; ZETTL FLORIAN (DE) ; DREIER NORSTEN (DE) ;
BAEUDERLE PATRICK A (DE) ; BORSCHERT KATRIN (DE) ; MICROMET GES FUER
BIOMEDIZINIS (DE)
FEATURES
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BASE COUNT    598 a      868 c      834 g      571 t
ORIGIN
Query Match      35.6%; Score 266; DB 9; Length 2871;
Best Local Similarity 64.4%; Pred. No. 9,1e-66;
Matches 433; Conservative 0; Mismatches 220; Indels 9; Gaps 2;
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Db	748	GTGCG 752	
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LOCUS	XXU49832 902 bp mRNA SYN 24-MAR-1996		
DEFINITION	Synthetic single chain Fv antibody against potato virus V coat protein, mRNA, partial cds.		
ACCESSION	U49832		
VERSION	U49832.1 GI:1236090		
KEYWORDS	synthetic construct.		
SOURCE	synthetic construct		
ORGANISM	artificial sequence.		
REFERENCE	1 (bases 1 to 902)		
AUTHORS	Chen,Z.C., Cockburn,W., Torrance,L., Barker,H. and Whitelam,G.C.		
TITLE	Cytoplasmic accumulation of a soluble functional scfv protein to a plant virus expressed as a thioredoxin fusion in <i>Escherichia coli</i>		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 902)		
AUTHORS	Chen,Z.C., Cockburn,W., Torrance,L., Barker,H. and Whitelam,G.C.		
TITLE	Direct Submission		
JOURNAL	Submitted (23-FEB-1996) 2 C. Chen, Botany, Univ. of Leicester, University Road, Leicester LE1 7RH, UK		
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BASE COUNT	223 a	239 c	234 g 206 t
ORIGIN			
Query Match	34.6%;	Score 258.6;	DB 56; Length 902;
Best Local Similarity	61.4%;	Pred. No. 1.3e-63;	
Matches 482;	Conservative 0;	Mismatches 249;	Indels 54; Gaps 2;
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QY	61	GTCCACCATCACCTGTGGCGCCAGCAAAACATCTATGTGGCGCTGAACTGGTATCAACGT	120
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QY	121	AAACCTGGGAAGCTCCGAAGCTTCTGATTACGGTTCGAGCAACCTGGCAGATGGAGTC	180
Db	130	AAACAGGAAATCTCTCAGCTCCCTGGTCTATAGTGGCAAAACCTTAGCAGAAGGTGTG	189
QY	181	CVTTCTCGCTTCTCTGGATCCGCTCCGGAACGATTCTACTCTGACCATCAGCAGCTGTG	240
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QY	241	CAGCCTGAAGACTTCGCTAGTATTTACTGTGCAACGTTTAAATATCTCGTGTGACTTTC	300
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Db	730	GACTATAG-----GAACGACCCCTTTGACTTTTGGGGCCAGGCACCACTCTCACA	780
QY	736	GTCTC 740	

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2001, 00:48:12 ; Search time 1948.2 Seconds
(without alignments)
3624.516 Million cell updates/sec

Title: US-08-487-283A-8
Perfect score: 747
Sequence: 1 ATGGCCGATTCAGATGAC.....TGGTCACTGTCTCAGCTGA 747

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 segs, 4726426750 residues
Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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67	ATCACCTGCGGGCGCCAGGAAGAAACATCTATGGCGGGCTGAACTGATCAACGTAACT	0	0	93	Indels	0	Gaps	0	
83	ATCACCTGCGGGCGCCAGGAAGCAATGACAGCACTTATTAATTGGTATCAGAGAAACCA	0	0	93	Indels	0	Gaps	0	
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203	AGGTTCAGTGGCAGTGGAGATCTGGGACAGATTTCACTCTACCATCAGCAGGTCTGAACT	0	0	93	Indels	0	Gaps	0	
247	GAAAGCTTGGTACGTATTTACTGTGAGAACGTTTAAATCTCCGTTGACTTGGGACAG	0	0	93	Indels	0	Gaps	0	

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES - source

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/note="Vector: p7T3-Pac; Site.1: Site.2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
157 c 143 q 128 t

BASE COUNT	138 a	157 c	143 g	128 t
ORIGIN				

Query Match 24.7%; Score 184.6; DB 115; Length 566;
Best Local Similarity 71.1%; Pred. NO.2.9e-46;
Matches 244; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY	7	GATATCCAGATGACCCAGTCCCGTCTCCCTGTCCGCTCTCTGGCGGATAGGGTCACC	66
Db	65	GATATCCAGATGACCCAGTCTCCATCTCCCTGTCCGATCTCTGAGAGACAGAGTCACC	124
QY	67	ATCACCTGCGGGCCAGCGAAAAATCTATGCGCGCGTGAACCTGGTATCAACGTAAACCT	136
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QY	127	GGGAAGCTCCGAAGCTTCTGATTTACGGTCCGACGAACTGGCAGATGGAGTCCCTTCT	186
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QY	247	GAAGACTTCCCTAGGTATTACTGTCCAGAACGTTTTAAATCTCCGTTGACTTTCGGACAG	306
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LOCUS	864 bp	mRNA
DEFINITION	602575248F1 NTH_WGC_77 Homo sapiens cDNA clone IMAGE:4703483 5', mRNA EST	04-APR-2001
ACCESSION	BG548281	
VERSION	BG548281.1	GI:13546946
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
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REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
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Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 864)
NIH-MGC <http://mgc.ncbi.nlm.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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High quality sequence stop: 726.

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2. Feature 2	Source 2
3. Feature 3	Source 3
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5. Feature 5	Source 5
6. Feature 6	Source 6
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50. Feature 50	Source 50
51. Feature 51	Source 51
52. Feature 52	Source 52
53. Feature 53	Source 53
54. Feature 54	Source 54
55. Feature 55	Source 55
56. Feature 56	Source 56
57. Feature 57	Source 57
58. Feature 58	Source 58
59. Feature 59	Source 59
60. Feature 60	Source 60
61. Feature 61	Source 61
62. Feature 62	Source 62
63. Feature 63	Source 63
64. Feature 64	Source 64
65. Feature 65	Source 65
66. Feature 66	Source 66
67. Feature 67	Source 67
68. Feature 68	Source 68
69. Feature 69	Source 69
70. Feature 70	Source 70
71. Feature 71	Source 71
72. Feature 72	Source 72
73. Feature 73	Source 73
74. Feature 74	Source 74
75. Feature 75	Source 75
76. Feature 76	Source 76
77. Feature 77	Source 77
78. Feature 78	Source 78
79. Feature 79	Source 79
80. Feature 80	Source 80
81. Feature 81	Source 81
82. Feature 82	Source 82
83. Feature 83	Source 83
84. Feature 84	Source 84
85. Feature 85	Source 85
86. Feature 86	Source 86
87. Feature 87	Source 87
88. Feature 88	Source 88
89. Feature 89	Source 89
90. Feature 90	Source 90
91. Feature 91	Source 91
92. Feature 92	Source 92
93. Feature 93	Source 93
94. Feature 94	Source 94
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96. Feature 96	Source 96
97. Feature 97	Source 97
98. Feature 98	Source 98
99. Feature 99	Source 99
100. Feature 100	Source 100

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1. 864
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="NIH_MGC_77"
/clone_lib="NIH_MGC_183"
/lab_host="DH10B (T1 phage-
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="NIH_MGC_77"
/clone_lib="NIH_MGC_183"
/lab_host="DH10B (T1 phage-
/note="organ: lung; Vector:
SfiI (ggccgcctggcc); Site_
3' adaptors were used in cl
sequence: 5'-CACGCCCATTTG
5'-ATTCTAGAGCCGAGCGGCCG
C, or G and N = A, C, G, o
kb (range 0.5-4.0 kb). 12/11
by PCR. This library was en
and was constructed by Clont
CA). Note: this is a NIH_MGC
253 c 209 g 187 t

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[illegible]

Query Match	24.7%;	Score 184.6;	DB 155;	Length 864;
Best Local Similarity	71.1%;	Pred. No. 3.3e-46;		
Matches 244;	Conservative 0;	Mismatches 99;	Indels 0;	Gaps 0;
7	GATATCCAGATGACCCAGTCCCGCTCCCTGTGCGGCTCTGTGGCGGATAGGGTCACC	66		
93	GACATCCAGATGACCCAGTCTCCATCTCTCCCTGTGTCATCTGTAGGACAGAGTCACC	152		
67	ATCACCTCGGGGCCAGCGAAACACTCTATGCGGGCTGAACTGCTATCAACGTAACACT	126		
153	ATCACTTGGCGGCAAGTACAGCATTAGCACTATTTAAATTGTTATCAGCAGAAACCA	212		
127	GGAAAGCTCCGAAGCTTCTGATTTACGGTGGCGAGAACTGGCAGATGGAGTCCTTTCT	186		
213	GGAAAGCCCTTAAGATCCTGATCTATGGTGCATCCAGTTTCAAGTGGGTCCCATCA	272		
187	CGCTTCTTGATCCGGCTCCGGAAGGATTTCACTCTGACCATCAGCAGTCTGCAGCT	246		
273	AGGTTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACT	332		
247	GAAGACTTCGGCTACGTTACTGTCTCAGAACGTTTTAAATCTCCGTTGACTTTCCGACAG	306		
333	GRAGATTTTGCACTTACTGTCTCAGACAGCTTACACTACACCCTCACTTTCGGCGGA	392		
307	GGTACCAGGTGGAATAAAACGTACTGGCGGTGGTGGTTCTG	349		
393	GGGACCAAGGTGGAGATCAAAAGAACTTGGCTGCACCACTTC	435		

RESULT 8

RESULT	8
BG341934	
LOCUS	
DEFINITION	BG341934 957 bp mRNA EST 27-FEB-2001
ACCESION	G0246327.GF1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4576170.5,
VERSION	mRNA sequence.
	BG341934
	BG341934.1 GI:13148372

KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE	1 (bases 1 to 957)
JOURNAL	NIH-MGC http://mgc.ncl.nih.gov/ .
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabbs-remail.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://Image.lnl.gov Plate: L10M1288 row: 9 column: 19 High quality sequence stop: 673.
FEATURES	Location/Qualifiers
Source	1..957
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	/db_xref="taxon:9606"
	/clone="IMAGE:4576170"
	/clone_lib="NIH_MGC_48"
	/tissue_type="Primary B-cells from tonsils (cell line)"
	/lab_host="DH10B (phage-resistant)"
	/note="Organ: B-cells; Vector: pOTB7; Site.1: XhoI; Site.2: EcoRI; cDNA made by oligo-dT priming. directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGAG(G). Size-selected >500bp for average insert size 1.kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA Synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT	242 a 266 c 231 g 217 t 1 others
ORIGIN	
Query Match	24.7%; Score 184.6; DB 152; Length 957;
Best Local Similarity	71.1%; Pred. No. 3,4e-46;
Matches	244; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
QY	7 GATATCCAGATGACCCAGTCCCGCTCCCTGTCGGCTGTGGGCGATAGGGTCACC 66
Db	
QY	53 GACATCCAGATGACCCAGTCCCGCTCCCTGTCGGCTGTGGGCGATAGGGTCACC 112
Db	
QY	67 ATCACCCTGGCGCGCCAGGAAACATCTATGCGCGCTGAAGTGGTATCAACGTAACT 126
Db	
QY	113 ATCACCCTGGCGCGCCAGGCGCATTAACAATTTTATGACCTGGTATCAGCAGAACTA 172
Db	
QY	127 GGGAAAGCTCCGAACCTCTGTATTAAGGTGGAGCAACCTGGCAGATGGAGTCCCTCT 186
Db	
QY	173 GGGAAAGTCTTAACCTCTGTATTAAGGTGGAGCAACCTGGCAGATGGAGTCCCTCT 232
Db	
QY	187 CGCTTCTGTGATCCGCTCCGGAAGGATTTCACTGTGACCATCAGCAGTGTGACGCT 246
Db	
QY	223 CGGTTCAAGTGGAGTGGCTGGGACAGATTTCATCTCCACATCAGCAGCCTTGACGCT 292
Db	
QY	247 GAAGACTTCGCTAGCTATTACTGTGAGAAGCTTTTAAATCTCGTGGACTTTGGACAG 306
Db	
QY	293 GAAGATGTTGGAAACTTATTACTGTCAAAAGTATTAACACTGCCCCCTCAGACAGCTTGGCCAA 352
Db	
QY	307 GGTACCAAGGTGGAATAAAGCTCTGGCGGTGGTGGTCTG 349
Db	
QY	353 GGGACCAAGGTGGAATAAAGCTCTGGCGGTGGTGGTCTG 395
Db	
RESULT	9
LOCUS	BG341941 959 bp mRNA EST 27-FEB-2001

[illegible]

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RESULT 10
AW404714      608 bp      mRNA      EST      16-FEB-2000
LOCUS
DEFINITION
IMAGE:3058580 5', mRNA sequence.
ACCESSION
AW404714
VERSION
AW404714.1   GI:6923771
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 608)
AUTHORS
NIH-MGC http://mgi.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES
source
Location/Qualifiers
1..608
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/clone="IMAGE:3058580"
/clone_lib="NIH_MGC_37"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/lab_host="MGC85"
/notes="Vector: p7T3-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT
158 a 169 c 146 g 135 t

Query Match 24.5%; Score 183.2; DB 115; Length 608;
Best Local Similarity 71.2%; Pred. No. 8.le-46;
Matches 242; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 10 ATCCAGATGACCCAGTCCCGTCTCCCTGTCGCGCTCTGTGGCGGATAGGCTACCATC 69
Db 45 ATCCAGATGACCCAGTCCCGTCTCCCTGTCGCGCTCTGTGGCGGATAGGCTACCATC 104

QY 70 ACCTGCGCGCCAGCGAAACATCTATGGCGGCTGAACCTGGTATCAACGTAACCTGGG 129
Db 105 ACTTGCGGGCAAGTCAGAGCATATAGCAGCTATTAAATTGGTATCAGCAGAAATCAGG 164

QY 130 AAAGCTCGGAAGCTTGTGATTACGGTGGGAGAACCTCGGAGGATGGAGTCCCTTCGCG 189
Db 165 AAAGCCCTTAACCTCCCTGATCTATGCTGCATCCAGTTTGCAGAAATGGGTCCATCAAG 224

QY 190 TTCTCTGATCCGCTCGGAGCGGATTTCACTCTGACCATCAGCAGTCTGAGGCTGAA 249
Db 225 TTGAGTCGAGTGTGATCTGGGAGAGATTTCACTCTCAACATCAGGAGTCTGCAACCTGAA 284

QY 250 GACTTCGCTAGCTATTACTGTGACAGACGTTTAAATACTCTCCGTTGACTTTCGACAGGCT 309
Db 285 GATTTCGAACTACTTCTGTGACAGAGATTTCACCTACCCCGTACAGTTTTCGCGGAGG 344

QY 310 ACCAAGGTGGAAATAAAGCTACTGCGGCTGGTGTCTG 349
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Db 345 ACAGACTGGAGATCAACGAAGTGTGGTGCACCATCTG 384

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RESULT 11
AW406886      431 bp      mRNA      EST      16-FEB-2000
LOCUS
DEFINITION
IMAGE:3061499 5', mRNA sequence.
ACCESSION
AW406886
VERSION
AW406886.1   GI:6925943
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 431)
AUTHORS
NIH-MGC http://mgi.nci.nih.gov/.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES
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Location/Qualifiers
1..431
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/clone_lib="NIH_MGC_37"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/lab_host="DH10B (LT1)"
/notes="Vector: p7T3-Pac; Site 1: NotI; Site 2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT
101 a 125 c 105 g 100 t

Query Match 24.5%; Score 183; DB 115; Length 431;
Best Local Similarity 70.8%; Pred. No. 8.5e-46;
Matches 243; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 7 GATATCAGATGACCCAGTCCCGTCTCCCTGTCGCGCTCTGTGGCGGATAGGTCACC 66
Db 60 GATATCAGATGACCCAGTCCCGTCTCCCTGTCGCGCTCTGTGGCGGATAGGTCACC 119

QY 67 ATCACTCGCGCGCCAGCGAAACATCTATGGCGGCTGAACCTGGATCAACGTAACCT 126
Db 120 ATCACTCGCGCGCGCGAGTCAGAGCATATAGCAGCTTTTAAATTGGTATCAGCAGAAACCA 179

QY 127 GGGAAAGCTCCGAAGCTTCTGATTACGGTGGCAGCAACCTGGCAGATGAGTCCCTTCT 186
Db 180 GGGAAAGCCCTCAGCTCCCTGATCTATGGAGCATCCAGTTTGCAAGTGGGTCCCATCA 239

QY 187 CGTTCTCTGATCGCGCTCCGGAACGGATTCTACTCTGACCATCAGCAGTCTGCGACCT 246
Db 240 AGTTTCAGTGGAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 299

QY 247 GAGACTTCGCTACGATTACTCTCAGAACGTTTAAATACTCCGTTGACTTCGGGACAG 306
Db 300 GAAGATTTTGCACCTTACTACTGTCAACAGAGATTACACCTCCCTCGCATCTTCGGGGGA 359
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Db	438	ATCAAGGTTACAGCGCAGTGTGATCGGACAGAAATTCACCTCTCACAATCAACAGCCTGCA	379
Qy	243	GCCCTGAAGACTTCGCTAGCTATTACTGTCGACAAAGCTTTTAAATACCTCGTTGACTTTTCGG	302
Db	378	GCCCTGAAGATTTTGCACCTTATTGCTTCACATAGTACTTACCTCGGACTTTTGG	319
Qy	303	ACAGGGTACCAAGGTGGAATAAACAACCTACTGGGGTGGTGGTCTG	349
Db	318	CCAGGGACCAAGCTGGAGATCAACGAACCTGTGGCTGCACCATCTG	272
RESULT	15		
LOCUS	BG539961	867 bp	mRNA EST 03-APR-2001
DEFINITION	602567476F1 NIH_MGC_77	Human sapiens cDNA clone IMAGE:4692138	5', mRNA sequence.
ACCESSION	BG539961		
VERSION	BG539961.1	GI:13532194	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Human sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	NIH-MGC (bases 1 to 867)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: ccapbs@mail.nih.gov Tissue Procurement: CLONTECH Laboratories, Inc. cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: L12CM1512 row: g column: 19 High quality sequence stop: 704.		
FEATURES	source		
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	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:4692138"		
	/clone_lib="NIH_MGC_77"		
	/lab_host="DH10B (T1 phage-resistant)"		
	/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site:1: SfiI (ggccattatggcc); Site:2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGCGCATATGGC-3' and 3' adaptor sequence: 5'-ATTCTAGACGCGGAGCGGCGGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."		
BASE COUNT	241 a 250 c 217 g 159 t		
ORIGIN			
Query Match	24.3%	Score 181.6; DB 155; Length 867;	
Best Local Similarity	70.9%	Pred. No. 2.8e-45;	
Matches	241; Conservative	0; Mismatches 99; Indels 0; Gaps 0;	
Qy	10	ATCCAGATGACCCAGTCCCGCTCTCCCTGTGCCGCTCTGTGGGGATAGGGTCAACATC	69
Db	91	ATCCAGTTGACCCAGTCTCCATCTCCCTGTCTGTCATCTGTAGGAGAGAGAGTCAACATC	150
Qy	70	ACCTGCGGCGCCAGGAAAAACATCTATGGCGCGCTGAACCTGGTATCAACGTAAACCTGGG	129
Db	151	ACTTGCGGGGCAAGTACGGGCACTAGCAGTCTTTAGCTGGTATCAGCAAAAAACAGGG	210
Qy	130	AAAGCTCGGAAGCTTCGATTATACGGTSCGACGAACCTGGCAGATGGAGTCCCTTCGCG	189

[illegible]

Search completed: July 20, 2001, 01:57:44
Job time: 4172 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2001, 01:24:47 ; Search time 181.81 Seconds

(Without alignments)
2579.850 Million cell updates/sec

Title: US-08-487-283A-8

Perfect score: 747
Sequence: 1 ATGCCCATATCCAGATGAC.....TGCTCTCTCTCGAGCTGA 747

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

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- 2: /SIDSI/gcgdata/geneseq/geneseqn/NA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	747	100.0	747	16	AAAT08480 Humanised CDR-graf
2	729.4	97.6	747	16	AAAT08488 Humanised CDR-graf
3	396.6	53.1	747	16	AAAT08479 Murine 5G1.1M1 scf
4	371	49.7	750	16	AAAT08484 Humanised 5G1.1 VH
5	358.2	48.0	750	16	AAAT08487 Humanised 5G1.1 VH
6	350.2	46.9	750	16	AAAT08483 Humanised 5G1.1 VH
7	328.8	44.0	726	16	AAAT10706 Humanised 5G1.1 VL
8	323.8	43.3	711	16	AAAT08486 Humanised 5G1.1 VL
9	322.4	43.2	726	16	AAAT08485 Humanised 5G1.1 VL
10	314.8	42.1	1612	22	AAAC86562 DNA encoding a fus
11	294	39.4	819	13	AAQ20381 Sequence encoding

12	290.6	38.9	1925	21	AAA15019	DNA encoding a CD-
13	290.4	38.9	1637	21	AAZ88358	Bispecific anti-ze
14	285.4	37.9	723	14	AAQ42284	V-J(Kappa)/I(Gly)4
15	269.4	36.1	1803	21	AAA58773	DNA encoding an Im
16	267	35.7	1065	18	AAAT94963	R. pipiens recombl
17	267	35.7	1065	18	AAAT94967	R. pipiens recombl
18	267	35.7	1074	18	AAAT94965	R. pipiens recombl
19	267	35.7	1074	18	AAAT94968	R. pipiens recombl
20	267	35.7	1086	18	AAAT94966	R. pipiens recombl
21	267	35.7	1137	18	AAAT94964	R. pipiens recombl
22	266	35.6	2871	21	AAZ50586	DC8scFv-erbB2EC fu
23	260.4	34.9	1457	21	AAA39167	Apoptobody3sc fusl
24	259	34.7	1630	21	AAZ50587	HD70scFv-CH1-GM-CS
25	259	34.7	1630	21	AAZ50588	HD70scFv-CK-interl
26	250	33.5	729	15	AAQ73679	Ev(GP-4) Immunosp
27	249.2	33.4	783	16	AAAT08490	Anti-C5 Mab N19/8
28	247.2	33.1	913	15	AAO81076	Bispecific CD3-L6f
29	245.2	32.8	1371	21	AAZ50584	M79scFv-interleuk1
30	245.2	32.8	1389	21	AAZ50585	M79scFv-interleuk1
31	242	32.4	1611	21	AAZ30332	Nucleotide sequen
32	241.6	32.3	925	21	AAZ58663	Antibody 4H5 H cha
33	241.6	32.3	925	21	AAZ44205	Murine derived DNA
34	239.6	32.1	1149	18	AAAT90514	DNA encoding chime
35	239.6	32.1	1212	18	AAAT90511	DNA encoding chime
36	238.6	32.1	1422	18	AAAT90509	DNA encoding chime
37	238.6	32.1	1545	18	AAAT90510	DNA encoding chime
38	239.6	32.1	1956	18	AAAT90512	DNA encoding chime
39	239.6	32.1	2079	18	AAAT90513	DNA encoding chime
40	238.6	31.9	1239	22	AAAC86563	DNA encoding a fus
41	236.6	31.7	733	20	AAV99766	A33/218 single-cha
42	236.6	31.7	733	20	AAZ37398	Linked fusion prot
43	236.6	31.7	1938	19	AAV58929	A33 chimeric recep
44	234.4	31.4	721	20	AAV99765	A33/212 single-cha
45	234.4	31.4	721	21	AAZ37397	Linked fusion prot

ALIGNMENTS

RESULT	1
ID	AAAT08480
XX	AAAT08480 standard; DNA; 747 BP.
AC	AAAT08480;
XX	
DT	15-MAR-1996 (first entry)
XX	
DE	Humanised CDR-grafted 5G1.1 scFv CB DNA.
XX	
KW	Complement C5; haemolysis; kidney; glomerulonephritis;
KW	monoclonal antibody; antiinflammatory; antibody engineering;
KW	humanised antibody; complementarity determining region; CDR;
KW	single chain antibody; scFv; ds.
XX	
OS	Synthetic.
XX	
FE	Key
FT	CDS
XX	
PN	W09529697-A1.
PD	09-NOV-1995.
XX	
PR	01-MAY-1995; 95WO-US05688.
XX	
PR	02-MAY-1994; 94US-0236208.
XX	
PA	(ALEX-) ALEXION PHARM INC.
XX	
PI	Evans MJ, Matlis L, Mueller EE, Nye SH, Rollins S;
PI	Rother RP, Springhorn J P, Squinto SP, Thomas TC;
PI	Wang Y, Wilkins JA;
XX	


```

OY 121 AACCTGGGAAGACTCCGAAGCTTCTGATTAGCGTCGACGAACCTGGCAGATGAGTGC 180
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Db 121 aaacctgggaagaactccgaagctcttgattacggtgcgaacacccggcagagagctc 180
OY 181 CCTTCGCTTCCTTCGGATCGGCTCCGGAAGCGATTCTACTGACCATCAGCAGCTG 240
    |||||||
Db 181 ccttcgcttccttcggatcggctccggaagcgattctactgaccatcagcagctc 240
OY 241 CAGCCTGAAGACTTCGCTACGATTATGTCAGAACGTTTTTAATACCTCGTTCATTTC 300
    |||||||
Db 241 cagcctgaagacttcgctacgtactactgtcagaacgttttaatactccgttgacttc 300
OY 301 GGACAGGGTACCAAGTGGAAATAAAACGTAAGTGGCGGTGCTTGGTGGCGGTGGA 360
    |||||||
Db 301 ggacagggtaaccaagtggaataaaaacgtactggcggtgtgtctgtggtcggtgga 360
OY 361 TCTGGTGGGAGCGGCTTCTCAAGTCCAACTGCTGCAATCCGCGCGGAGGTCGAAGGCA 420
    |||||||
Db 361 tctggtgggagcggtctctcaagtcctcaactgtgtcaatccgcggcgaggtccaaagcca 420
OY 421 GGGGCTCAGTCAAGTGTCTTAAAGCTAGCGGCTATATTTTCTAATTTATTTGAT 480
    |||||||
Db 421 ggggctcagtcgaagtgctctgttaaagctagcggtatatttcttaattatgtgatt 480
OY 481 CAATGGGTGCTAGAGCCCCCGGCGAGGCGCTGGAATGATGGTGAATCTTACCGGCG 540
    |||||||
Db 481 caatgggtgctagagccccggcgagcgctggaatgatgggtgaatctttaccggcg 540
OY 541 TCTGTAGAGACGGAATATACGAAATTTTAAAGACGCTGTACTATGACCGCGTACACT 600
    |||||||
Db 541 tctgtagagacggaatatatgcgaaatttttaaagacgctgtactatgacccggtacact 600
OY 601 TCGACTAGTACATATATAGATGAGCTCTCCAGCTCGCATCGAGACACGCGCTCTAT 660
    |||||||
Db 601 tcgactagatacataatagagctctccagctcgcatcgagagacagcgccgtctat 660
OY 661 TATTGCGCGCGTATTTTGTGTTCTAGCCCGAATTTGATTTGATTTGGGCTCAA 720
    |||||||
Db 661 tattgcgcggtattttgtgttctagcccgaaattgtattgtgtgtgtggtctaa 720
OY 721 GGAACCTGTGCTACTGTCTGACACTGA 747
    |||||||
Db 721 ggaacctgtgctactgtctgagactga 747

```

RESULT 3

AA08479 standard; DNA: 747 BP.

AC AA08479;

DT 15-MAR-1996 (first entry)

DE Murine 5G1.1M1 scFv DNA.

KM Complement C5; haemolysis; kidney; glomerulonephritis;
 KM monoclonal antibody; antinflammatory; antibody engineering;
 KM humanised antibody; complementarity determining region; CDR;
 KW scFv; single chain antibody; ds.

OS Mus sp.

EH Key Location/Qualifiers

FT CDS 1..747

PN W09529697-1.

XX 09-NOV-1995.

PF 01-MAY-1995; 95WO-US05688.

```

PR 02-MAY-1994; 94US-0236208.
XX
XX (ALEX-) ALEXION PHARM INC.
XX
XX Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;
PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;
PI Wang Y, Wilkins JA;
XX
XX WPI: 1995-392923/50.
DR P-PSDB: AAR77606.
XX
XX Treating glomerulonephritis with antibody against complement C5
PT component - to inhibit complement induced cell lysis
XX
XX Claim 24; Page 107-110; 181p; English.
XX
XX DNA (AA08479) coding for murine scFv 5G1.1M1 (AAR77606) was obt. by
CC PCR cloning of DNA from hybridoma ATCC HB 11625, the producer of
CC anti-C5 monoclonal antibody (MAb) 5G1.1. The DNA was subcloned into
CC pET 3c/SOS/Nr for expression in Escherichia coli. The light and/or
CC heavy chain CDRs of scFv 5G1.1M1 can be combined with CDRs from other
CC 5G1.1-derived antibodies, Fds and light chains (AAR77607-16) in the
CC prodn. of recombinant, including humanised, antibodies that retain
CC the ability of MAb 5G1.1 to block human complement C5a generation
CC and thus to reduce glomerular inflammation and kidney dysfunction
CC associated with glomerulonephritis.
XX
XX Sequence 747 BP; 183 A; 174 C; 211 G; 179 T; 0 other;
SQ

```

Query Match 53.1%; Score 396.6; DB 16; Length 747;
 Best Local Similarity 70.7%; Pred. No. 1.7e-101;
 Matches 528; Conservative 0; Mismatches 219; Indels 0; Gaps 0;

```

OY 1 ATGGCGAATATCCAGATGACCCAGTCCCGTCCCTCCGCTCGGCGGATGAG 60
    |||||||
Db 1 atggcgaaatattccagatgacccagtcccgctccgctcggcggaatgag 60
OY 61 GTACACATCACCTGGGCGCCAGCAAAACATCTATGGCGCGCTGAACGTATACAGT 120
    |||||||
Db 61 gtacacatcacctgggcgccagcaaaaacatctatggcgcgctgaacgtatagct 120
OY 121 AAACCTGGGAAAGCTCCGAACTTCTGATTACGGTGCAGACGACCTGCGAGTGA 180
    |||||||
Db 121 aaacctgggaaagctccgaacttctgattacgggtgcagacgacctgagtgagctg 180
OY 181 CCTTCTCGCTTCTGAGATCCGCGTCCGAGACGANTTACCTGACATCGACAGTCTG 240
    |||||||
Db 181 ccttctcgcttctgagatccgcgctccgagacganttacctgacatcgacagtctg 240
OY 241 CAGCCTGAAGACTTCGCTACGATTATGTCAGAACGTTTTTAATACCTCGTTCATTTC 300
    |||||||
Db 241 cagcctgaagacttcgctacgtactactgtcagaacgttttaatactccgttgacttc 300
OY 301 GGACAGGGTACCAAGTGGAAATAAAACGTAAGTGGCGGTGCTTGGTGGCGGTGGA 360
    |||||||
Db 301 ggacagggtaaccaagtggaataaaaacgtactggcggtgtgtctgtggtcggtgga 360
OY 361 TCTGGTGGGAGCGGCTTCTCAAGTCCAACTGCTGCAATCCGCGCGGAGGTCGAAGGCA 420
    |||||||
Db 361 tctggtgggagcggtctctcaagtcctcaactgtgtcaatccgcggcgaggtccaaagcca 420
OY 421 GGGGCTCAGTCAAGTGTCTTAAAGCTAGCGGCTATATTTTCTAATTTATTTGAT 480
    |||||||
Db 421 ggggctcagtcgaagtgctctgttaaagctagcggtatatttcttaattatgtgatt 480
OY 481 CAATGGGTGCTAGAGCCCCCGGCGAGGCGCTGGAATGATGGTGAATCTTACCGGCG 540
    |||||||
Db 481 caatgggtgctagagccccggcgagcgctggaatgatgggtgaatctttaccggcg 540
OY 541 TCTGTAGAGACGGAATATACGAAATTTTAAAGACGCTGTACTATGACCGCGTACACT 600
    |||||||
Db 541 tctgtagagacggaatatatgcgaaatttttaaagacgctgtactatgacccggtacact 600

```


QY 601 TCAGTACTACAGTATACATGAGCTCTCCAGCCTCGCATCGGAGGACACAGCCGCTCTAT 660
 Db 601 tctccaacacagcctacatcaactcagcagcctgacatcagagactctccgtctat 660
 QY 661 TATTGGCGCGCTTATTTTGGTTCAGCCGGAATGGTATTTTGGGGTCAA 720
 Db 661 tactgtcaagatatcttcggtagtagcccaactggtactctgctggtggtcgca 720
 QY 721 GGAACCTGGTCACTGCTCGAGCTGA 747
 Db 721 gggaccacggtcacgcgtctctcatga 747

RESULT 4

AAT08484

ID AAT08484 standard; DNA; 750 BP.

XX AAT08484;

XX 02-APR-1996 (first entry)

XX Humanised 5G1.1 VH + IGHRLC DNA.

XX Complement C5; haemolysis; kidney; glomerulonephritis;
 KW monoclonal antibody; antiinflammatory; antibody engineering;
 KW humanised antibody; complementarity determining region; CDR;
 KW ds.

XX Synthetic.

XX Key Location/Qualifiers

FH CDS 1..750

FT /*tag= a

FT sig_peptide 1..57

FT /*tag= b

FT mat_peptide 58..747

FT /*tag= c

XX WO9529697-A1.

XX 09-NOV-1995.

XX 01-MAY-1995; 95WO-US05688.

XX 02-MAY-1994; 94US-0236208.

XX (ALEX-) ALEXION PHARM INC.

XX Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;

PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;

PI Wang Y, Wilkins JA;

XX WPI; 1995-392923/50.

DR P-PSDB; AAR77611.

XX Treating glomerulonephritis with antibody against complement C5
 component - to inhibit complement induced cell lysis
 XX Claim 38; Page 123-125; 181pp; English.

XX A DNA construct (AAT08483) codes for a humanised CDR-grafted and
 framework sequence-altered Fd 5G1.1 VH + IGHRL (AAR77610), which
 includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1.
 The DNA can be subcloned together with DNA (AAT08484) coding for a
 humanised light chain (AAR77612) into vector APEX-3P (AAT08476) for
 expression of humanised antibody in human 293 EBNA cells. Such
 recombinant antibodies retain the ability of Mab 5G1.1 to block
 human complement C5a generation and thus to reduce glomerular
 inflammation and kidney dysfunction associated with
 glomerulonephritis.

XX Sequence 750 BP; 163 A; 220 C; 197 G; 170 T; 0 other;

Query Match 49.7%; Score 371; DB 16; Length 750;

Best Local Similarity 97.4%; Pred. No. 2.4e-94;

Matches 377; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 358 GGATCTGTGGTGGCGGTTCCTCAAGTCCAACTGCTGCAATCCGCGCCGAGGTCAAGAAG 417

Db 37 gtaactgcggcgctccactcccaagtccaactggtgcaatccggcgccgaggtcaagaag 96

QY 418 CCAGGGCCCTCAGTCAAGTGTCTCTAAAGCTAGCGGCTATATTTTCTAATATTGG 477

Db 97 ccagggcctcagtcacaagtgtctgtaaaagctagcggtatatttttctataattgg 156

QY 478 ATTCAATGGTGTGCTCAGGCCCGCGGCTGGAATGGGTGAGATCTTACCG 537

Db 157 attcaatgggtgcgtcagggcccccgggcctggaaatggatgggtgagatcttaccg 216

QY 538 GGCTCTGGTAGCACCGGAATATACCGAAATTTTAAAGACCGTGTACTATCACCGGTGAC 597

Db 217 ggctcgttagcacccgaataataccgaaaattttaaagaccgtgttactatgacgcgtgac 276

QY 598 ACTTCGACTAGTACAGTATACATGGAGCTCTCCAGCCTCGATCGGAGGACACGGCCGTC 657

Db 277 acttcgactagtagtatacatggagctctccagctcgatcgatcgagacacgcccgtc 336

QY 658 TATTATTGCGCGGTTATTTTGGTTCCTAGCCGGAATGGTATTTTGGGGT 717

Db 337 tattattgcgcgcttatttttttggcttcagcccggaattggtatttgcgttgggggt 396

QY 718 CAAGAACCCCTGGTCACTGCTCTCGAGC 744

Db 397 caagaaacctggtcactgctcgcagc 423

RESULT 5

AAT08487

ID AAT08487 standard; DNA; 750 BP.

XX AAT08487;

XX 02-APR-1996 (first entry)

XX Humanised 5G1.1 VH + IGHRLD DNA.

XX Complement C5; haemolysis; kidney; glomerulonephritis;
 KW monoclonal antibody; antiinflammatory; antibody engineering;
 KW humanised antibody; complementarity determining region; CDR;
 KW ds.

XX Synthetic.

XX Key Location/Qualifiers

FH CDS 1..750

FT /*tag= a

FT sig_peptide 1..57

FT /*tag= b

FT mat_peptide 58..747

FT /*tag= c

XX WO9529697-A1.

XX 09-NOV-1995.

XX 01-MAY-1995; 95WO-US05688.

XX 02-MAY-1994; 94US-0236208.

XX (ALEX-) ALEXION PHARM INC.

XX Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;

PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;

PI Wang Y, Wilkins JA;

CC expression of humanised antibody in human 293 EBNA cells. Such
 CC recombinant antibodies retain the ability of Mab 5G1.1 to block
 CC human complement C5a generation and thus to reduce glomerular
 CC inflammation and kidney dysfunction associated with
 CC glomerulonephritis.
 XX
 SQ Sequence 711 BP; 174 A; 206 C; 183 G; 148 T; 0 other:

Query Match 43.3%; Score 323.8; DB 16; Length 711;
 Best Local Similarity 96.5%; Pred. No. 3,7e-81;
 Matches 331; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 7 GATATTCAGATGACCAAGTCCCGTCCCTGTCGCGCTGTGGCGATAGGATCAC 66
 DB 67 gatatacagatgacccagctccgcctcctgctgcgcctctggygcgataggatacc 126
 QY 67 ATACCTGGCGGCGCCAGCAAAACATATAGGCGCGCTGAACCTGATCAACGTAACCT 126
 DB 127 atcaactgcgycgcagcgaatacatctatgycgcgtgactggtatcaacagaataacc 186
 QY 127 GGGAAAGCTCCGAAGCTTCGATTACGATGCGAGCAAGCTGCGAGATGAGTCCCTTCT 186
 DB 187 gggaaagctccgaagcttcctgattacggtgcgaagaaactgacagatgagtccttct 246
 QY 187 CGCTTCTGATCCGCGCTCCGGAACGATTTCACTCTGACCATCAGCTGCAGCCT 246
 DB 247 cgtctctctgacgcgcgcgcgaagcagattcactctgacacacagcagctgcagcct 306
 QY 247 GAAGACTTCGCTACGATTTACTGTCAGAACGTTTAAATACTCCGTTGACTTTGGGACAG 306
 DB 307 gaagacttcgctacgattactcgtcagaacgttttaataactccgttgcgttcgacag 366
 QY 307 GGTACCAAGGTGGAATAAACGTACTGCGGCTGTGTTCTG 349
 DB 367 ggtaccaaggtggaataaacaagaactgtgctgcacacatctg 409

RESULT 9

AAT08485
 ID AAT08485 standard; DNA; 726 BP.

AC AAT08485;
 XX
 DT 15-MAR-1996 (first entry)
 XX
 DE Humanised 5G1.1 VL + KLV56 DNA.
 XX
 KW Complement C5; haemolysis; kidney; glomerulonephritis;
 KW monoclonal antibody; antiinflammatory; antibody engineering;
 KW humanised antibody; complementarity determining region; CDR;
 KW ds.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH 1..726
 FT /*tag- a
 FT sig_peptide 1..75
 FT /*tag- b
 FT mat_peptide 76..723
 FT /*tag- c
 XX
 PN WO9529697-A1.
 XX
 PD 09-NOV-1995.
 XX
 PF 01-MAY-1995; 95WO-US05688.
 XX
 PR 02-MAY-1994; 94US-0236208.
 XX
 PA (ALEX-) ALEXION PHARM INC.
 XX

PI Evans MJ, Matis L, Mueller EF, Nye SH, Rollins S;
 PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;
 PI Wang Y, Wilkins JA;
 XX
 DR WPI: 1995-392923/50.
 DR P-PSDB; AAT08485.
 XX

PT Treating glomerulonephritis with antibody against complement C5
 PT component - to inhibit complement induced cell lysis
 XX
 PS Example 11; Page 126-128; 181pp; English.
 XX

CC A DNA construct (AAT08485) codes for a humanised CDR-grafted and
 CC framework sequence-altered light chain, 5G1.1 VL + KLV56 (AAR7612),
 CC which includes CDRs derived from mouse anti-C5 monoclonal antibody
 CC 5G1.1. The DNA can be subcloned together with DNA (AAT08483) coding
 CC for a humanised Fd (AAR7610) into vector APEX-3P (AAT08476) for
 CC expression of humanised antibody in human 293 EBNA cells. Such
 CC recombinant antibodies retain the ability of Mab 5G1.1 to block
 CC human complement C5a generation and thus to reduce glomerular
 CC inflammation and kidney dysfunction associated with
 CC glomerulonephritis.
 XX

SQ Sequence 726 BP; 176 A; 207 C; 186 G; 157 T; 0 other:

Query Match 43.2%; Score 322.4; DB 16; Length 726;
 Best Local Similarity 95.4%; Pred. No. 9,2e-81;
 Matches 332; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 2 TGGCCGATATCCAGATGACCCAGTCCCTGCTCCGCTGTGGCGATAGG 61
 DB 77 tgcagatataccagatgaccagctccctcctcctgctgcgcctctgtgycgatagg 136
 QY 62 TCACATACCTCGCGCGCGCCAGCAAAACATATAGCGCGCTGAACCTGATCAACGTA 121
 DB 137 tcaccatacactgcgycgcgcgaataacatctatgycgcgtgaaactggtatacagta 196
 QY 122 AACCTGGGAAGCTCCGAAGCTTCGATTACGATGCGAGCAAGCTGCGATGAGTCC 181
 DB 197 aacctgggaagctccgaagcttcgatttaacggtgcgaacacctggaagtgaagtc 256
 QY 182 CTTCGCTTCTCTGATCCGCGCTCCGGAAGGATTTCACTGTGACCATCAGCTGTC 241
 DB 257 ctctcgtctctctgatacgcgctccggaacgattacactctgacacacagctctgc 316
 QY 242 AGCCTGAAGACTTCGCTAGCTATTAATCTGATGAGCAAGCTTTAAATACTCCGTTGACTTCG 301
 DB 317 aacctgaagacttcgctactactctgcagaacgttttaataactccgttgcacttcg 376
 QY 302 GACAGGATCAAGGTGGAATAAACGTACTGCGGCTGTGTTCTG 349
 DB 377 gacaggtaccagaagtggaaataaacaagaactgtgctgcacacatctg 424

RESULT 10

AAC86562
 ID AAC86562 standard; DNA; 1612 BP.

AC AAC86562;
 XX
 DT 02-APR-2001 (first entry)
 XX
 DE DNA encoding a fusion of single chain antibody/streptavidin.
 XX
 KW Streptavidin; tumour cell; cancer; adenocarcinoma;
 KW hematological malignancy; hnuR-LU-10; EGP40; EPCAM; ss.
 XX
 OS Synthetic.
 OS Streptomyces avidinii.
 OS Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH

Db 719 gtcgaagatgagctactatagcactatccgtcccttgctactggygccaag 778
Qy 722 GAACCCGTGCTACTGTCCTGAGCTGA 747
Db 779 gcactctgctactgctctccgga 804

RESULT 14
AA042284
ID AA042284 standard; CDNA; 723 BP.
XX
AC AA042284;
XX
DT 13-SEP-1993 (first entry)
XX
DE V-(kappa)/[(G1y)4Ser]3/V-(gamma) single chain antibody.
XX
DE Type I ribosome-inactivating protein; ricin; gelonin;
XX immunonjugate; autoimmune disease; cell killing; toxin;
XX overlap extension polymerase chain reaction; H65 variable region;
XX RMA; rabbit muscle aldolase; cathepsin cleavage;
XX SLT; E.coli Shiga-like toxin; human engineered antibody; ss.
OS Synthetic.
XX
PN W09309130-A.
XX
PD 13-MAY-1993.
XX
PE 04-NOV-1992; 92MO-US09487.
XX
PR 04-NOV-1991; 91US-0787567.
XX
PR 19-JUN-1992; 92US-0901707.
XX
XX (XOMA) XOMA CORP.
PA
XX
PI Bernhard SL, Better MD, Carroll SF, Lane JA, Lei SP;
XX
XX WPI; 1993-167617/20.
XX
XX Analogues of type I ribosome inactivating protein - useful as
XX cytotoxic agents, immuno toxins for treating autoimmune diseases,
XX cancer, graft versus host disease and selective cell killing in-vivo
XX
XX Example 12; Page 123-124; 163pp; English.
XX
XX A single chain antibody form of the he3 H65 variable domain was
XX assembled from previously constructed genes. This scab segment
XX consisted of the entire V and J region of one chain (heavy or
XX light) linked to the entire V and J segment of the other (light or
XX heavy) via a 15 amino acid flexible peptide. The scab was assembled
XX in two orientations (see AA042284 and AA042285). A fusion construct was
XX prepared in which the natural sequence gelonin gene was positioned
XX at the N-terminus and the SLT or RMA linker peptide was positioned
XX between the gelonin and scab domains.
XX
XX Sequence 723 BP; 178 A; 162 C; 207 G; 176 T; 0 other;
XX

Query Match 37.9%; Score 283.4; DB 14; Length 723;
Best Local Similarity 63.7%; Pred. No. 7.3e-70;
Matches 472; Conservative 0; Mismatches 251; Indels 18; Gaps 2;

Qy 7 CATATCCAGATACCCAGTCCCGTCTCCGCTCTGCTGGCGGAGGTCACC 66
Db 1 gacatccagatgactcactcctcctcctgctcgtcgtacgagacagact 60
Qy 67 ATCAGCTGGGGCGGCAAGAAACATCTATGCGGCGCTGAACGTATCAAGTAACT 126
Db 61 atcacctccgggagcagcagacataatagcatltaagcgggtccagcgaacca 120
Qy 127 GGAAGAGTCCGAGACCTTGTACGTTGCGAGCAGAACCTGGCAATGAGTCCCTTCT 186
Db 127 GGAAGAGTCCGAGACCTTGTACGTTGCGAGCAGAACCTGGCAATGAGTCCCTTCT 186

Db 121 gggaaagctcctaagaccctgatctatcgtgcaaacagattggaatctgggtcccatca 180
Qy 187 CGCTTCTCTGATCCGGCTCCGGAACGATTTCACTGTACCATAGACATGTGAGCCT 246
Db 181 aggttcagtgagcagtgatcctcgagacagattactcctccatcagcagcctgcaaat 240
Qy 247 GAAGACTTCGCTAGCTATTACTGTCAAGACGTTTAAATACCTCGTACTTTCGACAG 306
Db 241 gaagatttgaattatlatitgtaacagatgatgatgcctcggtgagcttggtga 300
Qy 307 GGTACCAAGGTGGAATTAACGTACTGCGGTGCTGCTTCTGCGGGGTGATCTGCT 366
Db 301 ggcaccaaagcttgatgataa-----gttgcggtgagcttggtgaggtggtcgga 354
Qy 367 GGTGCGGTCTCAAGTCAACCTGATCGAATCCGCGCCGAGTCAAGAACCCAGCGCC 426
Db 355 ggtgagagatctgagatcagcttggtgagcttggaagagcctgtgagcctggaagg 414
Qy 427 TCAGTCAAGTGTCTCTGTAACGTAGCGGCTATATTTTCTAATTATTTGATTCATAG 486
Db 415 tccgtcgaatctcctcgtgcagctctggtatatacttcaacaactatggaatgaa 474
Qy 487 GTGCGTCAAGCCCGCGGAGGCGCTGGAATGATGATGATCTTACCGGCTCTGCT 546
Db 475 gtgcgccaagctccaggaaggtttagatggtgctggtatataacaccacactgga 534
Qy 547 AGCACGAATATACCGAAATTTTAAAGACCGTGTACTATGACCGTGCACATTCGACT 606
Db 535 gagccaacataatgctgattcttcaaggagcgttacccttcttgtagacattctaa 594
Qy 607 AGTACATATACATGAGACTCTCCAGCTCGATGGAGAGACGCGCTATATATTCG 666
Db 595 aacactgcctatttcaagatcaacagcctcagagcgagacagcgtgtgatttcgt 654
Qy 667 GCGGTTATTTTGTGTTAGCCCAATGATGTTTGTGATGTTGGGTCGAAGAAC 726
Db 655 acaagcagggttacg-----actgtacttcgagtgctggtggtgccaaggacc 702
Qy 727 CTGCTCACTGCTCGAGCTGA 747
Db 703 acgttcacgctcctcatga 723

RESULT 15
ID AA58773 standard; DNA; 1803 BP.
XX
XX AA58773;
XX
XX 20-OCT-2000 (first entry)
XX
XX
XX DNA encoding an immunotoxin comprising a CD3 binding domain and PE28.
XX
XX Immunotoxin; CD3-binding domain; Pseudomonas exotoxin A; immune system;
XX scfv(UCHL-1)-PE28; T-cell mediated disease; transplant rejection;
XX host versus graft disease; graft versus host disease;
XX bone marrow transplant; ss.
XX
XX Synthetic.
XX
XX Mus sp.
XX Pseudomonas aeruginosa.
XX
XX W0200041474-A2.
XX
XX 20-JUL-2000.
XX
XX 13-JAN-2000; 2000MO-EP00245.
XX
XX 15-JAN-1999; 99US-0232445.
XX
XX 25-JAN-1999; 99US-0236968.
XX
XX 07-OCT-1999; 99US-0414134.
XX
XX (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

PI Digan ME, Lake P, Wright RM;

DR WPI; 2000-482739/42.
DR P-PSDB; AAB07461.

DR P-PSDB; AAB07461.

PT Recombinant immunotoxin used for prophylaxis and treatment of T-cell mediated diseases e.g. transplantation rejection -

PS Disclosure; Page 55-59; 75pp; English

CC The present sequence encodes a recombinant immunotoxin comprising a
CC CD3-binding domain and a Pseudomonas exotoxin A component. It is
CC designated scFv(UCHL1)-PE28. The immunotoxins of the invention are
CC used for the prophylaxis or treatment of T-cell mediated diseases or
CC conditions of the immune system. They are also used to condition a
CC patient to be transplanted with cells, or a tissue or an organ of a
CC donor and for the prophylaxis and/or treatment of acute or chronic
CC transplantation rejection, host versus graft disease and/or graft
CC versus host disease in a patient to undergo a bone marrow transplant,
CC where the CD3-bearing cell population in the patient is depleted and
CC an inoculum comprising isolated bone marrow and/or stem-cell enriched
CC peripheral blood cells of the donor treated with immunotoxin is
CC inoculated into the patient.

Sequence 1803 BP; 363 A; 575 C; 567 G; 298 T; 0 other;

Query Match	36.18;	Score 269.4;	DB 21;	Length 1803;
-------------	--------	--------------	--------	--------------

Best Local Similarity 0.18; Pred. NO. 88-00;
Matches 454; Conservative 0; Mismatches 286; Indels 3; Gaps 1.

QY	1	ATGGCCCATATCCGAGTACCGCAATCCCGCTCCCTCCCTCCGCTGTCGCGCTGTGGGGGAGT	60
Db	1	atggcgacatcccaatgacacccagaccactctccctgctgcctcttcggygaaga	60
QY	61	GTCACATCACTCGCGGCCACGAAACATCTATGCGCGCTGAACCTGGTATCAAGT	120
Db	61	gtccaccatcagtttcaggagcaagtcagagacattagaattatctaacttgaactgatlcaacag	120
QY	121	AAACCTGGGAAAGCTCCGAGAGCTTCTATTTACGTCGCAAGAACCTGGCAGATGGAGTC	180
Db	121	aaacacagatggaactgtltaactctcgtatcctacacacatcaagaattacaactcaagagtc	180
QY	181	CCTTCTCGCTTCTCTGGATCCGCGCTCCGGAAGCGATTTCATCTGCAGCATCAGACGTCG	240
Db	181	ccatcaaatgttcagttgagtcagtgagtcggaacagattatctctccacattagcaactg	240
QY	241	CAGCTGAAGACTTCGCTACGATTTACTGTGCAGAACGTTTTAAATACCTCGGTGACTTTC	300
Db	241	gagcaagagagatattgcacttacttttgcacacaggtlaatacgttcgltgagcttc	300
QY	301	GGACAGGCTTACCAAGGTGGGAATTAACGTAACCTGCTGGCGTGTTCTGGTCG---CGGT	357
Db	301	gcttgagagccaccaagctcygaatcaaacagggctltgagcgagtagtgcgtgagtcaggt	360
QY	358	GGATCTGCTGGTGGCGGTTTCCAAAGTCCAACTGGTGCATATCCGCGCGGAGGTCACAAAG	417
Db	361	ggagagcagcgatgcygagtcgaagtgbcagctcccaagagctctgagcctcgatcggtgaag	420
QY	418	CCAGGGGCTCTCAGTCAAAAGTCTCTCTGTAAGACTGACGCGCTATATTTTCTTAATTATTCG	477
Db	421	ccctgagcttcaatgaagaatatactctgaaagccttcctgttattcattcaactgctaacac	480
QY	478	ATTTCATGEGTGCCTCAGGCCCCCGGCGACGGGCTGGAATGATGGTGGAATCTTACCG	537
Db	481	atgagactggtggaagcagagctcatalgaaagaacaccttgatgagtgagacttaataacct	540
QY	538	GGCTCTGGTAGCACCGAATTTACGGAATTTTAAACACCGCTGTACTATAGACCGGTGAC	597
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[illegible]

Search completed: July 20, 2001, 02:38:19
Job time: 4412 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2001, 00:52:07 ; Search time 86.76 Seconds

(without alignments)
1629.961 Million cell updates/sec

Title: US-08-487-283A-8

Perfect score: 747

Sequence: 1 ATGGCCGATATCCAGATGAC.....TGATCATCTCTCAGCTGA 747

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapept 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database : Issued_Patents_NA:*

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- 2: /cgn2_6/ptodata/2/1na/5B_COMB.seq:*
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- 5: /cgn2_6/ptodata/2/1na/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/2/1na/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	294	39.4	819	2	US-08-400-115-3
2	283.4	37.9	723	1	US-07-988-430-92
3	283.4	37.9	723	1	US-08-425-336-89
4	283.4	37.9	723	1	US-08-488-113B-89
5	283.4	37.9	723	1	US-08-477-484B-89
6	283.4	37.9	723	2	US-08-646-360-89
7	283.4	37.9	723	3	US-08-839-765-89
8	283.4	37.9	723	3	US-09-136-389-89
9	283.4	37.9	723	5	PCT-US92-09487-92
10	267	35.7	1065	3	US-08-875-811-48
11	267	35.7	1074	3	US-08-875-811-44
12	267	35.7	1074	3	US-08-875-811-50
13	267	35.7	1074	3	US-08-875-811-50
14	267	35.7	1086	3	US-08-875-811-46
15	267	35.7	1137	3	US-08-875-811-42
16	250	33.5	729	1	US-08-230-843-3
17	250	33.5	729	2	US-08-636-936-3
18	247.2	33.1	916	1	US-08-121-054C-29
19	247.2	33.1	916	3	US-08-539-436-29
20	236.6	31.7	733	2	US-08-224-591-17
21	236.6	31.7	733	2	US-08-926-789-17
22	234.4	31.4	721	2	US-08-224-591-15
23	234.4	31.4	721	2	US-08-926-789-15
24	233.4	31.1	2178	1	US-08-463-587A-24
25	233.4	31.1	2178	2	US-08-463-667A-2
26	233.4	31.1	2178	2	US-08-923-854-24
27	233.4	31.1	2178	5	PCT-US91-09133-25

28	231	30.9	6727	2	US-08-125-462-2	Sequence 2, Appl
29	231	30.9	6727	2	US-08-891-848-2	Sequence 2, Appl
30	230.6	30.9	1299	2	US-08-125-462-6	Sequence 6, Appl
31	230.6	30.9	1299	2	US-08-891-848-6	Sequence 6, Appl
32	230.6	30.9	1320	2	US-08-125-462-3	Sequence 3, Appl
33	230.6	30.9	1320	2	US-08-891-848-3	Sequence 3, Appl
34	230.6	30.9	6799	2	US-08-125-462-5	Sequence 5, Appl
35	230.6	30.9	6799	2	US-08-891-848-5	Sequence 5, Appl
36	227.6	30.5	2143	3	US-09-097-309-5	Sequence 5, Appl
37	227.6	30.5	2143	4	US-09-097-712B-1	Sequence 9, Appl
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39	224.4	30.0	732	1	US-08-230-843-1	Sequence 1, Appl
40	224.4	30.0	732	2	US-08-636-936-1	Sequence 1, Appl
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42	223.2	29.9	6127	4	US-09-109-207C-1	Sequence 1, Appl
43	221.8	29.7	720	1	US-08-061-092A-2	Sequence 1, Appl
44	220.6	29.5	7305	1	US-08-286-740-4	Sequence 4, Appl
45	220.6	29.5	7305	5	PCT-US95-09576-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-400-115-3
; Sequence 3, Application US/08400115
; Patent No. 5864019
; GENERAL INFORMATION:
; APPLICANT: KING, David John
; APPLICANT: MOUNTAIN, Andrew
; APPLICANT: OWENS, Raymond John
; APPLICANT: YARRANTON, Geoffrey Thomas
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/400,115
; FILING DATE: 06-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,136
; FILING DATE: 27-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/842,193
; FILING DATE: 17-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/00935
; FILING DATE: 11-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9012995.8
; FILING DATE: 11-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: ISACSON, John P.
; REGISTRATION NUMBER: 33,715
; REFERENCE/DOCKET NUMBER: 040283/0106 CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 819 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

TOPOLOGY: linear
 NAME/KEY: CDS
 LOCATION: 1..816
 US-08-400-115-3

Query Match 39.4%; Score 294; DB 2; Length 819;
 Best Local Similarity 66.3%; Pred. No. 6.2e-84;
 Matches 439; Conservative 0; Mismatches 220; Indels 3; Gaps 1;

4 GCCGATATCCAGATGACCCAGTCCCGCTCCCTGCTGCGCTGTGGCGATAGGCTC 63
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 124 ACCATACATCTCGAGCAAGTAGAATTTACAGTAATTTAGCATGTATCAACGANA 183
 124 CCTGGGAAAGCTCCGAGCTTCTGATTTACGGTGGAGCAACCTGGCAGATGGTCCCT 183
 184 CAGGAAATCTCCTCCTCCTGCTATGTGTGCAACAACTTAGCAGATGGTGGCA 243
 184 TCTGCTTCTGTGATCCGCTCCGGAACGATTTCACTTACCATTCAGCTGTGCA 243
 244 TCAAGTTTCACTGGCAGTGGATCGGGCACAGTATTCCTCAGATCAACAGCTGCA 303
 244 CCTGAAGATTCGCTAGCTATTTACTGTGAGAGCTTTTAAATACCTGTTGCTTGG 303
 304 TCTGAAGATTTTGGAGATTTACTGTCAACATTTTGGGTACTCTGACAGTTTGG 363
 304 CAGGATACCAAGTGGAAATAAACGTACTGGCGGTGTGTCTGCTGGCGGTGATCT 363
 364 GGGGGACCAAGCTTGAATATAAAG---TGGTGGGGGGGATCCGGGGGAGGTCA 420
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 544 GGTACACCGAATATACGAAATTTTAAAGACCGTGTACTATGACGGCTGACACTTG 603
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 661 TCCACACTGCTCATCATGAGCTCAACAGCCGACATCTGAGAGATTTCTCAGTATTTTC 720
 664 TG 665
 721 TG 722

RESULT 2
 US-07-988-430-92
 Sequence 92. Application US/07988430
 Patent No. 5416202

GENERAL INFORMATION:
 APPLICANT: Bernhard, Susan L.
 APPLICANT: Better, Marc D.
 APPLICANT: Carroll, Stephen F.
 APPLICANT: Lane, Julie A.
 APPLICANT: Lei, Shau-Ping
 TITLE OF INVENTION: Materials Comprising and Methods of
 Preparation and Use for Ribosome-Inactivating Proteins
 NUMBER OF SEQUENCES: 101

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ADDRESSEE: Bicknell
 STREET: Two First National Plaza, 20 South Clark
 STREET: Street
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60603
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/988,430
 FILING DATE: 19921209
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/901,707
 FILING DATE: 19-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/787,567
 FILING DATE: 04-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5416202and, Greta E.
 REGISTRATION NUMBER: 35302
 REFERENCE/DOCKET NUMBER: 31133
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 346-5750
 TELEFAX: (312) 984-9740
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 92:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 723 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 US-07-988-430-92

Query Match 37.9%; Score 283.4; DB 1; Length 723;
 Best Local Similarity 63.7%; Pred. No. 1.4e-80;
 Matches 472; Conservative 0; Mismatches 251; Indels 18; Gaps 2;

7 GATATCCAGATGACCCAGTCCCTCCCTGCTGCGCTGTGGCGATAGGCTAC 66
 1 GACATCCAGATGACTCAGTCTCCATCTTCCCTGCTGATCTGAGAGACAGATCA 60
 67 ATCACTGGCGGCGGAGGAAACATCTATGGCGCGCTGAACTGTATCAAGTAACT 126
 61 ATCACTGGCGGCGGAGGAGATGAGATTAATTAATTAATTAATTAATTAATTA 120
 127 GGGAAAGCTCCGAGCTTGTATTAAGTGTGCGAGAACCTGGCAGATGAGATCTTCT 186
 121 GGGAAAGCTCTTAAGACCTGATCTATCTGCAACAGATTTGAGATCTGGGCTCCATCA 180
 187 CGCTTCTGTGATCCGCTCCGGAACGATTTCACTGTGACCATCAGCATGTCCAGCT 246
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 307 GGTACCAAGGAGGAAATAAACGACTGCGGCTGTGCTGCTGCTGCTGCTGCTGCT 366
 301 GGCACCAAGCTTGAATGAAA-----GTTGGCGGTGATCTGTTGGAGTGGTCCGGA 354
 367 GGTGGCGGTTCTCAAGTCAAGTGTGCAATCCGGCGGAGGTCAAGAGAGGAGGCC 426
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Db 415 TCCGTCAAGATCTCCTGCGCAGCTTCTGGTATACCTTCAACAACTATGAATGACTGG 474
QY 487 GTGCGTCAAGGCGCCGCGGAGGCTGGAATGATGGGAGATCTTACCGGCTCTGCT 546
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Db 655 ACAGACGCGGTTACG-----ACTGTACTTCTGATGTCTGGGCGCAAGGAGCC 702
QY 727 CTGCTCACTGTCTCGAGCTGA 747
Db 703 ACGTCAACGCTCTCCATCA 723

RESULT 3
US-08-425-336-89
; Sequence 89, Application US/08425336
; Patent No. 5621083
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studinka, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 140
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,336
; FILING DATE: 18-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/064,691
; FILING DATE: 12-MAY-1993
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Thomas C.
; REGISTRATION NUMBER: P-36,989
; REFERENCE/DOCKET NUMBER: 31394
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 723 base pairs
; TYPE: nucleic acid

STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-425-336-89

Query Match 37.9%; Score 283.4; DB: 1; Length 723;
Best Local Similarity 63.7%; Pred. No. 1.4e-80;
Matches 472; Conservative 0; Mismatches 251; Indels 18; Gaps 2;

QY 7 GATATCCAGATGACCCAGTCCCGCTCCCTGTCGCGCTGTGGGCGATAGGATACC 66
Db 1 GACTTCCAGATGACTCACTCTCCATCTTCCCTGCTGATCTGTAGGAGACAGATCACT 60
QY 67 ATCACTGCGCGCGCAGGAAACATATGAGCGCGCTGAACCTGATATCAAGTAACT 126
Db 61 ATCACTTCCGCGCGGAGTACAGACATTAATGATATTAATTAAGCTGGTTCCAGCAAGCA 120
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QY 187 CGCTTCTGTGATCCGCGTCCGGAACGATTTCACTGTGACCATCAGCATGCTGAGCT 246
Db 181 AGTTCACTGAGTGGAGTGTCTGCGACAGATTAATCTCACCATCAGCATGCTGCAATAT 240
QY 247 GAAGACTTTCGCTACGATATTAATCTGAGAACCTTTAAATACCTGCTGATTTGGACAG 306
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QY 307 GGTACCAAGGTGGAATTAACGATCTGCGGTGCTGTTGTTGGTGGTGGATCTGCT 366
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Db 595 AACACTGCTATTTACGATCAACAGCCTCAGAGCCGAGACAGCGCTGTATTTCTGT 654
QY 667 GCGGCTATTTTGTGTTAGCCGAAATTTGATTTGATTTGGTGGGCTCAAGAAC 726
Db 655 ACAGACGCGGTTACG-----ACTGTACTTCTGATGTCTGGGCGCAAGGAGCC 702
QY 727 CTGCTCACTGTCTCGAGCTGA 747
Db 703 ACGTCAACGCTCTCCATCA 723

RESULT 4
US-08-488-113B-89
; Sequence 89, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studinka, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins

```

NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
City: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/300-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-488-113B-89

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Query Match      37.9%; Score 283.4; DB 1; Length 723;
Best Local Similarity 63.7%; Pred. No. 1.4e-80;
Matches 472; Conservative 0; Mismatches 251; Indels 18; Gaps 2;

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QY 307 GGTACCAAGGTGGAATAAAGCTACTGGCGGTGTCTGGTGGCGGTGATGTG 366
   || ||||| || || || || || || || || || || || || || || || ||
DB 301 GGACCAACAGCTTGAGATGAA-----GGTGGCGGTGAGATCTGTGAGTGGTCCGGA 354
QY 367 GGTGGCGGTTCACAGTCAACTGCTGCAATCCGGCCGAGAGTCAAGAACCCAGGGCC 426
   ||||| || || || || || || || || || || || || || || || || || ||
DB 355 GGTGGAGATCTGAGATCCAGTTGGTCAGTGTGAGAGAGCCCTGGTGAAGCTTGAGAG 414
QY 427 TCAGTCAAGTGTCCCTGTAAGCTACCGGCTATATTTTCTATATATGATTCATG 486
   || ||||| || ||||| || || || || || || || || || || || || || ||
DB 415 TCCGTGAGATCTCTCGCCACCTCTGTGATACCTTCAACAACTATGAAATGAAGTGG 474
QY 487 GTGGCTAGCGCCCGCGGAGCCCTGGAATGAGTGGTGAATCTTACCGGGCTGTG 546
   ||||| ||||| || || || || || || || || || || || || || || || ||
DB 475 GTCCCGCAGGCTCCAGAAAGGGTTAGATGATGGCTGGATTAACACCCACATGGA 534
QY 547 AGCACCAGATATACGGAATTTTAAAGACCGTGTACTATGACGGGTGACACTTGCAGT 606
   | ||||| || || || || || || || || || || || || || || || || ||
DB 535 GAGCCAAATATATGATGATCTTCTTCAAGGAGCGGTTTACCTTCTTGGACATCTAAG 594
QY 607 ACTACAGTATACATGAGCTCTCCAGCTCGCATCGAGACACGGCCGTCTATTTG 666
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DB 595 AACACTGCTTATTTACAGATCAACACCCCTCAGAGCCGAGACAGCGCTGTATTTCTGT 654
QY 667 GCGCGTATTTTGTCTAGCCCGAATGTGATTTGATGTTGGGCTCAAGGAC 726
   | | | || || || || || || || || || || || || || || || || || ||
DB 655 ACAAGACGGGGTTAC-----ACTGTACTTGATGTCTGGGCGCAAGGGACC 702
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DB 703 ACGGTACCGCTTCCCTCAGCA 723

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RESULT 5
US-08-477-484B-89
; Sequence 89, Application US/08477484B
; Patent No. 5756699
;
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studilka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
City: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992

```

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/787,567
 FILING DATE: 04-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REGISTRATION NUMBER: 32,918
 REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-8889
 TELEFAX: 312/707-9155
 TELEX: 650 388-1248
 INFORMATION FOR SEQ ID NO: 89:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 723 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 US-08-477-484B-89

Query Match 37.9%; Score 283.4; DB 1; Length 723;
 Best Local Similarity 63.7%; Pred. No. 1.4e-80;
 Matches 472; Conservative 0; Mismatches 251; Indels 18; Gaps 2;

QY 7 CATATCCAGATACCACTCCCGCTCCCTGTCGCGCTCTGTGGCGATAGGTCACC 66
 Db 1 GACATCCAGATACCTACGCTCCATCTCCCTGTCGATCTAGAGACAGATCACT 60
 QY 67 ATCACTGGGGGGCGGCAAAACATCTATNGCGCGCTGACATGATCAACGTAACCT 126
 Db 61 ATCACTGGGGGGCGGCAAAACATCTATNGCGCGCTGACATGATCAACGTAACCT 120
 QY 127 GGGAAAGCTCCCAAGCTTCTGATTTACGGTGCAGCAGACCTGCGAGATGAGTCTCT 186
 Db 121 GGGAAAGCTCCCAAGCTTCTGATTTACGGTGCAGCAGACCTGCGAGATGAGTCTCT 180
 QY 187 CGCTTCTCTGGATCCGGCTCGGAGATTCACCTCTGACATCAGACGATCTGCACCT 246
 Db 181 AGCTTACGAGGAGATGATCTGGGACAGATTTACTCTCACCATCAGCAGCTGCATAT 240
 QY 247 GAAGACTCGTACGATTAAGTCTGACAGCTTTAAATACCTCCGTTGATTCGGGACAG 306
 Db 241 GAAGACTTTGGAATTTATTTGTCACAGTATGATGAGTCTCCGTTGATTCGGGACAG 300
 QY 307 GGTACCAAGTGGAAATAAAGCTACTGCGGCTGTGTTCTGTGGCGGTGATCTGCT 366
 Db 301 GGTACCAAGTGGAAATAAAGCTACTGCGGCTGTGTTCTGTGGCGGTGATCTGCT 360
 QY 367 GGTGGCGGTTCTCAAGTCCAGCTGTCATCCGCGCGCGAGGTCAAGAACCCAGGGGCC 426
 Db 365 GGTGGCGGTTCTCAAGTCCAGCTGTCATCCGCGCGCGAGGTCAAGAACCCAGGGGCC 424
 QY 427 TCAGTCAAAAGTCTCTGTAAGCTTACGGCTATATTTTCTTAATTTGATTCGAATG 486
 Db 425 TCAGTCAAAAGTCTCTGTAAGCTTACGGCTATATTTTCTTAATTTGATTCGAATG 484
 QY 487 GTGGCGTCAAGGCGCGGCGGAGGCGTGAATGATGGGTGATCTTACGGGCTCTGCT 546
 Db 475 GTGGCGTCAAGGCGCGGCGGAGGCGTGAATGATGGGTGATCTTACGGGCTCTGCT 544
 QY 547 AGCACCAGATATACGCAAAATTTTAAAGACCGTGTACTATGACGCGTCACTTGCAGT 606
 Db 535 GAGCCACATATATGCTGATCTTTCAAGGACGCTTACCTCTCTTTGGACGATTTCAAG 594
 QY 607 AGTACAGATATACGAGCTTCCAGCTGCGATGCGAGACACAGCGCGCTATTTATTC 666
 Db 595 AACACTGCTATTTACAGATCAACAGCTCAGAGCGAGACACAGCGCTGATTTCTGT 654
 QY 667 GCGGCTATTTTGGTCTAGCCCGAATGTGATTTTGTATTTGGGTCAAGGAC 726
 Db 655 ACAAGACGGGTTAGC-----ACTGTACTTGATGTCTGGGGCGCAAGGAC 702

QY 727 CTGTCAGTCTGTCAGCTGA 747
 Db 703 ACGTCCAGCTCTCTCATGA 723

RESULT 6
 US-08-646-360-89
 Sequence 89, Application US/08646360
 Patent No. 5837491
 GENERAL INFORMATION:
 APPLICANT: Better, Marc D.
 APPLICANT: Carroll, Stephen F.
 APPLICANT: Studinika, Gary M.
 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
 NUMBER OF SEQUENCES: 173
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
 STREET: 500 West Madison Street, 34th floor
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60661
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/646,360
 FILING DATE: 13-MAY-1996
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PC/US94/05348
 FILING DATE: 12-MAY-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/064,691
 FILING DATE: 12-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/988,430
 FILING DATE: 09-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/901,707
 FILING DATE: 19-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/787,567
 FILING DATE: 04-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: McNicholas, Janet M.
 REGISTRATION NUMBER: 32,918
 REFERENCE/DOCKET NUMBER: 200-70.P4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/707-8889
 TELEFAX: 312/707-9155
 TELEX: 650 388-1248
 INFORMATION FOR SEQ ID NO: 89:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 723 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 US-08-646-360-89

Query Match 37.9%; Score 283.4; DB 2; Length 723;
 Best Local Similarity 63.7%; Pred. No. 1.4e-80;
 Matches 472; Conservative 0; Mismatches 251; Indels 18; Gaps 2;

QY 7 CATATCCAGATACCACTCCCGCTCCCTGTCGCGCTCTGTGGCGATAGGTCACC 66
 Db 1 GACATCCAGATACCTACGCTCCATCTCCCTGTCGATCTAGAGACAGATCACT 60

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QY 67 ATCACTGGGGGCGGAGGAAACATCTATGCGCGCTGAACCTGATCAACGTAACCT 126
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 ATCACTGGGGGCGGAGGAGTCAAGACATTAATAGCTATTAAGCTGTCACAGAAACA 120
QY 127 GGGAAAGCTCCGAAGCTTCTATTTACGGTGGACGAACCTGGCAGATGAGTCCCTCT 186
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 GGGAAAGCTCCGAAGCTTCTATTTACGGTGGACGAACCTGGCAGATGAGTCCCTCT 180
QY 187 CGTCTCTGTCGATCGGCTCGGAAACGATTTCACTGACCATAGACAGTCCGAGCT 246
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 AGTTCAGTGGCAGATGATCTGGGACATTAATCACTGACCATAGACAGCTCCGAAT 240
QY 247 GAAGACTTCCGATGATTAATCTGCAAGCTTTAAATTAATCTCCGTTACTTCCGAG 306
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Db 241 GAAGATTTTGAATTTATTTATTTCAACAGATGATGATGTCGCTGGACGTTCCGATGA 300
QY 307 GGTACCAAGTGGAAATTAACGTAAGTGGCGTGGTGTCTGTTGGTGGCGGTGATCTGT 366
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 GGCACCAAGCTTGAATGATAA-----GGTGGCGGTGATGCTGGTGGAGTGGTCCGA 354
QY 367 GGTGGCGGTCTCAAGTCCAGTGGTCAATCCGGCGCGGAGTCAAGACGCGAGGGGCC 426
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Db 355 GGTGGAGATCTGAGATTCAGTGGTCAATCTGAGAGAGCGCTGGTGAAGCTGGAGGG 414
QY 427 TCAGTCAAGTGTCTGTAAAGCTAGCGCTATATTTTCTAATTAATGATGATGATG 486
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 415 TCCGTCAAGATCTCTGGCGAGCTTCTGGGTATACCTTCAACAACTATGAAATGAAGT 474
QY 487 GTGGTCAAGGCGGCGGCGGCGCTGGAATGATGGTGAATCTTACCGGGCTCTGT 546
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 475 GTGGCGCAAGCTTCAAGGAAAGGTTTAAAGTGAAGTGGCTGATTAACCAACCACTGA 534
QY 547 AGCACCGAATTAACGAAATTTTAAAGACGCTTACTATGACGCGTGAACCTGAC 606
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 535 GAGCAACATATGCTGATCTTTCAAGGAGCGCTTACCTTCTTTGACCATTTCTAG 594
QY 607 AGTACAGTATACATGAGACCTCTCCAGCTGAGAGGAGACACGCGCTATTAATG 666
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 595 AACACTGGCTATTAACATCAACAGCCTCAAGCGGAGAGCGCTGTATTTCTGT 654
QY 667 GCGGCTATTTTGTGTTCTAGCCCGCAATTTGATTTGATTTGGGCTTAAGAAC 726
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 655 ACAAGAGCGGGGTTAG-----ACTGTACTTCTGATGCTGGGGCCAAAGGAGC 702
QY 727 CTGCTCACTGCTCGAGCTGA 747
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Db 703 ACGGTCAACCTCTCTCATGA 723

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APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70..P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-839-765-89

Query Match      37.9%; Score 283.4; DB 3; Length 723;
Best Local Similarity 63.7%; Pred. No. 1.4e-80;
Matches 472; Conservative 0; Mismatches 251; Indels 18; Gaps 2;

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QY 7 GATATCCAGATGACCAATCCCGCTCTCCCTGCGCTCTGTGGCGATPAGGTCACC 66
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 GATATCCAGATGACCAATCCCGCTCTCCCTGCGCTCTGTGGCGATPAGGTCACC 60
QY 67 ATCACTGGGGGCGGAGGAAACATCTATGCGCGCTGATGAGTCCGTAACGTAACCT 126
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 ATCACTGGGGGCGGAGGAGTCAAGACATTAATAGCTATTAATGAGTTCACGAAACA 120
QY 127 GGGAAAGCTCCGAAGCTTCTGATTTACGTCGACGAAACCTGGCAGATGAGTCCCTCT 186
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 GGGAAAGCTCCGAAGCTTCTGATTTACGTCGACGAAACCTGGCAGATGAGTCCCTCT 180
QY 187 CGTCTCTGTCGATCGGCTCGGAAAGGATTTCACTGCAACATGACAGTCTGACCT 246
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 AGTTCAGTGGCAGTGAATCTGGGACAGATTAATCACTCAACCACTGCAATAT 240
QY 247 GAAGACTTCCGATGATTAATCTGCAAGCTTTAAATTAATCTCCGTTACTTCCGAG 306
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 GAAGATTTTGAATTTATTTATTTCAACAGATGATGATGATGCTGAGAGTTCGGGGA 300
QY 307 GGTACCAAGTGGAAATTAACGTAAGTGGCGGTGTTCTGTTGGTGGCGGTGATCTGT 366
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 GGCACCAAGCTTGAATGATAA-----GGTGGCGGTGATGCTGGTGGAGTGGTCCGA 354
QY 367 GGTGGCGGTCTCAAGTCCAGTGGTCAATCCGGCGCGGAGGTCAAGAACGAGGGGCC 426
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 355 GGTGGAGATCTGAGATCCAGTGGTCAATCTGAGAGAGCGCTGGGAGAGCTGGAGGG 414
QY 427 TCAGTCAAGTGTCTGTAAGTGAAGTGAAGGCTATATTTTCTAATTAATGATTCATGG 486
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 415 TCCGTGAATCTCTGGCGAGCTTCTGGGTATACCTTCAACAACTATGGAATGAAGTGG 474
QY 487 GTGGTCAAGGCGGCGGCGGCGCTGGAATGATGGTGAATGATGATGATGATGATGAT 546

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Db 475 GTGGCGGAGGCTCCAGGAAGGTTAGATGGATGGCTGGATTAACACCCACACTGGA 534
Oy 547 AGACCCGATATACGAAATTTTAAAGACCGTGTACTATGACGGCTGACACTTGCAGT 606
Db 535 GAGCCAAATATGCTATCTTCTCAAGGAGCGTTTACTTCTTCTTGGACGATTCTAAG 594
Oy 607 AGTACGATATACGAGCTCTCCAGCCCTGCGATCGAGAGACAGCGGCTGTATTATTCG 666
Db 595 AACACGCTATTTTACGATCAACAGCCTCAGAGCGAGACAGCGCTGTATTCTGT 654
Oy 667 GCGCGTATTTTGTGTTCTACCGCAATTTGGTATTGTTGTTGGGCAAGAAC 726
Db 655 ACAAGACGGGGTTAGC-----ACTGTTACTTTCATGTCTGGGCCAAGGAGAC 702
Oy 727 CTGGTACTGTCTGAGCTGA 747
Db 703 ACGTCAACGCTCTCCATGA 723

RESULT 8
US-09-136-389-89
; Sequence 89, Application US/09136389
; Patent No. 6146850
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studinka, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESS: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09136,389
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/646,360
; FILING DATE: 13-MAY-1996
; APPLICATION NUMBER: PCT/US94/05348
; FILING DATE: 12-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 200-70_P4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 89:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 723 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-09-136-389-89

Query Match 37.9%; Score 283.4; DB 3; Length 723;
Best Local Similarity 63.7%; Pred. No. 1.4e-80;
Matches 472; Conservative 0; Mismatches 251; Indels 18; Gaps 2;

Oy 7 GATATCCAGATGACCCATCCCGCTCTCTCTGCTCCGCTCTGTGGGATAGGCTAC 66
Db 1 GACATCCAGATGACATGCTCCATCTCCCTGTCTGCTGCTGAGAGACGAGTACT 60
Oy 67 ATACCTCGGGGCGCGAAGAAACATATGAGCGGGCTGACCTGATACAGTAACT 126
Db 61 ATCACTTCCGGGCGAGTCAGACATTAATTAATTAAGTGTTCAGAGAAACCA 120
Oy 127 GGAAGAGCTCCGAACTCTGATTTACGTTGCGAGAACCTGACAGATGAGTCCCT 186
Db 121 GGAAGAGCTCTTAAGACCTGATGATGTCGAACAGATGGAATCTGGGCTCCATCA 180
Oy 187 CGCTTCTGTGATCCGCTCCGGAACGATTTCACTCTGACCATGACAGTCTCA 246
Db 181 AGTTCAGTGGGAGATGATCTGGGACAGATTTACTCTCCATCAGCAGCTGCAAT 240
Oy 247 GAAGCTTCGCTACTATTAATGATGAGAACTTTAAATACCTGCTTGGACAG 306
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Oy 307 GATACCAAGTGGGAATTAACGTAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 366
Db 301 GGCACCAAGCTTGATGATGAA-----GGTGGCGGTGATCTGTGGAGATGGTCC 354
Oy 367 GGTGGCGGTCTCAAGTCCAACTGCTGCAATCGGCGGCGGAGGTCAAGAGCCAG 426
Db 365 GGTGAGGATCTGAGATCCAGTGTGAGTGTGAGTGTGAGGAGGCGGTGAAGCTG 414
Oy 427 TCAGTCAAGTGTCTCTGTAAGCTAGCGCTATATTTTCTAATTAATTAATTA 486
Db 415 TCCGTCAGAAATCTCTGCGCACTTCTGGGTATACCTTCACAACTATGGAATGA 474
Oy 487 GTGGTCAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 546
Db 475 GTGGCGGAGGCTCCAGGAAGGTTTGAATGATGGCTGATTAACCCACACTGGA 534
Oy 547 AGACCGAATATACGAAATTTTAAAGACCGTGTACTATGACCGCTGACACTT 606
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Db 595 AACACTGCTATTTTACGATCAACAGCCTCAGAGCGAGACAGCGGCTGTATTCT 654
Oy 667 GCGGCTATTTTGTGTTCTAGCCGAAATTTGATTTTGAATTTGGGTTGAAGAAC 726
Db 655 ACAAGACGGGGTTAGC-----ACTGTTACTTTCATGTCTGGGCCAAGGAGAC 702
Oy 727 CTGGTACTGTCTGAGCTGA 747
Db 703 ACGTCAACGCTCTCCATGA 723

RESULT 9
PCT-US92-09487-92
; Sequence 92, Application PC/TUS9209487
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.

```



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: LENGTH: 1065 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1065
: OTHER INFORMATION: /note="SFvBmetcJluonc"
US-08-875-811-40

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Query Match          35.7%; Score 267; DB 3: Length 1065;
Best Local Similarity 63.4%; Pred. No. 2.7e-75;
Matches 427; Conservative 0; Mismatches 240; Indels 6; Gaps 1;

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QY 7 GATATCCAGATGACCCAGTCCCGTCCCTCCGCTCTGCGGCGATGAGGTCACC 66
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DB 1 GACATCAAGATGACCCAGTCTCATCTCTCATGTATGATGATAGAGAGAGTCACT 60
QY 67 ATACCTCGGCGGCCAGCAAAACATCTATGCGCGCTGAAGTGTATCAACGTAACT 126
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DB 61 TTCACCTTGAAGCGAGTGAAGACATTAATTAATTAATTAATTAATTAATTAAT 120
QY 127 GGGAAAGCTCCGAGCTTGTGATTTACGGTGCAGCAGCACTGCGAGTGCCTTCT 186
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DB 121 GGGAAATCTCCAAAGCCCTGATCTGCGCAACAGACTGGTAGTGGGTCCCATCA 180
QY 187 CGCTTCTCGATCCGCGTCCGAGAGGATTTCACTGACCATCACAGCTGACGCT 246
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DB 181 AGTTTAGTGGCAGTGGATCTGGACAAGATTATTTCTCACCATTAACAGCTGAGAT 240
QY 247 GAAGACTTGCCTACGATTTACTGTGACAGCTTTAAATACCTCGTTGACTTTGCGACAG 306
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DB 241 GAAGATATGGAAATTTATTTATTTCTACAGATGATGATGATGATGATGATGATG 300
QY 307 GGTACCAAGCTGGAATTAACCTACTGGCGGTGGTGTCTGTGCGCGGTGATCTGCT 366
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DB 301 GGGACCAAGCTGGAATTAACCTACTGGCGGTGGTGTCTGTGCGCGGTGATCTGCT 354
QY 367 GGTGGCGGTTCGAACTGCAATCGGAGTCCGCGCGGCGAGGTCAGAAAGCCGAGGCC 426
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DB 355 GGGCGGCGCTCTGAGTTTCACTGCTCCAGCACTCTGGGACTTACTGGCAAGCGCTGGGGCT 414
QY 427 TCAGTCAAGATGCTCTGTAAGCTAGCGGCTATATTTTCTATTAATTTGATTAATG 486
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DB 415 TCAGTCAAGATGCTCTGTAAGCTAGCGGCTATATTTTCTATTAATTTGATTAATG 474
QY 487 GTGCGTCAAGCGCCCGCGGCGAGGCTGGAATGATGGGTGATCTTAACGGGCTCTGCT 546
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 475 ATTAACCAAGAGGCTGAGAGGCTGAGTGGATGCTGCTATTTGATCTCGAAATAGT 534
QY 547 AGCAGCGAATATACGAAATTTAAAGACGTTTACTATGACGGCTGACACTTCGACT 606
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DB 535 GATACATATTTCACCCGCAATTCACACACAGGCCAAACTGACGAGTCACTCCACC 594
QY 607 AGTACAGTATACATGAGGCTCTCCAGCTGCGATTCGAGAGCAGACGCTTATTTATG 666
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DB 595 AGCAGCTCTACATGAGTCACTCAACAGCTGACAAATGAGAGACTCTGGGCTTATTA 654
QY 667 GCGCGTTATTTT 679
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DB 655 ACCCCCTTTTAT 667

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RESULT 11
US-08-875-811-48
: Sequence 48, Application US/08875811
: Patent No. 6045793
: GENERAL INFORMATION:
: APPLICANT: Rybak, Susanna M.
: APPLICANT: Newton, Dianne L.
: APPLICANT: Boque, Luis

```

```

APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 1065 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1065
OTHER INFORMATION: /note="SFvBmetcJluonc"
US-08-875-811-48

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Query Match          35.7%; Score 267; DB 3: Length 1065;
Best Local Similarity 63.4%; Pred. No. 2.7e-75;
Matches 427; Conservative 0; Mismatches 240; Indels 6; Gaps 1;

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QY 7 GATATCCAGATGACCCAGTCCCGTCCCTCCGCTCTGCGGCGATGAGGTCACC 66
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 GACATCAAGATGACCCAGTCTCATCTCTCATGTATGATGATAGAGAGAGTCACT 60
QY 67 ATACCTCGGCGGCCAGCAAAACATCTATGCGCGCTGAAGTGTATCAACGTAACT 126
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 TTCACCTTGAAGCGAGTGAAGACATTAATTAATTAATTAATTAATTAATTAAT 120
QY 127 GGGAAAGCTCCGAGCTTGTGATTTACGGTGCAGCAGCACTGCGAGTGCCTTCT 186
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 GGGAAATCTCCAAAGCCCTGATCTGCGCAACAGACTGGTAGTGGGTCCCATCA 180
QY 187 CGCTTCTCGATCCGCGTCCGAGAGATTTCACTGTGACCATGACAGTCTGAGCT 246
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 181 AGTTTAGTGGCAGTGGATCTGGACAAGATTATTTCTCACCATTAAGCAGCTGAGAT 240
QY 247 GAAGACTTGCCTACGATTTACTGTGCAAGAGTTTAAATACTCCGTTGACTTTGCGACAG 306
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 241 GAAGATATGGAAATTTATTTATTTCTACAGATGATGATGATGATGATGATGATG 300
QY 307 GGTACCAAGCTGGAATTAACCTACTGGCGGTGGTGTCTGTGCGCGGTGATCTGCT 366
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 301 GGGACCAAGCTGGAATTAACCTACTGGCGGTGGTGTCTGTGCGCGGTGATCTGCT 354

```



```

Db 901 ATAAACAGAGCCCTGGACAGGCTCTGGACTGGATTGTCCTATTGATCCTCGAATAGT 960
QY 547 AGCACCAGATATATCCGAAAAATTTTAAAGACCGTGTACTATGACGGGTGACACTTGACT 606
Db 961 GATACTATTACACCCGCAATTCAAACACAGAGCCCAACTGACTGACAGTCACTCCACC 1020
QY 607 AGTACAGTATACATGAGCTCTCCAGCCTGCGATCGAGAGACACGGCCGCTCTATTATTCG 666
Db 1021 AGCACTGCTTACATGAACTCAACAGCCTGACAAATGAGGACTCTCGTCTATTACTGT 1080
QY 667 GCGGCTATTATT 679
Db 1081 ACCCTCTTATT 1093

```

Search completed: July 20, 2001, 02:35:04
 Job time: 6177 sec

OM US-08-487-283a-8 to: PIR_68:* out_format : pfs
Date: Jul 19, 2001 8:17 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL=frame+12p.model -DEV=xlp
-O=/cgn2_1/USPPO.spool/US08487283/runat_19072001_075937_3832/app_query.fasta_1.817
-DB=PIR_68 -QEXT=fastan -SUPERX=tra.rpr -GAPOP=12.000
-GAEXP=4.000 -MINMATCH=0.100 -LOOPEXT=0.000 -LOOPEXT=0.000
-GAPOP=4.500 -GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blissum62
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR_SCORE=pc
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NOR=ext -MINLEN=0 -MAXLEN=300000000
-USER=US08487283 -CGN1_1_126 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPRX
-WAIT -THREADS=1

Search information block:

Query: US-08-487-283a-8
Query length: 747
Database: PIR_68:*
Database sequences: 219241
Database length: 76174552
Search time (sec): 46.350000

Sequence	Strid Orig	ZScore	EScore	len	Documentation
PIR2:PC4402	586.00	838.87	3.4e-39	287	Ig heavy chain anti
PIR2:A33548	481.50	694.66	7.4e-31	142	Ig heavy chain V region - human
PIR2:S40317	481.00	694.87	8.1e-31	127	Ig kappa chain V-J-C region - human
PIR2:S36265	476.00	688.30	2.0e-30	118	Ig heavy chain V region (clone
PIR2:S46593	471.50	681.10	4.7e-30	119	Ig heavy chain V region (human
PIR2:CS0562	467.50	676.03	9.7e-30	119	Ig heavy chain V region (27.7.2
PIR2:B49047	466.00	674.68	1.3e-29	108	Ig kappa chain V region (monoclonal
PIR2:S49530	465.00	671.39	1.5e-29	135	anti-Sm antibody VH chain (VH1)
PIR2:E30562	464.50	671.72	1.7e-29	119	Ig heavy chain V region (27.10.
PIR2:S40317	462.00	667.86	2.7e-29	123	Ig kappa chain - human
PIR2:S23623	461.00	663.87	3.3e-29	171	Ig heavy chain V region (precurs
PIR2:D30562	460.50	662.98	3.5e-29	119	Ig heavy chain V region (27.4b.
PIR2:D33548	458.50	662.83	5.1e-29	123	Ig heavy chain V-1 region (WIL2
PIR2:PT0358	457.00	661.31	6.7e-29	114	Ig kappa chain V region (7D2.G1
PIR2:PH0954	456.00	658.65	8.1e-29	132	Ig heavy chain V region (G6+ C1
PIR2:S31598	455.00	658.81	9.6e-29	109	Ig kappa chain - human (fragment
PIR2:S31600	453.00	656.97	9.7e-29	136	Ig heavy chain V region (human
PIR2:PH0952	453.00	654.60	1.4e-28	128	Ig heavy chain V region (G6+ C1
PIR2:S52793	452.00	653.10	1.7e-28	129	Ig kappa chain V region - human
PIR2:S20783	450.50	651.48	2.2e-28	121	Ig heavy chain V region - human
PIR2:PH0959	450.00	651.11	2.4e-28	116	Ig heavy chain V region (G6+ T-1
PIR2:PH0957	449.50	649.77	2.7e-28	125	Ig heavy chain V region (G6+ C1
PIR2:S31981	449.00	650.19	2.9e-28	109	Ig kappa chain - human (fragment
PIR2:S36260	448.50	648.08	3.2e-28	129	Ig heavy chain V region (clone
PIR2:S14683	448.50	634.93	3.6e-28	627	Ig mu chain precursor, membrane
PIR2:PH0962	448.00	647.96	3.5e-28	120	Ig heavy chain V region (G6+ T-1
PIR2:S40317	448.00	647.36	3.5e-28	129	Ig kappa chain - human
PIR2:PH0961	446.50	645.87	4.6e-28	119	Ig heavy chain V region (G6+ T-1
PIR2:S44122	445.00	644.53	6.1e-28	108	Ig kappa chain V region - human
PIR2:S19665	445.00	643.38	6.1e-28	124	Ig heavy chain V region (alpha-
PIR2:PH0955	444.50	642.46	6.7e-28	127	Ig heavy chain V region (G6+ C1
PIR2:K1KH0U	444.00	643.09	7.3e-28	108	Ig kappa chain V-1 region (Hau)
PIR2:S40349	444.00	641.88	7.3e-28	125	Ig kappa chain V-J region - human
PIR2:S29257	443.50	639.75	8.1e-28	148	Ig heavy chain V region (precurs
PIR2:S36269	443.00	641.73	8.7e-28	107	Ig lambda chain V region (clone
PIR2:CS3548	442.50	639.21	9.7e-28	133	Ig heavy chain V-1 region (783)
PIR2:S36264	442.00	640.30	1.1e-27	107	Ig lambda chain V-1 region (clone
PIR2:K1KH0Y	442.00	640.22	1.1e-27	108	Ig kappa chain V-1 region (Lay)
PIR2:S47182	442.00	640.22	1.1e-27	108	Ig kappa chain - human
PIR2:S40370	442.00	639.21	1.1e-27	122	Ig kappa chain - human

PIR2:B33548 + 442.00 638.94 1.1e-27 126 I Ig heavy chain V-1 region (A
PIR2:A33548 + 441.50 638.02 1.2e-27 129 I Ig heavy chain V-1 region (N
PIR2:JL0139 + 441.00 638.86 1.3e-27 107 I Ig kappa chain V region (AND
PIR2:S24217 + 440.50 637.84 1.4e-27 111 I Ig kappa chain - mouse (frag
PIR2:S34014 + 440.50 636.72 1.4e-27 127 I Ig heavy chain V region - hu

seq_name: PIR2:PC4402

seq_documentation_block:

peib leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protei
C:Species: Synthetic
C:Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 06-Nov-1998
C:Accession: PC4402
R:Suzuki, C.; Ueda, H.; Suzuki, E.; Nagamune, T.
J. Biochem. 122, 322-329, 1997
A:Title: Construction, bacterial expression, and characterization of hapten-specific
A:Reference number: PC4402
A:Accession: PC4402
A:Molecule type: DNA
A:Residues: 1-287 <SD2>
C:Keywords: fusion protein

alignment_scores:

Quality: 586.00 Length: 263
Ratio: 3.151 Gaps: 7
Percent Similarity: 70.722 Percent Identity: 49.430

alignment_block:

US-08-487-283a-8 x PC4402 ..

Align seg 1/1 to: PC4402 from: 1 to: 287

7 GATATCAG.....ATGACCCAGTCCCGCTCCCTGCGGCTGT 50
||||||| |||||:||||:|||||
24 ASPLIEGhAlaValhIngInu...SerAlaLeuthrSerP 39
51 GGGCGATGAGGTCACCATCATCTGCGCGGCGACGAACATGATGCGC 100
|||||: |||||:|||||: |||||
39 oGlygUthrValThrLeuthrCysArgSerThr.....GlyA 53
101 CGGTG.....ACTGTTATCACTGAACCTGGGAA 132
|||: ||||| |||||:|||||
53 lAlValhThrSerAsnTyAlaAsnTrValgIngluTyProSPHs 69
133 GCGCCGACCTGTGATTACGGTGGAGACCTGGACATGAGTCC 182
70 LeuPherThrGlyLeuThrLeuThrAsnAsnArgAlaProGlyValPr 86
183 TTCTCCCTCTGTGATCCGCTCCGAGACGATTTCACCTGACATCA 232
|||||:|||||:|||||: |||||
86 oAlaArgPheSerGlySerLeuLeuLeuGlyAspLysAlaAlaLeuThrLet 103
233 GCAGTCTGACCTGAAGACTTGGTACGTATCTGTCGAACGTTTA 282
|||: ||||| |||||: |||||
103 hGcLysAlaGlnThrGlyAspGlyAlaIleTyRhecysAlaLeuTrpTy 119
283 AATACCCGCTGACTTGGACAGGATACCAAGTGAATTAACGTAC 332
|||: ||||| |||||: |||||
120 SerAsnHisTrpAlaPheGlyGlyGlyThrLysLeuThrValLeuSerSe 136
333 TGCGCGTGTGTGTGTGTCGCGGCTGATCTGGTGGCGT..... 375
136 rAlaAspAlaLysLysAspAlaLysLysAspAlaLysLys 153
|||: ||||| |||||: |||||
376TCTCAAGTCAACTGGTGAATCCGCGCGAC 408
153 sPaSPaLysLysAspGlyGlnValGlnLeuGlnInProGlyAlaGln 169
409 GTCAGACACCGAGGCGCTGACAAAGTCTCTGTAACCTAGCGGCTA 458
|||: ||||| |||||: |||||
170 LeuValLysProGlyLysSerValLysLeuSerCysLysAlaSerGlyTy 186

```

459 TATTTTAAATATGATTCATGCGTGCAGAGCCCGGCGAG 508
186 rThpetherSeryTrpMethistripallysGlnarProglyArag 203
509 GCGTGAATGATGGGTGAGTCTACCGGGCTGTGATACCAAGAT 558
203 lYleuGluTrpIleGlyArgIleAspProAsnSerGlyGlyThrLysTyr 219
559 ACCGAAATTTAAAGACCGGTACTATGACCGGTGACACTTCAGATAG 608
220 AangluLysPheLysSerLysAlaThrLeuThrValAspLysProSerSe 236
609 TACAGTATACATGAGCTCTCCAGCCTCGAGAGAGACAGCGCGCTCT 658
236 rThralaTyrMetGlnLeuSerSerLeuThrSerGluAspSerAlaValr 253
659 ATTATTCGCGCGGTAT...TTTTGGTTCTAGCCCGAATTGGTATTT 705
253 YTYTCysAlaArgYrAspTYrTYrGlySerSer.....TyrPhe 266
706 GATGTTTGGGTCAAGAACCCGTGCTGCTGCTGAGC 744
267 AspTYrTrpGlyGlnGlyThrThrLeuThrValSerSer 279

```

seq_name: pir2:A32483

seq_documentation_block:

Ig heavy chain V region - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996
 C:Accession: A32483
 R:Larriock, J.W.; Danielsson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck, C
 Biochem. Biophys. Res. Commun. 160, 1250-1256, 1989
 A:Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells usi
 A:Reference number: A32483; MUID:89273586
 A:Accession: A32483
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-142 <L&R>
 A:Cross-references: GB:M26463
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:25-108/Domain: immunoglobulin homology <IMM>

alignment_scores:

Quality:	481.50	Length:	131
Ratio:	4.261	Gaps:	1
Percent Similarity:	86.260	Percent Identity:	74.809

alignment_block:

US-08-487-283a-8 x A32483 ..

Align seg 1/1 to: A32483 from: 1 to: 142

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367 GGTGGGGTTCACAGTCCAGTGGTGAATCGGGCGGAGCAGAA 416
7 gIyAlaHisSerGlnValGlnLeuValGlnSerGlyAlaGluValLysly 23
417 GCCAGGGGCTCAGTCAAGTCTCTGTAAGCTAGCGGCTATATTTT 466
23 sProGlyAlaSerValLysValSerGlyLysAlaSerGlyTyrThrPhe 40
467 CTAATTTATGATTCATGCGTGCAGAGCCCGGCGAGCGCTGGAA 516
40 hAsnTYrTYrMetHisTrpValArgGlnAlaProGlyGlnGlyLeuGln 56
517 TCGATGGGAGATCTTACCGGGCTGGAGACCGAATATACCGAAA 566
57 TrpMetGlyTyrIleLeuAsnProSerGlyAsnSerThrAsnTYrAlaGlnly 73
567 TTTTAAAGACCGGTACTATGACCGGTGACACTTCGACTAGTACAGTAT 616

```

```

73 spheGlnGlyArgValThrMetThrArgAspThrSerThrValr 90
617 ACATGAGCTCTCCAGCCTGCGATCGAGAGACAGCGCGCTCATTTATGAC 666
90 YrMetGlnLeuSerSerLeuArgSerGluAspThrAlaValTyrTrpGly 106
667 GCGCGT.....TATTTTGGTTCTACCCGGAATTGGTA 701
107 AlaArgGluLysLeuAlaThrThrLePheGlyValLeuIleThrGln 123
702 TTTGATGTTGGGTCAAGAACCCGTGCTGCTGCTGAGC 744
123 YMetAspTYrTrpGlyGlnGlyThrLeuValThrValSerSer 137

```

seq_name: pir2:S40367

seq_documentation_block:

Ig kappa chain V-J-C region - human
 C:Species: Homo sapiens (man)
 C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C:Accession: S40367
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
 A:Reference number: S40312; MUID:94080891
 A:Accession: S40367
 A>Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-127 <KLE>
 A:Cross-references: EMBL:X72477
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:33-107/Domain: immunoglobulin homology <IMM>

alignment_scores:

Quality:	481.00	Length:	109
Ratio: <td>4.716 <td>Gaps: <td>0</td> </td></td>	4.716 <td>Gaps: <td>0</td> </td>	Gaps: <td>0</td>	0
Percent Similarity: <td>93.578 <td>Percent Identity: <td>86.239</td> </td></td>	93.578 <td>Percent Identity: <td>86.239</td> </td>	Percent Identity: <td>86.239</td>	86.239

alignment_block:

US-08-487-283a-8 x S40367 ..

Align seg 1/1 to: S40367 from: 1 to: 127

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7 GATATCCAGATGACCCAGTCCCGTCTCCCTGTCGCGCGCA 56
18 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAs 34
57 TAGGGTCACATACACCTGCGGGCGGAGGAAACAATCATAGCGCGCTGA 106
34 pArgValThrIleThrCysArgAlaSerGlnSerIleSerAsnTYrLeuA 51
107 ACTGATATCAACGTAAACCTGGGAAGCTCGAAGCTTCTGATTACGAT 156
51 snrTPTYrGlnArgLysProGlyLysAlaProLysLeuLeuIleTYrAla 67
157 GCGAGAACTGGGCAATGAGATCCCTTCGCTTCGCTTGATCCGGCTC 206
68 AlaSerSerLeuGlnSerGlyValProSerArgPheSerGlySerGlySe 84
207 CGGAAGGATTTCACTGACCATCAGACAGCTGACGCTGAGCAACTCG 256
84 rGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspPheA 101
257 CTAGATATTACTGTCAGAACCTTTTAATACCTCCCTTACCTTTCGAGAG 306
101 IaThrTYrTYrCysGlnGlnSerTyrAsnThrProTrpThrPheGlyGln 117
307 GGTACCAAGGTGAAATAAAGTACT 333
118 GlyThrLysValGluIleLysArgThr 126

```



```

seq_name: p1r2:S36265

seq_documentation_block:
ig heavy chain V region (clone alpha-MUc1-1) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C:Accession: S36265
R:Griffiths, A.D.; Malingvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448
A:Accession: S36265
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-118 <GR1>
A:Cross-references: EMBL:218846; NID:933121; PIDN:CAA79298.1; PID:9339900
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

alignment_scores:
Quality: 476.00 Length: 122
Ratio: 4.250 Gaps: 1
Percent Similarity: 91.803 Percent Identity: 76.230

alignment_block:
US-08-487-283a-8 x S36265 ..

Align seg 1/1 to: S36265 from: 1 to: 118

379 CAAGTCCAACTGCTGCAATCCGGCCGAGGTCAAGAACCGAGGCGCTC 428
1 GlnValGlnLeuValGlnSerGlyAlaGlnValLysProGlyAla 17
429 AGTCAAGTCTCCTGTAAGCTAGCGGTATATTTCTTAATTATTTGA 478
17 rValLysValSerGlySerGlyTyrThrPheThrGlyTyrTyrM 34
479 TTCATGGTGGTCCGTCAGACCCCGCGAGGCTGAAATGATGAGCTC 528
34 ethIstrpValArgGlnAlaProGlyGlnGlyLeuGlnTyrMetCylTyr 50
529 ATCTTACCGGCTCTGCTAGCACCAGCAATATACCAAAATTTAAAGCG 578
51 IleAsnProAsnSerGlyGlyThrAsnTyrAlaGlnLysPheGlnGlyAr 67
579 TGTACTATATGACCGGTGACACTTGGACTAGTACAGTATACAGAGCTC 628
67 gValThrIleThrArgAspThrSerAlaSerThrAlaTyrMetGlnLys 84
629 CCAGCTGCGATCGAGGACACCGCGCTCTATTATTTGGCGGTATTTT 678
84 erAspLeuAlaGlySerGlnAspThrAlaValTyrTyrCysAlaArgAspPhe 100
679 TTTGGTCTAGCCGGAATGATTTGATTTGGAGGTGAGCAAGACCT 728
101 LeuSerGly.....TyrLeuAspTyrTrpGlyGlnGlyThrLe 113
729 GGTACTGCTCTCGAGC 744
113 uValThrValSerSer 118

seq_name: p1r2:S46393

seq_documentation_block:
ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C:Accession: S46393
R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by

```

```

A:Reference number: S46390; MUID:94254092
A:Accession: S46393
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-129 <FIG>
A:Cross-references: EMBL:231680; NID:9509786; PIDN:CAA83485.1; PID:91335146
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

alignment_scores:
Quality: 471.50 Length: 129
Ratio: 4.210 Gaps: 2
Percent Similarity: 86.822 Percent Identity: 72.093

alignment_block:
US-08-487-283a-8 x S46393 ..

Align seg 1/1 to: S46393 from: 1 to: 129

379 CAAGTCCAACTGCTGCAATCCGGCCGAGGTCAAGAACCGAGGCGCTC 428
1 GlnValGlnLeuValGlnSerGlyAlaGlnValLysProGlyAla 17
429 AGTCAAGTCTCCTGTAAGCTAGCGGTATATTTCTTAATTATTTGA 478
17 rValLysValSerGlySerGlyTyrThrPheThrGlyTyrTyrM 34
479 TTCATGGTGGTCCGTCAGACCCCGCGAGGCTGAAATGATGAGCTC 528
34 ethIstrpValArgGlnAlaProGlyGlnGlyLeuGlnTyrMetCylTyr 50
529 ATCTTACCGGCTCTGCTAGCACCAGCAATATACCAAAATTTAAAGCG 578
51 IleAsnProAsnSerGlyGlyThrAsnTyrAlaGlnLysPheGlnGlyT 67
579 TGTACTATATGACCGGTGACACTTGGACTAGTACAGTATACAGAGCTC 628
67 pValThrMetThrArgAspThrSerIleSerThrAlaTyrMetGlnLys 84
629 CCAGCTGCGATCGAGGACACCGCGCTCTATTATTTGGCGGTATTT 672
84 erArgLeuAlaGlySerAspThrAlaValTyrTyrCysAlaArgAspSer 100
673 ...TATTTTTCGCTCT.....AGCCGAATTGATTTTGA 707
101 AlaTyrTyrTyrAspSerSerGlyTyrTyrSerAlaAsnTyrTyrMetAs 117
708 TGTGGGGTCAAGAACCTGCTGCTGAGC 744
117 pValTyrPglYlyGlyThrThrValThrValSerSer 129

seq_name: p1r2:C30562

seq_documentation_block:
ig heavy chain V region (27.7.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 16-Aug-1996
C:Accession: C30562
R:Slinder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison,
J. Immunol. 142, 888-893, 1989
A:Title: Amino acid substitutions in V-H CDR2 change the idotype but not the antigen
A:Reference number: A30562; MUID:89110066
A:Accession: C30562
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <SKI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

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alignment_scores: Length: 122
 Quality: 467.50
 Ratio: 4.289
 Percent Similarity: 89.344 Percent Identity: 70.492

alignment_block:

US-08-487-283a-8 x C30562 ..

Align seg 1/1 to: C30562 from: 1 to: 119

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379 CAGATCCAGTGGTGCATCCGCGCCGAGGTACAGACAGCGGCGCTC 428
|||||
1 GlnValGlnLeuGlnGlnSerGlyAlaGluLeuMetLysProGlyAlaSer 17
429 AGTCAAGTGCCTGTAAAGCTAGCGGCTATATTTTCTTAATTATGA 478
|||||
17 rValLysIleSerCysLysAlaThrGlyTyrThrPheSerSerTyrTrpI 34
479 TTCATGGGTGCGTCAGGCGCCGCGGACAGGCGCTGGAATGATGGTGA 528
|||||
34 IeGluTrpValLysGlnArgProGlyHisGlyLeuGluTrpIleGlyLys 50
529 ACTTACCCGGGCTCTGTAGACACCGAATATACGAAATTTTAAAGCCG 578
|||||
51 IleLeuProGlySerGlySerThrAsnTyrAsnGluLysPheLysGly 67
579 TGTACTATGACGCGTACACTGACCTGACTAGTACGATACGAGAGCTCT 628
|||||
67 salathrPheThrAlaAspThrSerSerAsnThrAlaTyrMetGlnLeu 84
629 CGAGCTCGGATCGAGACGCGCGCTATATTGCGCGCTTATTTT 678
|||||
84 eSerLeuThrSerGluAspSerAlaValTyrTyrCysAlaArgHisTyr 100
679 TTGGTCTACGCCGATGATTTTGGATTTGGGGGTCAAGAACCTT 728
|||||
101 TyrGlySerSerSer.....PheAlaTyrTrpGlyGlnGlyThrLe 114
729 GGTCACTGCTCGAGC 744
|||||
114 vValThrValSerAla 119

```

seq_name: p1r2:B49047

seq_documentation_block:

Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragm
 C:Species: Homo sapiens (man)
 C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
 C:Accession: B49047
 R:Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
 Eur. J. Immunol. 22, 2231-2236, 1992
 A:Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
 A:Reference number: A49047; MUID:92387224
 A:Accession: B49047
 A>Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-108 <VIC>
 A:Experimental source: thymic B lymphocytes
 A>Note: Sequence extracted from NCBI Backbone (NCBIN:113208, NCBIPI:113209)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:16-90/Domain: immunoglobulin homology <IMM>

alignment_scores:

 Quality: 466.00 Length: 108
 Ratio: 4.614 Gaps: 0
 Percent Similarity: 93.519 Percent Identity: 84.259

alignment_block:

US-08-487-283a-8 x B49047 ..

Align seg 1/1 to: B49047 from: 1 to: 108

```

7 GATATCCAGATGACCCAGTCCCGCTCCTCCTGTCGCGCTGTGGCGCA 56
|||||
1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAs 17
57 TAGGGTCCACATCACCTCGCGGCGCAGGAAACATCTATGGCGGCGCA 106
|||||
17 pargValThrIleThrCysArgAlaSerGlnSerIleSerSerTyrLeuA 34
107 ACTGATATCAACGTAAACCTGGGAAAGCTCCGAAACCTCTGATTACGAT 156
|||||
34 snTrpTyrGlnGlnLysProGlyLysAlaProLysLeuLeuIleTyrAla 50
157 GCGAGCAACCTGCGAGATGAGATCCCTTCTGCTTCTGTGATCCGCTC 206
|||||
51 AlaSerSerLeuGlnSerGlyValProSerArgPheSerGlySerGlySe 67
207 CGGAACGATTTTCACTGTGACCATCAGACAGTCTGACGCTGAAGCTCG 256
|||||
67 rGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspPheA 84
257 CTACGATTTACTGTCGAGAACGTTTAAATACCTGCTGACTTTCGAGACG 306
|||||
84 laThrTyrTyrCysGlnGlnSerTyrSerThrProLeuThrPheGlyGly 100
307 GGTACCAAGTGGAAATPAAACGT 330
|||||
101 GlyThrLysValGluIleLysArg 108

```

seq_name: p1r2:S49530

seq_documentation_block:

anti-Sm antibody VH chain (VH1/DK1 or DM1/VH4b) - human
 C:Species: Homo sapiens (man)
 C:Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
 C:Accession: S49530
 R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
 submitted to the EMBL Data Library, October 1994
 A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
 A:Reference number: S48797
 A:Accession: S49530
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-135 <MAN>
 A:Cross-references: EMBL:246348; NID:9560839; PIDN:CAA86467.1; PID:9560840
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:34-117/Domain: immunoglobulin homology <IMM>

alignment_scores:

 Quality: 465.00 Length: 126
 Ratio: 4.265 Gaps: 1
 Percent Similarity: 86.508 Percent Identity: 73.016

alignment_block:

US-08-487-283a-8 x S49530 ..

Align seg 1/1 to: S49530 from: 1 to: 135

```

367 GGTGGCGGTTCTCAAGTCCAACTGTCGAATCGGCGCGGAGGTCAAGA 416
|||||
16 GlnAlaHisSerGlnValGlnLeuValGlnSerGlyAlaGluValLysLys 32
417 GCCAGGGGCTCAGTCAAGAGTCTCTGTAAGCTGACGGCTATATTTT 466
|||||
32 sproGlyAlaSerValLysValSerCysLysAlaSerIleTyrThrPheT 49
467 CTAATTATTTGATTCATGAGTGTGCTGACGCGCCGCGGACGCGCTGGA 516
|||||
49 hrGlyTyrTyrMetHisTrpValArgGlnAlaIleProGlyGlnGlyLeu 65
517 TGGATGGGTGAGATCTTACCGGGCTCTGTAGACACGGAATATACGGA 566
|||||
66 TrpMetGlyTrpIleAsnProAsnSerGlyGlyThrAsnTyrAlaGlnGly 82

```

```

567 TTTTAAGACCGCTGTACTATGACCGGTGACACTTCGACTAGTACAGTAT 616
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
82  spEgInGlyArValThrMetThrArgAspThrSerIleSerThrAla 99
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
617 ACATGAGACCTCCAGCTCGATCGAGGAGGAGCGCGCTATATATGCG 666
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
99  yMetGluLeuSerArgLeuArgSerAspThrAlaValIlyrIcys 115
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
667 GCGCGTATATTTTGGTCTAGCCGCAATGTATTTTGATGTTGGGG 716
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
116 AlaArgIlaArgThrIly.....TyrAsnTyrTrpGI 126
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
717 TCAAGGACACCTGGTCACTGTCTGAG 744
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
126 yGInGlyThrLeuValThrValSerSer 135

seq_name: p1r2:E30562

seq_documentation_block:
lg heavy chain V region (27.10.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 16-Aug-1996
C:Accession: E30562
R:Sticker, S.K.; Borden, P.; Gruneo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.L.
J. Immunol. 142, 888-893, 1989
A:Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-bi
A:Reference number: A30562; MUID:89110066
A:Accession: E30562
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <SIK>
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

alignment_scores:
Quality: 464.50      Length: 122
Ratio: 4.261         Gaps: 1
Percent Similarity: 89.344      Percent Identity: 69.672

alignment_block:
US-08-487-283A-8 x E30562 ..

Align seg 1/1 to: E30562 from: 1 to: 119

379 CAAGTCCAACTGTGCAATCCGGCGGAGGTCAAGACCGAGCGCTC 428
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1  GlnValGlnLeuGlnGlnSerGlyAlaGlnLeuMetIysProGlyAla 17
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
429 AGTCAAGTGTCTGTAAAGCTAGCGCTATATTTTCTAATTATTTGA 478
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17  ValIlyIleSerCysIysAlaTrnGlyTyrThrPheSerSerTyrTrpI 34
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
479 TTCATGTGGTGGTCAAGCGCCCGGAGGAGCGCTGAATGATGGGTGAG 528
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34  LeGIuTrpValIlyGlnArgProGIyHISGlyLeuGIuTrpIleGIlyIu 50
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
529 ATCTTACCGGGCTGTGTAGCACCGAATATACGAAATTTTAAAGACG 578
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51  IlePheProGIySerGIySerThrIlyTrpAsnGIuIlySPhelySgIly 67
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
579 TGTTCATATACCGGTGACACTTGACTAGTACATATCATGACGCTCT 628
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
67  salAThrPheThrAlaAspThrSerSerAsnThrAlaIlyMetGIuLeu 84
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
629 CGAGCCGCGCATGGAGACAGCGCGCTATATTTGCGCGCTATTTT 678
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
84  eArSerLeuTrnSerGIuAspSerAlaValIlyrIyCysAlaArgHISTr 100
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
679 TTGTGTTCTAGCCCGAATGTATTTGATTTGGGGTCAAGAACCT 728
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

101 TyrGIySerSerSer.....PheAlaTyrTrpGIyGInGlyThrIle 114
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
729 GGTCACTGTCTCGAGC 744
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
114 uValThrValSerAla 119

seq_name: p1r2:S40331

seq_documentation_block:
lg kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40331
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chl genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40331
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-123 <KLE>
A:Cross-references: EMBL:X72441; NID:q441350; PIDN:CAAS1109.1; PID:q441351
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:32-106/Domain: immunoglobulin homology <IMM>

alignment_scores:
Quality: 462.00      Length: 107
Ratio: 4.620         Gaps: 0
Percent Similarity: 93.458      Percent Identity: 84.112

alignment_block:
US-08-487-283A-8 x S40331 ..

Align seg 1/1 to: S40331 from: 1 to: 123

7  GATATCCAGATGACCGAGTCCCGCTCCCTGTCGCGCTGTGGCGA 56
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17  AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGIyAs 33
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
57  TAGGTCACCATCAGCTGCGCGCCGACGCAAAACATCTATAGCGCGCTGA 106
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
33  pArgValThrIleThrCysArgAlaSerGlnSerIleSerSerTyrIleuA 50
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
107 ACTGTATCAAGTAAACCTGGGAAGCTCCGAAGCTTGATTTACGCT 156
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
50  snTrpTyrGlnGlnIlySProGIyLysAlaProIlySLeuIleIyAla 66
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
157 GCGACGACCTGGCAGATGGAGTCCCTTCTGCTCTGATCCGCGCTC 206
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
67  AlaSerSerLeuGlnSerGIyValProSerArgPheSerGIySerGIySe 83
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
207 CGGACGAGATTCACCTGTGACCATCAGACAGTGTGACCGTGAAGACTTC 256
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
83  rGIyThrAspPheThrLeuThrIleSerSerLeuGlnProGIuAspPhea 100
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
257 CTACGATATACGTTCAGAACGTTTAAATCTCCGTTGATTTTCGGACAG 306
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
100  laThrTyrIyCysGlnGlnSerTyrSerThrProArgThrPheGIyGln 116
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
307 GGTACCAAGGTGGAATTAATA 327
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
117  GIyThrIlyValGIuIleIlyS 123

seq_name: p1r2:S23623

seq_documentation_block:
lg heavy chain V region precursor - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S23623
R:Olée, T.; Lu, E.W.; Huang, D.F.; Soto-Gill, R.W.; Defios, M.; Kozin, F.; Carson, D.A

```

J. Exp. Med. 175, 831-842, 1992
 A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from h
 A:Reference number: S23623; MUID:92156804
 A:Accession: S23623
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-171 <OLE>
 A:Cross-references: EMBL:X59702; NID:932010; PIDN:CAA42223.1; PID:932011
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:34-117/Domain: immunoglobulin homology <IMM>

alignment_scores:
 Quality: 461.00 Length: 130
 Ratio: 4.153 Gaps: 2
 Percent Similarity: 85.385 Percent Identity: 70.765

alignment_block:
 US-08-487-283A-8 x S23623 ..

Align seg 1/1 to: S23623 from: 1 to: 171

```

367 GGTGGCGGCTTCACAGTCCAACTGTGCAATCCGCGCGAGGTCAAGAA 416
|||||
16 GYALAHSSerGlnValGlnSerGlyAlaGluValIysIy 32
|||||
417 GCCAGGGCGCTCAGTCAAGTGCCTGTAAGAGTACGGCTATATTTT 466
|||||
32 SProlGlnAlaSerValIysValSerGlySerGlyTyrThrPheT 49
|||||
467 CTAATTATTGATTCATAGTGCCTGCTCAGGCCCGCGAGGCGCTGAA 516
:: |||
49 hValAlaTyrGlnMetHisTyrValArgGlnAlaProGlyGlnGlyLeuGlu 65
|||||
517 TCGATGGGTGAGATCTTACCGGGCTGTGTAGCAGCCGAATATACGAAA 566
|||||
66 TTPMetGlyTyrPheIleAsnProAsnSerGlyGlyThrGlyGlyGlnIy 82
|||||
567 TTTTAAAGCGGTGTTACTATGACGGGTGACATTCGACTAGTACGAT 616
:|||||
82 sPheGlnGlyArgValThrLeuThrArgAspThrSerIleSerThrAlaT 99
|||||
617 ACATGAGAGCTCTCAGCTCGCATCGAGACGAGCGCTCTATTATTCG 666
|||||
99 yMeGlnLeuSerArgLeuThrSerAspSerPheAlaValIyTyrCys 115
|||||
667 GCG...CGTTATTTTGGTCTTACG.....CCGAATTGTTATTT 704
|||
116 AlaIleGlnTyrPheTyrAspGlySerAspLeuLysProSerAspValPh 132
|||||
705 TGATGTTGGGTCAAGAAACCTGTCACCTGCTCGAGC 744
|||||
132 eAspIleTyrGlyGlnGlyThrMetValThrValSerSer 145

```

seq_name: p1r2:D30562

seq_documentation_block:

Ig heavy chain V region (27.4b.2) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 16-Aug-1996
 C:Accession: D30562
 R:Silkder, S.K.; Borden, P.; Grunezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.I.
 J. Immunol. 142, 888-893, 1989
 A:Title: Amino acid substitutions in V-H CDR2 change the idotype but not the antigen-bi
 A:Reference number: A30562; MUID:89110066
 A:Accession: D30562
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-119 <STR>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

alignment_scores:
 Quality: 460.50 Length: 122
 Ratio: 4.225 Gaps: 1
 Percent Similarity: 89.344 Percent Identity: 68.852

alignment_block:
 US-08-487-283A-8 x D30562 ..

Align seg 1/1 to: D30562 from: 1 to: 119

```

379 CAACTCCAACTGTGTCATCCGCGCGAGGTCAAGAACGAGGCGCTC 428
|||||
1 GlnValGlnLeuGlnGlnSerGlyAlaGluLeuMetLysProGlyAla 17
|||||
429 AGTCAAAGTGTCTGTAAAGCTACGCGCTATATTTTCTAATTATGGA 478
|||||
17 rValIysIleSerCysLysAlaThrGlyTyrThrPheSerSerTyrTrpI 34
|||||
479 TTCAATGGGTGCTCAGCGCCCGCGAGGCGCTGAGTGAATGATGGTGAG 528
|||||
34 lGluTyrPValLysGlnArgProGlyHisGlyLeuGlnTyrPheIyGlu 50
|||||
529 ATCTTACCGGCTCTGTAGCAGCGAATATACGAAATTTTAAAGCG 578
|||||
51 lIlePheProGlySerGlySerSerAsnTyrSerGlnLysPheLysGly 67
|||||
579 TGTACTATGACGCGTGCACCTGTGACTAGTACATATACATGAGCTCT 628
|||||
67 sAlaThrPheThrAlaAspThrSerSerAsnThrAlaTyrMetGlnLys 84
|||||
629 CCAGCTCCGATTCAGGAGCAGCGCGCTCTATTATGGCGGCTATTTT 678
|||||
84 eSerLeuThrSerGlnAspSerAlaValIyTyrCysAlaArgHisTyr 100
|||||
679 TTTGGTCTCAGCCGCAATTGTTGATTTGATGTTGGGGTCAAGAACCT 728
|||||
101 TyrGlySerSerSer.....PheAlaTyrTyrPglGlnGlyThrIle 114
|||||
729 GGTACCTGTCTCGAGC 744
|||||
114 uValThrValSerAla 119

```

seq_name: p1r2:D33548

seq_documentation_block:

Ig heavy chain V-1 region (W1L2) - human
 C:Species: Homo sapiens (man)
 C:Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
 C:Accession: D33548
 R:Klips, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
 Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
 A:Title: Developmentally restricted immunoglobulin heavy chain variable region gene e
 A:Reference number: A33548; MUID:89345575
 A:Accession: D33548
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
 A:Molecule type: mRNA
 A:Residues: 1-123 <RIP>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

alignment_scores:
 Quality: 458.50 Length: 123
 Ratio: 4.168 Gaps: 1
 Percent Similarity: 89.431 Percent Identity: 72.358

alignment_block:

US-08-487-283A-8 x D33548 ..

Align seg 1/1 to: D33548 from: 1 to: 123


```

629 CCAGCCTGGGATCGAGACACGCCGCTATATTGCGCGCT..... 672
      |||||||||||||||||||||||||||||||||||
84 erSerLeuArGSerGIuAsPThrAlaValTYrCYsAlaArgProHis 100
      |||||||||||||||||||||||||||||||||||
673 .....TATTTTGGTCTAGCCCGAATGGTATTTT.. 705
      |||||||:|||||:|||||:|||||:|||||:
101 AlaSerIleAspAspPheTrpSerGIuTYrTYrProAsnTYrTYrTY 117
      |||||||:|||||:|||||:|||||:|||||:
706 .....GATGTTGGGTCACAGAACCCCTGTCACCTGTCGAGC 744
      |||||||||||||||||||||||||||||||
117 rclYMetAspValTrpGIyInGIyThrThrValThrValSerSer 132

```

OM of: US-08-487-283a-8 to: SwissProt_39:* out_format : pfs
Date: Jul 19, 2001 8:20 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL-frame+12p.model -DEV-xlp
-O=/cgn2_1/USPRO.spool/US08487283/runat_19072001.075938.3923/app_query.fasta_1.817
-DB=SwissProt_39 -OFMT=fasta -SUFFIX=tra.rsp -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPL=0.000 -LOOPEXT=0.000
-OGAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPEXT=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blomsu62
-TRAS=human40.cdi -LIST=45 -DOCLALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NOR=ext -MINLEN=0 -MAXLEN=200000000
-USER=US08487283 -ECGN_1_56 -NCRU=6 -ICPU=3 -LONGLOG -NO_XLFPY
-WAIT -THREADS=1

Search information block:

Query: US-08-487-283a-8
Query length: 747
Database: SwissProt_39:*
Database sequences: 93435
Database length: 34255486
Search time (sec): 24.910000

score_list:

Sequence	Strd Orig	ZScore	EScore	Len	Documentation
SwissProt_39:KV1H_HUMAN	444.00	673.49	6.6e-30	108	P01600 homo sapiens (human)
SwissProt_39:KV1M_HUMAN	442.00	670.47	9.8e-30	108	P01605 homo sapiens (human)
SwissProt_39:KV1B_HUMAN	437.00	662.21	2.6e-29	117	P01743 homo sapiens (human)
SwissProt_39:HV07_MOUSE	437.00	660.68	2.7e-29	139	P01751 mus musculus (mouse)
SwissProt_39:KV1R_HUMAN	435.00	661.42	3.1e-29	108	P01610 homo sapiens (human)
SwissProt_39:KV1K_HUMAN	435.00	659.91	3.8e-29	108	P01603 homo sapiens (human)
SwissProt_39:KV1P_HUMAN	435.00	659.91	3.8e-29	108	P01608 homo sapiens (human)
SwissProt_39:KV1A_HUMAN	433.00	656.81	4.7e-29	129	P04431 homo sapiens (human)
SwissProt_39:KV1B_HUMAN	433.00	656.89	5.6e-29	108	P01594 homo sapiens (human)
SwissProt_39:KV1O_HUMAN	431.00	653.87	8.2e-29	108	P01607 homo sapiens (human)
SwissProt_39:KV1Q_HUMAN	430.00	652.36	1.0e-28	108	P01609 homo sapiens (human)
SwissProt_39:KV1C_HUMAN	429.00	650.85	1.2e-28	108	P01595 mus musculus (mouse)
SwissProt_39:KV1N_HUMAN	429.00	650.85	1.2e-28	108	P01606 homo sapiens (human)
SwissProt_39:KV1J_HUMAN	428.00	649.34	1.5e-28	108	P01602 homo sapiens (human)
SwissProt_39:KV1G_HUMAN	425.00	644.81	2.6e-28	108	P01599 homo sapiens (human)
SwissProt_39:KV1V_HUMAN	425.00	644.81	2.6e-28	108	P04330 homo sapiens (human)
SwissProt_39:KV1E_HUMAN	423.00	641.79	3.9e-28	108	P01597 homo sapiens (human)
SwissProt_39:KV1S_HUMAN	423.00	641.79	3.9e-28	108	P01611 homo sapiens (human)
SwissProt_39:HV01_MOUSE	419.50	635.50	7.7e-28	121	P01745 mus musculus (mouse)
SwissProt_39:KV1A_HUMAN	419.00	635.76	8.4e-28	108	P01593 homo sapiens (human)
SwissProt_39:HV1C_HUMAN	418.00	631.50	1.1e-27	147	P01744 homo sapiens (human)
SwissProt_39:KV1D_HUMAN	417.50	633.58	1.1e-27	107	P01596 homo sapiens (human)
SwissProt_39:KV1X_HUMAN	413.00	625.12	2.8e-27	129	P04432 homo sapiens (human)
SwissProt_39:HV1G_HUMAN	411.00	622.92	4.0e-27	117	P23083 homo sapiens (human)
SwissProt_39:KV1F_HUMAN	408.00	619.15	7.1e-27	108	P01598 homo sapiens (human)
SwissProt_39:HV1I_MOUSE	408.00	617.03	7.3e-27	137	P01755 mus musculus (mouse)
SwissProt_39:KV1T_HUMAN	405.50	615.30	1.1e-26	109	P01612 homo sapiens (human)
SwissProt_39:KV1L_HUMAN	405.00	614.93	1.3e-26	108	P01614 homo sapiens (human)
SwissProt_39:HV12_MOUSE	401.50	608.65	2.5e-26	117	P01756 mus musculus (mouse)
SwissProt_39:HV50_MOUSE	401.00	607.65	2.8e-26	120	P06329 mus musculus (mouse)
SwissProt_39:KV5D_MOUSE	399.00	605.57	4.0e-26	108	P01536 mus musculus (mouse)
SwissProt_39:HV03_MOUSE	399.50	603.88	4.5e-26	120	P01747 mus musculus (mouse)
SwissProt_39:HV13_MOUSE	397.50	602.59	5.5e-26	117	P01757 mus musculus (mouse)
SwissProt_39:HV48_MOUSE	389.50	589.92	6.8e-26	138	P03880 mus musculus (mouse)
SwissProt_39:HV02_MOUSE	389.50	589.92	6.8e-26	140	P01748 mus musculus (mouse)
SwissProt_39:KV5S_MOUSE	387.00	587.46	4.1e-25	108	P01552 mus musculus (mouse)
SwissProt_39:KV5L_MOUSE	387.00	587.46	4.1e-25	108	P06330 mus musculus (mouse)
SwissProt_39:KV5T_MOUSE	379.00	575.38	1.9e-24	108	P01533 mus musculus (mouse)
SwissProt_39:KV5Q_MOUSE	378.00	573.88	2.3e-24	108	P01550 mus musculus (mouse)
SwissProt_39:KV1J_HUMAN	378.00	573.16	2.4e-24	117	P01602 homo sapiens (human)

SwissProt_39:KV1A_HUMAN	376.50	570.90	3.2e-24	117	P01742 homo sapiens (human)
SwissProt_39:KV1L_HUMAN	376.50	570.03	3.2e-24	129	P18135 homo sapiens (human)
SwissProt_39:KV1O_HUMAN	374.00	567.51	5.1e-24	112	P01613 homo sapiens (human)
SwissProt_39:HV38_MOUSE	566.97	5.2e-24	119	P01808 mus musculus (mouse)	
SwissProt_39:KV5J_MOUSE	373.00	566.33	6.2e-24	108	P01643 mus musculus (mouse)

seq_name: SwissProt_39:KV1H_HUMAN

seq_documentation_block:	STANDARD:	PRT:	108 AA.
ID	KV1H_HUMAN		
AC	P01600:		
DC	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DI	15-JUL-1993 (Rel. 38, Last annotation update)		
DE	IG KAPPA CHAIN V-I REGION HAV.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OX	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
NCBI_Taxid	9606;		
NCBI	[1]		

SEQUENCE.
RP MEDLINE=71032830; PubMed=4097974;
RX Watanabe S, Hilschmann N.;
RA "The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subgroup I (Bence-Jones Protein Hau): subdivision within subgroups."

RT Hoppe-Seiler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR, A01868; K1H0HU.
DR HSSP; P80362; 1MTL.
DR InterPro: IPR003006; -
DR Pfam: PF00047; 1g; 1.
KW Immunoglobulin L region; Bence-Jones protein.

FT	DOMAIN	1	23	FRAMEWORK 1
FT	DOMAIN	24	34	COMPLEMENTARITY-DETERMINING 1.
FT	DOMAIN	35	49	FRAMEWORK 2.
FT	DOMAIN	50	56	COMPLEMENTARITY-DETERMINING 2.
FT	DOMAIN	57	88	FRAMEWORK 3.
FT	DOMAIN	89	97	COMPLEMENTARITY-DETERMINING 3.
FT	DOMAIN	98	107	FRAMEWORK 4.
FT	DISULFID	23	88	BY SIMILARITY.
FT	NON_TER	108	108	
SO	SEQUENCE	108 AA;	11671 MW;	08D3A6160D8D0618 CRC64;

alignment_scores:
Quality: 444.00 Length: 108
Ratio: 4.440 Gaps: 0
Percent Similarity: 92.593 Percent Identity: 79.630

alignment_block:
US-08-487-283a-8 x KV1H_HUMAN ..

Align seg 1/1 to: KV1H_HUMAN from: 1 to: 108

7	GATATTCAGATGACCCAGTCCGCTCCCTGCGCGCTGTGGCGA	56
1	ASPILEDIMETHRGINSERPROSERSERLEUSERLASERVALGLYAS	17
57	TAGGTCACCATCAGCTGCGCGCCAGCAAGAAACATCATATGCGCGTGA	106
17	PAHYVALTHILIEHCHYSARGALASERGINSELTSETTYRLEUS	34
107	ACTGATATCAGCTAAACCTGCGAAGCTCCGACCTTGATTTACGTT	156
34	ETRPYRGINGINLYSPROGLYSLAPROGINVALLEUITYALA	50
157	GCACAGACCTGCGACATGAGTCCCTTCGCTTCGATCGCGGCTC	206
51	ALASERLEUPROSERGLYVALPROSERFARPHESERDLYSERGLYSE	67
207	CGAAGGATTCACCTCTGACCATCAGCATGCTGACGCTGAGACTTCG	256

```

|||||
67 rGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspPheA 84
257 CTACGATTAAGTGTGAGACGTTTAAATACCGCTTGACTTCGGACG 306
|||||
84 lArhTrTyrcysGlnGlnAsnTrpTlTherProThrSerPheGlyGln 100
307 GGTACCAAGGTGGAATAAAGCT 330
|||||
101 GlyThrArgValGluIleLysArg 108

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seq_name: SwissProt_39:KV1M_HUMAN

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seq_documentation_block:
ID KV1M_HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION LAY.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human
RT IgM anti-gamma globulins (Iay/Pom) with shared idiotypic
RT specificities."
RT Scand. J. Immunol. 5:677-684(1976).
CC -I- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POW-V-III KAPPA CHAIN,
CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
CC PIR: A01871; K1HULY.
DR HSSP; P01607; IREI.
DR InterPro: IPR003006; -.
DR Pfam; PF00047; 1g; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 3 49 FRAMEWORK 2.
FT DOMAIN 4 50 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 5 56 FRAMEWORK 3.
FT DOMAIN 6 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 7 107 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

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alignment_scores:

Quality:	442.00	Length:	108
Ratio:	4.557	Gaps:	0
Percent Similarity:	89.815	Percent Identity:	79.630

alignment_block:

US-08-487-283a-8 x KV1M_HUMAN

Align seg 1/1 to: KV1M_HUMAN from: 1 to: 108

```

7 GATATCGACATGACCCAGTCCCTCCCTCCGCTCTGTGGCGCA 56
|||||
1 AspIleGlnMetThrGlnSerProSerSerLeuSerValSerValGlyAs 17
457 TAGGGTCACCATCAGCTCGGGCGCCGAGCAAAACATCTATGGCGCGCTGA 106
|||||
17 pArgValThrIleThrCysGlnAlaSerGlnAsnValAlaSnAlaTyrIleuA 34
107 ACTGTATCAAGCTAAACCTGGGAAAGCTCCGAAGCTTCTGATTACGCT 156

```

```

|||||
34 snTrpTyGlnGlnInLysProGlyLeuAlaProLysLeuLeuIleTyrGly 50
157 GCGAGCAACCTCGCGCATGGAGTCCCTTCGCTCTCGTATCCGGCTC 206
|||||
51 AlAserThrArgGluAlaGlyAlaProSerArgPheSerGlySerGlySe 67
207 CGAAGCATTTCACTCTGACCATCAGCAGTCTGCAGCCCTGAGACTTCG 256
|||||
67 rGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspPheA 84
lArhTrTyrcysGlnGlnAsnTrpProThrSerPheGlyGln 100
257 CTACGATTAAGTGTGAGACGTTTAAATACCGCTTGACTTCGGACG 306
|||||
84 lArhTrTyrcysGlnGlnAsnTrpProThrSerPheGlyGln 100
307 GGTACCAAGGTGGAATAAAGCT 330
|||||
101 GlyThrArgValGluIleLysArg 108

```

seq_name: SwissProt_39:HV1B_HUMAN

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seq_documentation_block:
ID HV1B_HUMAN STANDARD; PRT; 117 AA.
AC P01743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-I REGION HG3 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=83144028; PubMed=6298778;
RA Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
RT "Evolutionary aspects of immunoglobulin heavy chain variable region
RT (VH) gene subgroups."
RT Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; J00240; AAA52988.1; -.
DR PIR; A02024; HVHUNG.
DR InterPro: IPR003006; -.
DR Pfam; PF00047; 1g; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION HG3.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1EF7 CRC64;

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alignment_scores:

Quality:	437.00	Length:	102
Ratio:	4.505	Gaps:	0
Percent Similarity:	95.098	Percent Identity:	82.353

alignment_block:

US-08-487-283a-8 x HV1B_HUMAN

Align seg 1/1 to: HV1B_HUMAN from: 1 to: 117

```

367 GGTGGCGGTCTCAAGTCCAGTGTGCAATCCGGCGCGAGGTCAAGAA 416
|||||
16 GlyAlaHisSerGlnValGlnLeuValGlnSerGlyAlaGluValLysLys 32

```



```

417 GCCAGGGGCTCACTCAAGCTCTCTGTAAGCTAGCGGTATATTTT 466
|||||
32 sproglyalaserVallysalserGlysalserGlyThrpheta 49
467 CTATATTGATTCATGAGGTGCGTCAGCGCCCGGAGCGCTTGAA 516
|||||
49 snserYrTyrMetHisTyrValArgGlnAlaProGlyGlnGlu 65
517 TGGATGGGTGAGATCTTACCGGCTCTGGTAGACCGAATATACGAAA 566
|||||
66 TrpMetGlyIleIleAsnProSerGlyGlySerThrSerYrAlaGln 82
567 TTTTAAGACCGCTGTACTATGAGCGCTGACACTTCGCTAGTACAGTAT 616
|||||
82 spheGlnGlyArgValThrMetThrArgAspThrSerThrSerThrVal 99
617 ACATGAGCTCTCCAGCTCGCATCGAGACGAGCGCGCTATATTATGC 666
|||||
99 YrMetGlyLeuSerSerLeuArgSerGlyAspThrAlaValTyrTyrCys 115
667 GCGCGT 672
|||||
116 AlArg 117

```

seq_name: SwissProt_39:HV07_MOUSE

seq_documentation_block:

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ID HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION B1-8/186-2 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reih M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: J00529; AAA38170.1; -
CC PIR: A02034; MHMS18.
CC InterPro: IPR003006; -
CC DR Pfam: PF00047; 19; 1.
CC KW Immunoglobulin V region; Signal.
FT CHAIN 1 19
FT SIGNAL 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARTY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARTY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.

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FT NON_TER 139 139
SQ SEQUENCE 139 AA; 13419 MW; 1857DD4FD0C9F465 CRC64;

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alignment_scores:
  Quality: 437.00      Length: 127
  Ratio: 4.009        Gaps: 2
  Percent Similarity: 85.827      Percent Identity: 65.354

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alignment_block:
US-08-487-283a-8 x HV07_MOUSE ..

Align seg 1/1 to: HV07_MOUSE from: 1 to: 139

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367 GGTGGGGTTCACATGTCACATGTCACATCGCGCCGAGGTCAGAA 416
|||||
16 GlyValHisSerGlnValGlnLeuGlnProGlyAlaGlnLeuVal 32
417 GCCAGGGGCTCAGTCAAGCTGCTGTAAGCTAGCGGCTATATTTT 466
|||||
32 sproglyalaserVallylsleuSerGlysalserGlyTyrThrPhe 49
467 CTATATTGATTCATGAGGTGCGTCAGCGCCCGGAGCGGCTTGAA 516
|||||
49 hrSerYrTyrMetHisTyrValGlnArgProGlyArgGlyLeuGlu 65
517 TGGATGGGTGAGATCTTACCGGCTCTGGTAGACCGAATATACGAAA 566
|||||
66 TrpIleGlyArgIleAsnProAsnSerGlyGlyThrLysTyrAsnGlu 82
567 TTTTAAGACCGCTGTACTATGAGCGCTGACACTTCGACTAGTACAGTAT 616
|||||
82 spheLysSerLysAlaThrLeuThrValAspLysProSerSerThrAla 99
617 ACATGAGCTCTCCAGCTCGCATCGAGACGAGCGCGCTCTTTATATGC 666
|||||
99 YrMetGlnLeuSerSerLeuThrSerGlnAspSerAlaValTyrTyrCys 115
667 GCGCGTAT...TTTWTGGTCTTACCGCCGAATGATTTATGTTTG 713
|||||
116 AlArgTyrAspTyrTyrGlySerSer.....TyrPheAspTyrTr 129
714 GGGTCAGGAACCCGTGCTCAGCTCTCGAGC 744
|||||
129 pGlyGlnGlyThrThrLeuThrValSerSer 139

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seq_name: SwissProt_39:KV1R_HUMAN

seq_documentation_block:

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ID KV1R_HUMAN STANDARD; PRT; 108 AA.
AC P01610;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION WEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
RT (protein WEA) with antibody activity against 3,4-pyruvylated
RT galactose in Klebsiella polysaccharides K30 and K33.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC WALDENSTROM'S MACROGLOBULINEMIA.
CC PIR: A01876; K1HOME.
CC HSSP: P80362; 1WTL.
CC DR InterPro: IPR003006; -

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DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Monoclonal antibody.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;

alignment_scores:
Quality: 436.00 Length: 108
Ratio: 4.495 Gaps: 0
Percent Similarity: 89.815 Percent Identity: 78.704

alignment_block:
US-08-487-283a-8 x KV1R_HUMAN ..
Align seg 1/1 to: KV1R_HUMAN from: 1 to: 108

7 GATATCCAGATGACCCAGTCCCGCTCCCTGTCGCCCTGTGGCGCA 56
|||||
1 AspliegImethrGlnSerProserSerleuSerValGlyAs 17
57 TAGGTCACCATCCTCGCGCGCCAGCAAAATCATATGCGCGCTGA 106
|||||
17 parGValThrIleThrCysArgAlaSerGlnGlyIleArgAsnAspLeu 34
107 ACTGATCAAGTAACTCGGAAGCTCCGAAGCTCTGATTTAGGT 156
|||||
34 htrpPrglnGlnLysProGlyThrAlaProLysArgLeuIleTyrGly 50
157 GCGACGACCTGGCAGATGAGTCCCTCTCGCTCTGATCCGCGCTC 206
|||||
51 AlaThrSerLeuGlnSerGlyValProSerArgPheSerIleSerGly 67
207 CGGACGCGATTTCATCTGACCATCAGACATGCGACCTGGAAGACTTCG 256
|||||
67 rGlyThrGluPheThrLeuThrIleAsnSerLeuGlnProGluAspPhe 84
257 CTACGATTATCTGTCAGACGTTTAAATCTCCGTTGACTTCGCGAG 306
|||||
84 IaThrTyrTyrCysLeuGlnTyrSerSerPheProItrPheGlyGln 100
307 GGTACCAAGGTGGAATAAAGCT 330
|||||
101 GlyThrLysValGluValLysArg 108

seq_name: SwissProt_39:KV1K_HUMAN

seq_documentation_block:
ID KV1K_HUMAN STANDARD; PRT; 108 AA.
AC P01603;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION KA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76189985; PubMed=818073;
RA 'Shinoda T.;
RT Comparative structural studies on the light chains of human
RT immunoglobulins. I. Protein Ka with the Inv(3) allotypic marker.*;
RL J. Biochem. 77:1277-1296(1975).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01869; KIHUKA.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006;
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11900 MW; 768839FED5A2F4B CRC64;

alignment_scores:
Quality: 435.00 Length: 108
Ratio: 4.350 Gaps: 0
Percent Similarity: 92.593 Percent Identity: 73.148

alignment_block:
US-08-487-283a-8 x KV1K_HUMAN ..
Align seg 1/1 to: KV1K_HUMAN from: 1 to: 108

7 GATATCCAGATGACCCAGTCCCGCTCCCTGTCGCCCTGTGGCGCA 56
|||||
1 AspliegImethrGlnSerProserThrleuSerValGlyAs 17
57 TAGGTCACCATCCTCGCGCGCCAGCAAAATCATATGCGCGCTGA 106
|||||
17 parGValThrIleThrCysGluAlaSerGlnThrValLeuSerTyrLeu 34
107 ACTGATCAAGTAACTCGGAAGCTCCGAAGCTCTGATTTAGGT 156
|||||
34 sntrpTyrGlnGlnLysProGlyLysAlaProLysLeuLeuIleTyrAla 50
157 GCGACGACCTGGCAGATGAGTCCCTCTCGCTCTGATCCGCGCTC 206
|||||
51 AlaSerSerLeuGlnThrGlyValProSerArgPheSerGlyGlnGly 67
207 CGGACGCGATTTCATCTGACCATCAGACATGCGACCTGGAAGACTTCG 256
|||||
67 rGlyThrPheThrPheThrIleSerSerVal**Pro*****Phe 84
257 CTACGATTATCTGTCAGACGTTTAAATCTCCGTTGACTTCGCGAG 306
|||||
84 IaThrTyrTyrCysGln***TyrLeuAspLeuProArgThrPheGlyGln 100
307 GGTACCAAGGTGGAATAAAGCT 330
|||||
101 GlyThrLysValAspLeuLysArg 108

seq_name: SwissProt_39:KV1P_HUMAN

seq_documentation_block:
ID KV1P_HUMAN STANDARD; PRT; 108 AA.
AC P01608;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION ROY.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68362076; PubMed=5595110;
RA Hilschmann N.;

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RT 2Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
RT 'Cum.')";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN [2]
RN REVISIONS TO 39 AND 41.
RA Hiltmann N., Barntkol H.U., Hess M., Langer B., Ponsingl H.,
RA Steinmetz-Kayne M., Suter L., Matanabe S.;
RL (in) Franek F., Shugar D. (eds.);
RL Gamma globulins: structure and function, pp.57-74, Academic Press,
RL New York (1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01874; KIHURY.
DR HSSP: P80362; IWTU.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; 1g: 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 3 49 FRAMEWORK 2.
FT DOMAIN 4 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 5 57 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 6 88 FRAMEWORK 3.
FT DOMAIN 7 97 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 23 107 FRAMEWORK 4.
FT NON-TER 108 88 BY SIMILARITY.
SQ SEQUENCE 108 AA; 11782 MW; F5ACEDE5A313DF3A CRC64;

alignment_scores:
Quality: 435.00 Length: 108
Ratio: 4.485 Gaps: 0
Percent Similarity: 89.815 Percent Identity: 79.630

alignment_block:
US-08-487-283a-8 x KVIW_HUMAN ..

Align seg 1/1 to: KVIW_HUMAN from: 1 to: 108

7 GATATCCAGATGACCCAGTCCCGTCTCCGCTGCGCTGTGGCGA 56
1 AspilegImethrInserProserSerleuSerAlaSerValGlyAs 17
57 TAGGTCACCATCACCCTGCGCGCCAGCAAAACATCTATGCGCGCTGA 106
17 parGValThrIleThrcysGlnAlaSerGlnAspIleSerIlePheLeuA 34
107 ACTGATATCAGCTAAACCTGGGAAGCTCCGAAGCTTGTGATTACGGT 156
34 snrPtyrGlnGlnLysProGlyLysAlaProLysLeuIleTyrAsp 50
157 GCGAGCAACCTGGCAGATGAGTCCCTTCGCTTCCTGATCCGCTC 206
51 AlaserLysleuGlnAlaGlyValProserArgPheSerGlyThrGlySe 67
207 CGGAACGATTTCACTCTGACATCAGCATCTGACAGCTGAAAGACTTCG 256
67 rGlyThrAspPheThrIleSerSerleuGlnProGluAspIleA 84
257 CTACGATTAATCTGTCAGAACGTTTAAATACCTCGTTCGATTGGACAG 306
84 lathrIlyrTyrcysGlnGlnPheAspAsnLeuProLeuThrPheGlyGly 100
307 GGTACCAAGGTGGAATAAAGCT 330
101 GlyThrLysValAspPheLysArg 108

seq_name: SwissProt_39: KVIW_HUMAN

seq_documentation_block:
ID KVIW_HUMAN STANDARD; PRT; 129 AA.
AC P04431;

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DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION WALKER PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; Pubmed=6091049;
RA Klobbeck H.G., Combratio G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RL lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X00965; CAA25477.1; ALT-TERM.
DR PIR: A01883; KIHUWK.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; 1g: 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
FT DOMAIN 23 45 FRAMEWORK 1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 57 71 FRAMEWORK 2.
FT DOMAIN 72 78 FRAMEWORK 2.
FT DOMAIN 79 110 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 111 119 FRAMEWORK 3.
FT DOMAIN 120 129 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 45 110 FRAMEWORK 4.
FT NON-TER 129 129 BY SIMILARITY.
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4ARC2F9 CRC64;

alignment_scores:
Quality: 434.00 Length: 107
Ratio: 4.429 Gaps: 0
Percent Similarity: 91.589 Percent Identity: 79.439

alignment_block:
US-08-487-283a-8 x KVIW_HUMAN ..

Align seg 1/1 to: KVIW_HUMAN from: 1 to: 129

7 GATATCCAGATGACCCAGTCCCGTCTCCGCTGCGCTGTGGCGA 56
23 AspilegImethrInserProserSerleuSerAlaSerValGlyAs 39
57 TAGGTCACCATCACCCTGCGCGCCAGCAAAACATCTATGCGCGCTGA 106
39 parGValThrIleThrcysArgAlaSerGlnIleSerAspTyrLeuA 56
107 ACTGATATCAGCTAAACCTGGGAAGCTCCGAAGCTTGTGATTACGGT 156
56 snrPtyrGlnGlnLysProGlyLysAlaProLysLeuIleTyrAla 72
157 GCGAGCAACCTGGCAGATGAGTCCCTTCGCTTCCTGATCCGCTC 206
73 AlaserSerleuGlnSerGlyValThrSerArgPheSerGlySerGlySe 89
207 CGGAACGATTTCACTCTGACATCAGCATCTGACAGCTGAAAGACTTCG 256
89 rGlyThrAspPheThrIleSerSerleuGlnProGluAspIleA 106

```

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seq_name: SwissProt_39:KV1O_HUMAN
seq_documentation_block:
ID      KV1O_HUMAN          STANDARD;              PRT;           108 AA.
AC      P01607;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      IG KAPPA CHAIN V-I REGION REL.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_Taxid=9606;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE=76023758; PubMed=809329;
RA      Palm W., Hilschmann N.;
RT      "The primary structure of a crystalline monoclonal immunoglobulin
RT      kappa-type L-chain, subgroup I (Bence-Jones protein Rel.); isolation
RT      and characterization of the tryptic peptides; the complete amino acid
RT      sequence of the protein: a contribution to the elucidation of the
RT      three-dimensional structure of antibodies, in particular their
RT      combining site.";
RL      Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN      [2]
RP      X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX      MEDLINE=76039968; PubMed=1182131;
RA      Edp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT      "The molecular structure of a dimer composed of the variable portions
RT      of the Bence-Jones protein RFI refined at 2.0-A resolution.";
RL      Biochemistry 14:4943-4952(1975).
CC      CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (L,2)
CC      MARKER.
CC      -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR      PIR: A01873; KIHURE.
DR      PDB: 1REI; 17-FEB-84.
DR      InterPro: IPRO03006; -.
DR      Pfam: PF00047; 19; 1.
KW      Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT      DOMAIN             1         23       FRAMEWORK 1.
FT      DOMAIN             2         34       FRAMEWORK 2.
FT      DOMAIN             3         49       FRAMEWORK 3.
FT      DOMAIN             4         56       FRAMEWORK 4.
FT      DOMAIN             5         66       COMPLEMENTARITY-DETERMINING 1.
FT      DOMAIN             6         88       COMPLEMENTARITY-DETERMINING 2.
FT      DOMAIN             7         97       COMPLEMENTARITY-DETERMINING 3.
FT      DOMAIN             8         107      COMPLEMENTARITY-DETERMINING 4.
FT      DISUFID            23        88
FT      STRAND             4           7

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FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 45 52
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 85 90
FT STRAND 98 98
FT STRAND 102 106
FT NON_TER 108 108
SQ SEQUENCE 108 AA: 11902 MW: 9E8143E1188BCE2A CRC64;
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alignment_scores:
Quality: 431.00 Length: 108
Ratio: 4.537 Gaps: 0
Percent Similarity: 87.963 Percent Identity: 77.778

alignment_block:
US-08-487-283A-8 x KV10_HUMAN

Align seg 1/1 to: KV10_HUMAN from: 1 to: 108

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7 GATATCCAGATGACCCAGTCCCTCCCTGCGCTCTGCGCGA 56
|||||
1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAs 17
57 TAGGTCACCATCACCCTGCGCGCCAGCAAAACATCTATGGCGCTGA 106
|||||
17 pArgValThrIleThrCysGlnAlaSerGlnAspIleLeuStyLeuA 34
107 ACTGGATACAGCTGAACCTGGGAAGCTCGAAGCTTCGATTACGCT 156
|||||
34 snTrpTyrGlnGlnThrProGlyLysAlaProLysLeuLeuIleTyrGlu 50
157 GCGACGAACTGGCAGATGAGTCCCTGCTGCTGATCCGCGCTC 206
|||||
51 AlaSerThrLeuGlnAlaGlyValProSerArgPheSerGlySerGlySe 67
207 CGGAACGATTTCACTGACCATCAGCATCAGCTGACCGCTGAAGACTTCG 256
|||||
67 rGlyThrAspTyrThrPheThrIleSerSerLeuGlnProGlnAspIleA 84
257 CTACGATTACTCTGACGAACTTTTAATACCTCCGTTGACTTTCGGACAG 306
|||||
84 lAsnTyrTyrCysGlnGlnTyrGlnSerLeuProTyrThrPheGlyGln 100
307 GGTACCAAGCTGGAATAAATACG 330
|||||
101 GlyThrLysLeuGlnIleThrArg 108
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seq_name: SwissProt_39:KV10_HUMAN

seq_documentation_block:

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ID KV10_HUMAN STANDARD: PRT: 108 AA.
AC P01609;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION SCM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_taxid=9606;
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RN [1]
RP SEQUENCE.
RX MEDLINE=75059271; PubMed=4435756;
RA Eulitz M., Hilschmann N.;
RT "The primary structure of a human immunoglobulin L-chain of
RT kappa-type (Bence-Jones protein scw.), II: The chymotryptic peptides
RT and the complete amino acid sequence."
RL Hoppe-Seyler's Z. Physiol. Chem. 355:842-866(1974).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01875; KIHUSW.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; 1g; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA: 11764 MW: 32CECDDE9644414 CRC64;
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alignment_scores:
Quality: 430.00 Length: 107
Ratio: 4.388 Gaps: 0
Percent Similarity: 91.589 Percent Identity: 77.570

alignment_block:
US-08-487-283A-8 x KV10_HUMAN

Align seg 1/1 to: KV10_HUMAN from: 1 to: 108

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7 GATATCCAGATGACCCAGTCCCTCCCTGCGCTCTGCGCGA 56
|||||
1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAs 17
57 TAGGTCACCATCACCCTGCGCGCCAGCAAAACATCTATGGCGCTGA 106
|||||
17 pArgValThrIleThrCysGlnAlaSerGlnAspIleArgLysIleuA 34
107 ACTGGATACAGCTGAACCTGGGAAGCTCGAAGCTTCGATTACGCT 156
|||||
34 snTrpTyrAspGlnLysProGlyLysAlaProArgLeuLeuIleTyrGly 50
157 GCGACGAACTGGCAGATGAGTCCCTGCTGCTGATCCGCGCTC 206
|||||
51 AlaSerThrLeuGlnThrGlyValProSerArgPheSerGlySerGlySe 67
207 CGGAACGATTTCACTGACCATCAGCATCAGCTGACCGCTGAAGACTTCG 256
|||||
67 rGlyThrAspPheThrLeuThrIleSerThrLeuGlnProGlnAspIleG 84
257 CTACGATTACTCTGACGAACTTTTAATACCTCCGTTGACTTTCGGACAG 306
|||||
84 lAsnTyrTyrCysGlnGlnTyrAspAsnValProIleThrPheGlyGln 100
307 GGTACCAAGCTGGAATAAATAA 327
|||||
101 GlyThrArgValGlnAsnLys 107
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seq_name: SwissProt_39:KV1C_HUMAN

seq_documentation_block:

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ID KV1C_HUMAN STANDARD: PRT: 108 AA.
AC P01595;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
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DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-I REGION BI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=73029807; Pubmed=4563064;
 RA Braun M., Leibold W., Barikol H.U., Hilschmann N.;
 RT "Principle of antibody structure. The primary structure of a
 RT monoclonal kappa I-type immunoglobulin L-chain (Bence Jones protein
 RT B1). 3. The complete amino acid sequence and the genetic
 RT significance of the variability principles for the mechanism of
 RT antibody formation.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:1284-1306(1972).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENGE-JONES PROTEIN.
 DR PIR; A01863; KIHUBI.
 DR HSP; P01607; IREI.
 DR InterPro; IPR003006; -.
 DR Pfam; PF00047; Ig; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT 24 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 2 35 49 FRAMEWORK 2.
 FT DOMAIN 3 50 56 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 4 57 88 FRAMEWORK 3.
 FT DOMAIN 5 89 97 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 6 98 107 FRAMEWORK 4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 12026 MW; 7A83983986A431E7 CRC64;

alignment_scores:
 Quality: 429.00 Length: 108
 Ratio: 4.564 Gaps: 0
 Percent Similarity: 87.037 Percent Identity: 77.778

alignment_block:
 US-08-487-283a-8 x KV1C_HUMAN ..
 Align seg 1/1 to: KV1C_HUMAN from: 1 to: 108

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7 GATATCCAGATGACCAAGCCGCTCCCTGCTCCGCTGCGCTGCGGCGA 56
|||||
1 AsplieglnmetrlhlnserProserProleuserAlaservAlgylas 17
57 TAGGTCACCATCACCTGCGGCGCCAGCAAAACATCTATGCGCGCTGA 106
|||||
17 pserValthrIethrhcysglAlaservlAsplleargAsnserLeu 34
107 ACTGCTATCAACGTAACCTGGGAAAGCTCCGAAAGCTTGTGATTACGGT 156
|||||
34 IetrptylglnlInysprogllyslAProlyshleuIletryasp 50
157 GCGAGAACCTGGCAGATGAGTCCCTTCTGCTTCTGATGATCGGCTC 206
|||||
51 AlagluAnleuGlulIleGlYvalProserArgphearglYserIlyse 67
207 CGGACGAGATTTCACCTGACCATGACGAGTCTGCGCTGGAAGACTTCG 256
|||||
67 rglYthrspheAlaleuSerIleSerSerleuGlInProgluAsPheh 84
257 CTACGTATTACTGTCCAGAACGTTTAAATATCTCCGTTGACTTTCGACAG 306
|||||
84 laThrTyTrtyCysglnglnInyTrYrAsnleuProtyrThrPheglYgln 100
307 GGTACCAAGGTGGAATAAACCT 330
|||||
101 GlyThrIysleuGlulIleYsarY 108
  
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seq_name: SwissProt_39:KV1N_HUMAN
 seq_documentation_block:
 ID KV1N_HUMAN STANDARD; PRT; 108 AA.
 AC P01606;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-I REGION OU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=70201507; Pubmed=5447531;
 RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
 RT "Macroglobulin structure: variable sequence of light and heavy
 RT chains.";
 RL Science 169:56-59(1970).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
 CC MACROGLOBULIN.
 DR PIR; A01872; KIHOU.
 DR HSP; P01607; IREI.
 DR InterPro; IPR003006; -.
 DR Pfam; PF00047; Ig; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT 24 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 2 35 49 FRAMEWORK 2.
 FT DOMAIN 3 50 56 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 4 57 88 FRAMEWORK 3.
 FT DOMAIN 5 89 97 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 6 98 107 FRAMEWORK 4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11777 MW; 8283DA24105827E CRC64;

alignment_scores:
 Quality: 429.00 Length: 108
 Ratio: 4.248 Gaps: 0
 Percent Similarity: 93.519 Percent Identity: 69.444

alignment_block:
 US-08-487-283a-8 x KV1N_HUMAN ..
 Align seg 1/1 to: KV1N_HUMAN from: 1 to: 108

```

7 GATATCCAGATGACCAAGCCGCTCCCTGCTCCGCTGCGCTGCGGCGA 56
|||||
1 AsplieglnmetrlhlnserProserProleuserAlaservAlgylas 17
57 TAGGTCACCATCACCTGCGGCGCCAGCAAAACATCTATGCGCGCTGA 106
|||||
17 ArgvalThrIethrhcysArgAlaser***ThrIleSerSerYrleu* 34
107 ACTGCTATCAACGTAACCTGGGAAAGCTCCGAAAGCTTGTGATTACGGT 156
|||||
34 **TrpTyrr****LysProcllyslAPro****LeuIleulIeYrAla 50
157 GCGAGAACCTGGCAGATGAGTCCCTTCTGCTTCTGATGATCGGCTC 206
|||||
51 Alaser***LeuHlsSergYvalProserArgphearglYserIlyse 67
207 CGGACGAGATTTCACCTGACCATGACGAGTCTGCGCTGGAAGACTTCG 256
|||||
67 rglYThr***PheThrPheThrIleSerSerleu***Pro*****Pheh 84
257 CTACGTATTACTGTCCAGAACGTTTAAATATCTCCGTTGACTTTCGACAG 306
|||||
84 laThrTyTrtyCys****SerTySerSerProThrThrPheglY*** 100
  
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307 GGTACCAAGGTGGAATAAAACGT 330
      |||||:::|||||
101 GlyThrargLeu**IleIysarg 108

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57 TAGGTCACCATCCTGCGCGCCGCAAGCAAAACATCTATGCGCGCTGA 106
|||||
17 parValThrIleIleCysArgAlaSerGlnGlyIleArgAsnAspLeuT 34
|||||
107 ACTGATATCAACGTAACCTGGGAAGCTCCGAAGCTCTGATTACGCT 156
|||||
34 hTTPtyrGlnGlnLysProGlyLysAlaProLysGlnLeuIleTyrAla 50
|||||
157 GCGACGACCTGCGCAGATGAGTCCCTTCGCTCTCTGATCCGCGCTC 206
|||||
51 AlaSerAsnLeuGlnSerGlyValProSerArgPheSerGlyAla 67
|||||
207 CGGACGATTCATCTCTGACCATCAGCAGCTGCAAGCTGAAGACTTCG 256
|||||
67 aglyThrGlnPheThrLeuThrIleSerSerLeuGlnProGlnAspPheA 84
|||||
257 CTACGTATTAATCTCAGAACGTTTAAATACCTGCTGACTTCGCGACAG 306
|||||
84 IathrTyrTyrCysLeuGlnGlnAsnSerTyrProArgSerPheGlyGln 100
|||||
307 GGTACCACAGTGGAAATAAAACGT 330
|||||
101 GlyThrLysValGlnIleLysArg 108

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CM of: US-08-487-283a-8 to: SPTREMBL_16.* out_format : pfs

Date: Jul 19, 2001 8:21 AM

About: Results were produced by the Gencore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL=frame+...-DEV=xlp
-O/cgn2_1/USPO.spool/US08487283/runat_19072001_075938_3893/app.query.fasta_1.817
-DB=SPTREMBL_16 -OFMT=fastan -SUFFIX=tra.rspt -GAPOP=12.000
-GAPEXT=4.000 -NIMATCH=0.100 -LOOPTCL=0.000 -LOPEXT=0.000
-GAPOP=4.500 -GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -TGAPOP=10.000 -TGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blsum62
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR_SCORE=pcp
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -MINLEN=0 -MAXLEN=200000000
-USER=US08487283@cgn1_1.219 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPRX
-WAIT -THREADS=1

Search information block:

Query: US-08-487-283a-8
Query length: 747
Database: SPTREMBL_16.*
Database sequences: 425026
Database length: 132305027
Search time (sec): 76.780000

score_list:

Sequence	Strd Orig	ZScore	EScore	Len	Documentation
SP_human:Q9UL92	+	482.00	813.25	3.7e-37	124 Q9UL92 homo sapiens (human) . my
SP_human:Q9UL94	+	451.50	761.94	2.8e-34	119 Q9UL94 homo sapiens (human) . my
SP_human:Q9UL77	+	451.00	761.93	3.0e-34	108 Q9UL77 homo sapiens (human) . my
SP_human:Q9UL95	+	446.50	753.05	8.2e-34	125 Q9UL95 homo sapiens (human) . my
SP_human:Q9UL89	+	445.00	751.15	1.1e-33	116 Q9UL89 homo sapiens (human) . my
SP_invertebrate:Q9GY22	+	430.50	726.38	2.6e-32	119 Q9GY22 schistosoma japonicum
SP_human:Q9UL70	+	425.00	717.89	8.6e-32	108 Q9UL70 homo sapiens (human) . my
SP_rhodent:Q9Z1C4	+	423.00	713.74	1.3e-31	118 Q9Z1C4 mus musculus (mouse) . ar
SP_human:Q9UL81	+	421.50	712.04	1.8e-31	107 Q9UL81 homo sapiens (human) . my
SP_human:Q95978	+	416.50	700.29	5.7e-31	157 Q95978 homo sapiens (human) . v1
SP_human:Q9UL79	+	407.00	687.40	4.3e-30	108 Q9UL79 homo sapiens (human) . my
SP_rhodent:Q9QYF0	+	405.00	675.33	7.3e-30	158 Q9QYF0 mus musculus (mouse) . cr
SP_human:Q9X298	+	397.50	668.50	3.5e-29	150 Q9X298 homo sapiens (human) . id
SP_rhodent:Q9QXFO	+	389.00	657.08	1.9e-28	117 Q9QXFO mus musculus (mouse) . id
SP_rhodent:Q9R1A5	+	379.00	634.12	2.0e-27	214 Q9R1A5 mus musculus (mouse) . ka
SP_rhodent:Q9QXES	+	373.50	629.98	6.3e-27	117 Q9QXES mus musculus (mouse) . lit
SP_rhodent:Q9JL81	+	373.00	629.35	7.0e-27	114 Q9JL81 mus musculus (mouse) . ar
SP_human:Q9UL83	+	371.00	626.43	1.1e-26	108 Q9UL83 homo sapiens (human) . my
SP_rhodent:Q9JL77	+	371.00	626.27	1.1e-26	110 Q9JL77 mus musculus (mouse) . ar
SP_human:Q9UL85	+	368.50	622.12	1.8e-26	109 Q9UL85 homo sapiens (human) . my
SP_human:Q9UL78	+	368.50	622.12	1.8e-26	109 Q9UL78 homo sapiens (human) . my
SP_rhodent:Q9JL83	+	360.00	607.64	1.2e-25	110 Q9JL83 mus musculus (mouse) . ar
SP_rhodent:Q9JL75	+	356.00	600.94	2.8e-25	109 Q9JL75 mus musculus (mouse) . ar
SP_rhodent:Q9JL84	+	348.00	587.55	1.6e-24	107 Q9JL84 mus musculus (mouse) . ar
SP_human:Q9UL86	+	342.50	578.08	5.2e-24	109 Q9UL86 homo sapiens (human) . my
SP_rhodent:Q9Z1C6	+	341.50	575.78	6.6e-24	117 Q9Z1C6 mus musculus (mouse) . ar
SP_human:Q9UL88	+	341.50	574.81	6.6e-24	131 Q9UL88 homo sapiens (human) . my
SP_human:Q9UL71	+	339.50	572.10	1.0e-23	121 Q9UL71 homo sapiens (human) . my
SP_human:Q9Y504	+	334.00	561.12	3.9e-23	147 Q9Y504 homo sapiens (human) . v1
SP_human:Q9UL84	+	332.00	559.33	5.2e-23	122 Q9UL84 homo sapiens (human) . my
SP_human:Q9HCC1	+	328.00	553.29	1.2e-22	112 Q9HCC1 homo sapiens (human) . si
SP_human:Q9UL90	+	327.50	552.37	1.4e-22	113 Q9UL90 homo sapiens (human) . my
SP_human:Q9UL91	+	326.00	551.15	1.5e-22	118 Q9UL91 homo sapiens (human) . my
SP_rhodent:Q9ER72	+	326.00	549.45	1.9e-22	118 Q9ER72 homo sapiens (human) . my
SP_rhodent:Q9ER79	+	323.00	545.21	3.6e-22	107 Q9ER79 mus musculus (mouse) . ar
SP_invertebrate:Q9U410	+	322.50	544.44	4.0e-22	106 Q9U410 schistosoma japonicum
SP_rhodent:Q9JL85	+	318.50	537.47	9.6e-22	109 Q9JL85 mus musculus (mouse) . ar
SP_human:Q9UL93	+	315.50	531.82	1.9e-21	116 Q9UL93 homo sapiens (human) . my
SP_rhodent:Q9JL74	+	313.00	528.94	3.1e-21	99 Q9JL74 mus musculus (mouse) . ar
SP_mammal:Q9N0W4	+	312.00	525.32	4.0e-21	124 Q9N0W4 oryctolagus cuniculus (d

SP_mammal:Q9N0W6	+	309.00	520.24	7.7e-21	124 Q9N0W6 oryctolagus cuniculus
SP_mammal:Q9N0W5	+	306.00	516.26	1.5e-20	109 Q9N0W5 oryctolagus cuniculus
SP_rhodent:Q9JL80	+	304.00	513.36	2.2e-20	103 Q9JL80 mus musculus (mouse) .
SP_rhodent:Q9JL78	+	303.00	511.83	2.8e-20	101 Q9JL78 mus musculus (mouse) .
SP_human:Q9UL73	+	298.50	502.80	7.5e-20	119 Q9UL73 homo sapiens (human) .

seq_name: sp_human:Q9UL92

seq_documentation_block:

ID	Q9UL92	PRELIMINARY:	PRT:	124 AA.
AC	Q9UL92:			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)			
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE:98277139; PubMed:9614934;			
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,			
RT	Young D.C.;			
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal			
RT	fetus.";			
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).			
CC	-I SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX			
CC	DOMAIN			
DR	EMBL: AF035022; AAD56258.1; -			
DR	InterPro: IPR003006; -			
DR	InterPro: IPR003596; -			
DR	Pfam: PF00047; Ig; 1.			
DR	SMART: SM00406; Ig; 1.			
FT	NON_TER	1	124	
FT	NON_TER	124	124	
SQ	SEQUENCE	124 AA;	13580 MW;	1BAACBD96ACD2A2 CRC64;

alignment_scores:

Quality:	482.00	Length:	124
Ratio:	4.342	Gaps:	1
Percent Similarity:	89.516	Percent Identity:	76.613

alignment_block:

US-08-487-283a-8 x Q9UL92 ..
Align seg 1/1 to: Q9UL92 from: 1 to: 124

379	CAAGTCAACATGCTGCAATCCGCGCGGAGGTCAGAAAGCCAGGGGCTC	428
1	GlutValGlnLeuValGlnSerGlyAlaGlnValLysProGlyAlaSer	17
429	AGTCAAGTCTGCTGTAAGCTAGCGGCTATATTTTCTAATATTGGA	478
17	TallysValSerCysLysAlaSerGlyTyrThrPheSerSerTyrTm	34
479	TTCATGGGTGGTGGTGGGCGGCGGAGGCTGATGATGAGGGGAG	528
34	ethIstrPalargGlnAlaProGlyGlnGlyLeuGlnLutPheMetGlyIle	50
529	ACTTTCACGGGCTCTGTAGACACGATATACGAAATTTTAAAGACG	578
67	gallrhmethrArgAspThrSerThrValAlaGlnLysPheGlnGlyLeu	84
579	TGTTACTATGACCGCTGACACTTGACTGACTAGTACATACATGAGACTC	628
629	CCAGCTGCGATCGAGACACGCGGCTATATTGCGGCTTATTTT	678
84	erSerLeuArgSerGlnAspThrAlaValTyrTyrCysAlaArgGlyLeu	100

```

679 TTGGTCTAGCCGCAATGTAT.....TTTGATTTGGGCTGACG 722
      ::|||:::|||||
101 TTTValValValProAlaIAlaPheSerArgPheAspTyrTrpGlyGlnG 117
      |||||
723 AACCTGCTACTGCTCTGAGC 744
      |||||
117 TTTLeuValThrValSerSer 124

```

seq_name: sp_human:Q9UL94

seq_documentation_block:

```

ID Q9UL94 PRELIMINARY; PRT; 119 AA.
AC Q9UL94;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -! SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF035020; AAD56256.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 119
FT SEQUENCE 119 AA; 13205 MW; 13664F5345FA16E CRC64;

```

alignment_scores: Quality: 451.50 Length: 122
Ratio: 4.142 Gaps: 1
Percent Similarity: 89.344 Percent Identity: 71.311

alignment_block:

US-08-487-283a-8 x Q9UL94 ..

Align seg 1/1 to: Q9UL94 from: 1 to: 119

```

379 CAAGTCCAACTGGTCAATCCGCGCCGCGCAAGACAGACGAGCGGCTC 428
      ::|||:::|||||
1 GluValGlnLeuValGlnSerGlyAlaGlnValLysProGlyAlaSer 17
429 ACTCAAGTCTCTGTAAAGTACGCGCTATATTTTCTCAATATTATGGA 478
      |||||
17 rValLysValSerGlyAlaSerGlyTyrThrPheThrGlnGlyTyrTrp 34
479 TTCAATGGGTGCGTCAGCGCCCGGCGAGGCGCTGGAATGATGGTGAG 528
      ::|||
34 eHisTrpValArgGlnAlaProGlyGlnGlyLeuGlnLysTrpMetGlyTrp 50
529 ATCTTACCGGGCTCTGTGTCAGACCGCAATATACGAAATTTTAAAGCG 578
      |||
51 IleAsnProAsnSerTrpThrAsnTyrAlaGlnLysPheGlnGlyTrp 67
579 TGTACTATGACGCGTACACTTCGACTGACGATGATGACGACTCT 628
      :|||
67 sValThrMetThrLysAspThrSerIleSerThrAlaTyrMetGlnLeu 84
629 CCAGCCTCGGATCGAGGACGAGCGCGCTATATTATTCGCGCGCTATT 678
      |||

```

```

84 eArgLeuArgSerAspAspThrAlaValTyrTyrCysAlaArg..... 98
679 TTGGTCTAGCCGCAATGTATTTGATTTGGGCTGACGAAACCT 728
      |||:::|:::
99 ...GlyGlyGlyArgGlyLeuThrPheAspProTyrGlyGlnGlyThrLe 114
729 GGTCACTGCTCTGAGC 744
      |||||
114 uValThrValSerSer 119

```

seq_name: sp_human:Q9UL77

seq_documentation_block:

```

ID Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -! SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF035037; AAD56273.1; -.
DR HSSP: P01607; 1RET.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 108
FT SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

```

alignment_scores: Quality: 451.00 Length: 108
Ratio: 4.510 Gaps: 0
Percent Similarity: 92.593 Percent Identity: 81.481

alignment_block:

US-08-487-283a-8 x Q9UL77 ..

Align seg 1/1 to: Q9UL77 from: 1 to: 108

```

7 GATATCCAGATGACCCAGTCCCGCTCTCTGCTCCGCGCTCTGTGGCGA 56
      |||||
1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAs 17
57 TAGGGTACCATTCACCTGCGCGCCGCGAGGAAACATCTATGCGCGCTGA 106
      |||||
17 pArgValThrIleThrCysArgAlaSerGlnSerIleSerSerTyrLeu 34
107 ACTGTATCAAGCTAAACCTGGGAAGCTCGGAAGCTCTGATTTAGCGT 156
      |||||
34 snTrpTyrGlnGlnLysProGlyLysAlaProAsnLeuLeuIleTyrAla 50
157 GCGAGCACTGCGCAGATGAGATCCCTTCTGCTTCTGATCCGCGCTC 206
      |||
51 AlaSerSerLeuGlnSerGlyValProSerArgPheSerGlySerGlySe 67
207 CGGACGAGATTTCACCTGACCATTCAGACGCTGACGCTGACGCTTGC 256
      |||||
67 rGlyThrAspThrLeuThrIleSerSerLeuGlnProGlnAspPhe 84

```

257 CTACGATATCTGTCACAGCTTTAAATCTCCGTTGACTTCGCACAG 306
 |||||
 84 lathyrtrycysglnlsertryserthrsertrphtpheglylu 100
 |||||
 307 GGTACCAAGGTGGAATAAACGT 330
 |||||
 101 GlyThrLysValGlnIleLysArg 108

seq_name: sp_human:Q9UL95

seq_documentation_block:

ID Q9UL95: PRELIMINARY: PRT: 125 AA.
 AC Q9UL95:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 Young D.C.;
 RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus";
 RT Clin. Immunol. Immunopathol. 87:184-192(1998).
 RL -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 CC EMBL: AF035019; AAD56255.1; -.
 DR InterPro: IPR003006; -.
 DR InterPro: IPR003596; -.
 DR Pfam: PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 FT NON_TER 1 125
 FT NON_TER 1 125
 SO SEQUENCE 125 AA; 13516 MW; 0D3CD5C23248BAC CRC64;

alignment_scores:

Quality: 446.50 Length: 125
 Ratio: 4.096 Gaps: 1
 Percent Similarity: 87.200 Percent Identity: 69.600

alignment_block:

US-08-487-283a-8 x Q9UL95 ..

Align seg 1/1 to: Q9UL95 from: 1 to: 125

379 CAAGTCCAATGTCGCAATCCGGCCGAGGTCAAGAACCCAGGGCCTC 428
 :|||
 1 GluValGlnLeuValGlnSerGlyAlaValLysLysProGlyAlaSe 17
 429 AGTCAAGTGCCTGTAAGCTAGCGGCTATTTTCTAATATATGCA 478
 |||||
 17 ValLysValSerCysLysAlaSerGlyTrpTherhrglytryrm 34
 479 TTCAGTGGTGGTCAGCGCCCGGCGAGGCGCTGAATGATGGTGAG 528
 :|||
 34 ethlstrpvalarglnalaproglnglyleuglutrmpmetglytrp 50
 529 ATCTTACCGGGCTCTGTAGCACCAGATATACGAAATTTTAAAGCCG 578
 |||||
 51 IleAspProAsnserglylyThrAsnTyrAlaGlnLysValGlnGlyAr 67
 579 TGTACTATATACGGGTGACACTTGTAGTACTAGTACTATGAGCTCT 628
 |||||
 67 gValThrMetThrArgAspThrThrIleSerThrAlaTyrMetGluLeuS 84
 629 CCAAGCCGCGATCGAGACACGCGCTGTATATTGCGCGCGTTATTTT 678

|| |||||
 84 etArgLeuArgSerAspSPThralaValTyrTrycysAlaArgSerGln 100
 679 TTYGAT.....TCTAGCCCAATTTGATTTGAGTGGGTCA 719
 |||||
 101 GlyGlyGlyArgGlnAlaAlaGlnGlyAspAlaPheAspIletrpGly 117
 720 AGGACCTGTGCTACTGTCTCGAGC 744
 |||||
 117 nglyThrMetValThrValSerSer 125

seq_name: sp_human:Q9UL89

seq_documentation_block:

ID Q9UL89: PRELIMINARY: PRT: 116 AA.
 AC Q9UL89:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 Young D.C.;
 RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus";
 RT Clin. Immunol. Immunopathol. 87:184-192(1998).
 RL -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 CC EMBL: AF035025; AAD56261.1; -.
 DR InterPro: IPR003006; -.
 DR InterPro: IPR003596; -.
 DR Pfam: PF00047; Ig; 1.
 DR SMART; SM00406; IgV; 1.
 FT NON_TER 1 116
 FT NON_TER 1 116
 SO SEQUENCE 116 AA; 12605 MW; C8F9131DE13EA898 CRC64;

alignment_scores:

Quality: 445.00 Length: 118
 Ratio: 4.320 Gaps: 1
 Percent Similarity: 87.288 Percent Identity: 73.729

alignment_block:

US-08-487-283a-8 x Q9UL89 ..

Align seg 1/1 to: Q9UL89 from: 1 to: 116

391 GTGCAATCCGCGCCGAGTCAAGAACCCAGGCGCTCAAGTGC 440
 |||||
 1 ValGlnSerGlyAlaGlnValLysLysProGlySerSerValLysValSe 17
 441 CGTAAAGCTAGCGGCTATATTTTCTAATATATGATCAATGGGTGC 490
 |||||
 17 rcysLysAlaSerGlyGlyThrPheSerSerTyrAlaIleSerTrpAla 34
 491 CTCAGGCCCCCGGCGAGGCGCTGGAATGATGGGTGAGATCTTACCGGC 540
 |||||
 34 rglAlaIleProGlyGlnGlyLeuGlnLutrpmetIlyArgIleIleProIle 50
 541 TCTGTAGCACCAGATATACGAAATTTTAAAGACGCTGTCTATGAC 590
 |||||
 51 LeuGlyIleAlaAsnTyrAlaGlnLysPheGlnGlyArgValThrIleTh 67
 591 CGGTGACTTGCACCTAGTACATATACATGAGAGCTCTCCAGCCTCGAT 640
 |||||
 67 rAlaAspLysSerThrSerThrAlaTyrMetGluLeuSerSerLeuArgS 84

641 CGAGGACACGCGCTATTTATTCGCGCGTATTTTGGTCTAGC 630
 |||||
 84 enGluaspHraIaValTyrTyrCysAlaSerSerSnrtpgLy..... 98
 691 CGGAATTTGGTATTTGATGATTTGGGGTCAAGAACCTGGTCACTGCTC 740
 |||||
 99 ProTyrTrpTyrPheaspLeuTrpGlyArgGlyThrLeuValThrValSe 115
 741 GAGC 744
 |||||
 115 rSer 116

seq_name: sp_invertebrate:Q9GYZ2

seq_documentation_block:
 ID Q9GYZ2 PRELIMINARY; PRT: 119 AA.
 AC Q9GYZ2;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE MONOCLONAL ANTI-IDIOtypIC ANTIBODY NP30 HEAVY CHAIN VARIABLE REGION
 (FRAGMENT).
 OS Schistosoma japonicum (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
 OC Trematoda; Digenea; Strigeiida; Schistosomatidae; Schistosomatidae;
 OC Schistosoma.
 OX NCBI_TaxID=6182;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Song X.T., Feng Z.Q., Guan X.H.;
 RT "Amplification, cloning and sequence analysis of the heavy chain
 variable region gene of monoclonal anti-idiotypic antibody NP30 of
 RT Schistosoma japonicum."
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF282622; AAG01452.1;
 FT NON_TER 1 1
 FT 119 119
 SO SEQUENCE 119 AA; 13567 MW; BA893873FD5FA6AB CRC64;

alignment_scores:
 Quality: 430.50 Length: 122
 Ratio: 4.100 Gaps: 1
 Percent Similarity: 86.066 Percent Identity: 67.213

alignment_block:

US-08-487-283a-8 x Q9GYZ2 ..

Align seg 1/1 to: Q9GYZ2 from: 1 to: 119

379 CAAGTCCAACTGGTGCATTCGCGCGCGAGTCAAGAACGCGGCGCTC 428
 |||||
 1 GlnValGlnLeuValGlnSerGlyAlaGlnValArgLysProGlyAlaSe 17
 429 AGTCAAGTGCCTCTTAAGCTAGCGGCTATTTTCTAATTAATGGA 478
 |||||
 17 rValArgValSerCysLysAlaSerGlyTyrThrPheThrGlyTyrTyrM 34
 479 TTCATGGGTGGTGCAGGCCCGCGGCGAGGCGCTGGAATGATGGTGA 528
 |||||
 34 eLAsnrTrpValArgGlnAlaProGlyHisGlyLeuGlnTrpIleGlyTyr 50
 529 AACTTACCGGGCTCTGTAGCACCGCAATATACGAAATTTTAAAGCCG 578
 |||||
 51 IleAsnProSerArgGlyTyrThrAsnTyrAsnGlnLysPheLysAspAr 67
 579 TGTATATAGAGCGGTGACACTGCACTAGTACATGATGAGGCGCTC 628
 |||||
 67 gValThrMetThrThrAspLysSerPheSerThrAlaTyrMetAspLeuA 84
 629 CCAGCGTGCATCGAGACACGCGCTATTTATTCGCGCGCTATTTT 678
 |||||

84 rGSerLeuArgSerAlaAspSerAlaValTyrTyrCysAlaArgTyrTyr 100
 679 TTGGTTTACCCGGAATTTGATGATTTGGGGTCAAGAACCT 728
 |||||
 101AspAspHisTyrCysLeuAspTyrTrpGlyGlnGlyThr 114
 729 GGTCACTGCTCGAGC 744
 |||||
 114 rValThrValSerSer 119

seq_name: sp_human:Q9UL70

seq_documentation_block:
 ID Q9UL70 PRELIMINARY; PRT: 108 AA.
 AC Q9UL70;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98271139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berny S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus."
 RT Clin. Immunol. Immunopathol. 87:184-192(1998).
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR EMBL; AF035044; AAD56280.1;
 DR HSSP; P01607; IRET.
 DR InterPro; IPR003006;
 DR InterPro; IPR003596;
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Igv; 1.
 FT NON_TER 1 1
 FT 108 108
 SO SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

alignment_scores:
 Quality: 425.00 Length: 108
 Ratio: 4.381 Gaps: 0
 Percent Similarity: 89.815 Percent Identity: 77.778

alignment_block:

US-08-487-283a-8 x Q9UL70 ..

Align seg 1/1 to: Q9UL70 from: 1 to: 108

7 GATATCCAGATGACCCAGTCCCGCTCCCTGTCGCGCTGTGGGGA 56
 |||||
 1 AspieGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAs 17
 57 TAGGTCAACATCACCTCGCGCGCCAGCGAANAACATCTAATGGCGGCTGA 106
 |||||
 17 pArgValThrIleThrCysArgAlaSerGlnGlyIleSerAsnTyrLeuA 34
 107 ACTGTATCAACGTAAACCTGGGAAGCTCCGAACCTCTGATTACGCT 156
 |||||
 34 latrPtyGlnGlnLysProGlyLysValProLysSerLeuIleTyrAla 50
 157 GCGAGCAACTGGCAGATGAGATCCCTCTGCTCTGATCCGCGCTC 206
 |||||
 51 AlaSerThrLeuGlnSerGlyValProSerArgPheSerGlySerGlySe 67
 207 CGGAAGGATTTCACTTGACCATCAGAGTCTGCGAGCTGAAGACTTCG 256
 |||||
 67 rGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGlnAspValA 84

257 CTACGATATCTGTCAGAACGTTTAATACTCCGTTGACCTTGGACAG 306
 |||||
 84 lahrtyrtyrCysGlnLysTyrAsnSerAlaProArgThrPheGlyPro 100
 |||||
 307 GGTACCAAGGTGGAATAAAGCT 330
 |||||
 101 GlyThrLysLeuGlnIleLysArg 108

seq_name: sp_rodent:Q921C4

seq_documentation_block:

ID Q921C4 PRELIMINARY; PRT; 118 AA.
 AC Q921C4
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)
 DE ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA1B/C.
 RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
 Matis L.M., Evans M.J.;
 RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
 RT IgG2/g4 constant regions block human leukocyte binding to porcine
 RT endothelial cells."
 RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR EMBL; U78801; AAD0293.1; -.
 DR InterPro: IPR003006; -.
 DR InterPro: IPR003596; -.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 118
 SO SEQUENCE 118 AA; 13036 MW; 90EEC559D31EC4FC CRC64;

alignment_scores:

Quality: 423.00 Length: 122
 Ratio: 4.147 Gaps: 1
 Percent Similarity: 83.607 Percent Identity: 63.934

alignment_block:

US-08-487-283a-8 x Q921C4 ..

Align seg 1/1 to: Q921C4 from: 1 to: 118

379 CAAGTCAACTGTCGCAATCGCGCCGAGTCGAAGACCGAGGCGCTC 428
 |||||
 1 GlnValGlnValGlnGlnSerGlyAlaGlnLeuAlaArgProTyrPala 17
 429 AGTCAAGTGTCTGTAAGCTAGCGGCTATTTTCTAATATATGA 478
 |||||
 17 rValLysLeuSerCysLysAlaSerGlyTyrAsnPheAsnSerTyrTrpM 34
 479 TTCAAAGGTGTCGTCAGAGCCCGCGGAGGCGCTGGAATGGATGGAG 528
 ::|||
 34 eGlnTrpValLysGlnArgProGlyGlnGlnLysGlnIleTrpIleGlyAla 50
 529 ATCTACCGGGCTCTGTAGACACCGAATATACGAAATTTTAAAGCG 578
 |||||
 51 IleTyrProGlyAspGlyAspThrSerTyrThrGlnLysPheArgGly 67
 579 TGTATATGAGCGCGTACACTGCTAGCTAGTATACATGAGCTCT 628
 ::|||
 67 salatThrLeuThrAlaAspLysSerSerSerThrAlaTyrMetGlnLeu 84

629 CCAGCTGCGATCGAGACGCGCGCTCTATTATTGGCGGCTATT 678
 |||||
 84 erSerLeuAlaSerGlnAspSerAlaValTyrTyrCysAlaArgArgTr 100
 |||||
 679 TTTGGTTCAGCCCGAATGTTATTTGATGTTGGGTCAAGAACCT 728
 |||||
 101 ValGlyGly.....TyrPheAspTyrTrpGlyGlnGlyThr 113

729 GGTCACTGCTCGAGC 744
 ::|||
 113 rLeuThrValSerSer 118

seq_name: sp_human:Q9UL81

seq_documentation_block:

ID Q9UL81 PRELIMINARY; PRT; 107 AA.
 AC Q9UL81
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)
 DE MOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9827139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Fyosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus.";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 DR EMBL; AF035033; AAD56269.1; -.
 DR HSSP; P80362; IWTL.
 DR InterPro: IPR003006; -.
 DR InterPro: IPR003596; -.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 107
 SO SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

alignment_scores:

Quality: 421.50 Length: 108
 Ratio: 4.258 Gaps: 1
 Percent Similarity: 91.667 Percent Identity: 77.778

alignment_block:

US-08-487-283a-8 x Q9UL81 ..

Align seg 1/1 to: Q9UL81 from: 1 to: 107

7 GATATCCAGATGATCCAGACCCCGCTCCCTGCTCCGCTGTGGCGA 56
 |||||
 1 AspIleGlnMetThrGlnSerProSerLeuSerAlaSerValLys 17
 57 TAGGCTACACATCACCTGGCGCGCCAGCAAAACATCTATGGCGCCTA 106
 |||||
 17 pArgValThrIleThrCysArgAlaSerIleSerIleSerAsnTyrLeu 34
 107 ACTGATATCAACGTAACCTGGGAAAGCTCCGAAGCTTGTGATTACGT 156
 |||||
 34 snTrpTyrGlnGlnLysProGlyLysAlaProAsnLeuLeuIleTyrAla 50
 157 GCGAGAACCTGGCAGATGAGATCCCTTCTCGCTTCTGATCCGGCTC 206
 |||||
 51 AlaSerSerLeuGlnSerGlyValProSerArgPheSerGlySerLys 67
 207 CGAAGCATTTCACTCTGACCATCAGACGTCTGACGCTGAAGACTCG 256

```

|||||
67 rclYhrspNhrleuthrIleSerGlyLeuGlnAlaGluAspPheA 84
257 CACGCTAATCTACGAGAACGTTTAATACGCCGTGACTTGCGACAG 306
|||
84 lArhTyrIcysGlnGlnSerTyrSerAla...leuthrPheGlyPro 99
307 GGTACCAAGGTGGAATAAAGCT 330
|||||
100 GlyThrIysValAspIleArg 107

```

seq_name: sp_human:095978

```

seq_documentation_block:
ID_095978 PRELIMINARY; PRT; 157 AA.
AC 095978:
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE VH1 PROTEIN PRECURSOR (FRAGMENT).
GN VH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PERIPHERAL BLOOD:
RA Jox A., Zander T., Kuipers R., Irsch J., Kanzler H., Kornacker M.,
RA Bollen H., Diehl V., Wolf J.;
RT "Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a
RT patient with mixed cellularity Hodgkin's disease is associated with
RT somatic mutations within the untranslated regions of rearranged and
RT class switch recombined Ig genes."
RU Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
-i- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
CC EMBL: AJ005570; CAA06599.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
DR SIGNAL.
KW SIGNAL.
FT 1 21 POTENTIAL.
FT NON_TER 157 157
SQ SEQUENCE 157 AA; 17304 MW; 869866DDA84D8B5 CRC64;

```

alignment_scores: Quality: 416.50 Length: 126
Ratio: 4.083 Gaps: 1
Percent Similarity: 80.952 Percent Identity: 68.254

alignment_block: US-08-487-283A-8 x 095978 ..

Align seg 1/1 to: 095978 from: 1 to: 157

```

367 GGTGGCGGTTCAAGTCCAACTGTCGAATCCGCGCGAGGTCAAGAA 416
|||
16 GlyAlaHisSerGlnValGlnLeuValGlnSerGlyAlaGluIleLysar 32
417 GCCAGGGGCTCAGTCAAGTGTCTCTAAAGTACGGGTATATTTT 466
:|||||
32 gProGlyAlaSerValIscysIysThrSerGlyTyrValPheT 49
467 CTAATATATGATTCATGAGTGGTGGTCAAGCCCGGCGAGGCGCTGAA 516
:|||||
49 hSetTyrIleIleHisTyrValArgGlnProArgIleGlnGlyLeuGlu 65
517 TGAGATGGGTGAGATCTTACCGGGGCTCTGGTAGCAGCCGAATATACGAAA 566
|||||
66 TrpMetGlyGlyIleGlyProGlyValGlySerThrMetCysAlaGlu 82

```

```

567 TTTAAGACCGTGTACTATGACCGGTGACACTTCGACTGATACAGTAT 616
:|||||
82 sPheGlnGlyArgLeuThrMetThrArgAsnThrSerThrThrValT 99
617 ACATGAGCTCTCCAGCTCGCATCGAGACAGCGCGCTATATTATTCG 666
|||||
99 yMetGlnLeuSerArgLeuArgPheGlnAspThrAlaValTyrPheCys 115
667 GCGGCTATTTTGTGTTCTAGCCCGAATGTGATTTTGAATGTTGGGG 716
:|||||
116 GlyArgGlyGlyArgTyrPArgSerGlyAsn...TyrAsnGlyHisTrpG 131
717 TCAAGAACCCCTGCTGCTGCTGAGC 744
|||||
131 yGlnGlyThrProValThrValSerSer 140

```

seq_name: sp_human:090U79

```

seq_documentation_block:
ID_090U79 PRELIMINARY; PRT; 108 AA.
AC 090U79:
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RU Clin. Immunol. Immunopathol. 87:184-192(1998).
-i- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN
CC EMBL: AF035035; AAD56271.1; -.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
FT NON_TER 1 1
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

```

alignment_scores: Quality: 407.00 Length: 108
Ratio: 4.330 Gaps: 0
Percent Similarity: 87.037 Percent Identity: 75.000

alignment_block: US-08-487-283A-8 x 090U79 ..

Align seg 1/1 to: 090U79 from: 1 to: 108

```

7 GATATCCAGATGACCCAGTCCCGTCCTGTCGCGGCTGAGGCGGA 56
|||||
1 AspIleValMetThrGlnSerProSerIleuSerAlaSerThrGlyAs 17
57 TAGGTCACATCACTCGCGCGCCAGCGAACAATCATATGCGCGCTGA 106
|||||
17 pArgValThrIleSerGysArgMetSerGlnGlyIleSerSerTyrLeuA 34
107 ACTGTATCAACGTAAACCTGGGAAAGCTCCGAAGCTTCTGATTTACGCT 156
|||||
34 lArTrpTyrGlnGlnIysProGlyLysAlaProGlnLeuLeuIleTyrAla 50

```

```

157 GCGACGACCTGGCAGATGAGTCCCTTCCTCTGATCCGGCTC 206
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51 AlaserThrlengInserGlyValProSerArpHeserGlySerGlyse 67
207 CGGACGATTCACCTCTGACATCAGACAGTCTGACCTGAAGACTTCG 256
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67 rGlyThraSpHethrleuthrlethrlleserGlyleuGlnSerGluasphea 84
257 CTACGATTAATCTGACAGACGTTTAAATACCTCGTGAATTCGACAG 306
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84 laThrlyTrGysGlnGlnTyTrTySerPheProThrPheGlyGln 100
307 GGTACCAAGGTGGAATAAACGT 330
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101 GlyThlyValGlnIlelySarG 108

```

seq_name: sp_rodent:Q99YF0

```

seq_documentation_block:
ID Q99YF0 PRELIMINARY; PRT; 298 AA.
AC Q99YF0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE CN 8 SCFV.
GN CN 8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BALB/C; TISSUE=SPLEEN;
RA Shinozuka N., Demura T., Fukuda H.;
RN Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA STRAIN=BALB/C; TISSUE=SPLEEN;
RC shinozuka N., Demura T., Fukuda H.;
RT "Isolation of a novel type of vascular cell wall-specific monoclonal
RT antibody recognizing a cell polarity using a phage display subtraction
RT method."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB036341; BAA86633.1; -.
DR HSSP; P01607; IREI.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; Igv; 1.
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

```

alignment_scores:

Quality:	405.00	Length:	113
Ratio:	4.010	Gaps:	0
Percent Similarity:	89.381	Percent Identity:	67.257

alignment_block:

US-08-487-283a-8 x Q99YF0 ..

Align seg 1/1 to: Q99YF0 from: 1 to: 298

```

4 GCGCATATCCAGATGACCCAGTCCCTCCCTGTCGGCTCTGTTGGG 53
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
172 SerAspIleuThrInserProAlaSerleuSerAlaSerValGln 188
54 CGATAGGGTCCACATCAGTGCAGCCGCGCAGGAAACATCATGAGCGCGC 103
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
188 yGluThrValThrIleHrcysArgAlaSerGlyAsnIleHisnTrpYL 205
104 TGAAGTGTATCAACGTAACCTGGGAAGCTCCGGAAGCTTCTGATTTAC 153
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
205 euAlaTrpTyGlnGlnIlyGlnIlySerSerProGlnIleuValTrpYL 221

```

```

154 GGTGGACGACACCTGACATGAGTCCCTTCCTCTGATCCGGCTC 203
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
222 AsnAlaIlyThrleuAlaaspGlyValProSerArpHeserGlySerG 238
204 CTCCGGAACGATTCACCTCTGACATCAGACAGTCTGACCTGAAGACT 253
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
238 ySerGlyThrGlnTyTrSerleuIlyleuSerleuGlnProGluasp 255
254 TCGCTACGATTAATCTGACAGACGTTTAAATACCTCGTGAATTCGGA 303
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
255 heGlySerTyTrGysGlnHisPheTrpThrProTyTrThrPheGly 271
304 CAGGTACCAAGGTGGAATAAACGTAAGCTACTGCGGTGCT 342
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
272 GlyGlyThrlyleuGlnIlelySarGAlaAlaIlyGly 284

```

seq_name: sp_human:Q9Y298

```

seq_documentation_block:
ID Q9Y298 PRELIMINARY; PRT; 150 AA.
AC Q9Y298;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE Igg VH PROTEIN PRECURSOR (FRAGMENT).
GN IGG VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98322155; PubMed=9657749;
RA Jacquemin M.G., Vander Elst L.P.L.;
RT "Mechanism and kinetics of factor VIII inactivation: study with an
RT Igg4 monoclonal antibody derived from a hemophilia A patient with
RT inhibitor."
RL Blood 92:496-506(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AJ224083; CAAl1829.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT NON_TER 150 150
SQ SEQUENCE 150 AA; 16031 MW; 563D164AB22802D5 CRC64;

```

alignment_scores:

Quality:	397.50	Length:	126
Ratio:	3.786	Gaps:	2
Percent Similarity:	83.333	Percent Identity:	64.286

alignment_block:

US-08-487-283a-8 x Q9Y298 ..

Align seg 1/1 to: Q9Y298 from: 1 to: 150

```

367 GGTGGGGGTTTCACATCCAGTGGTGCATCCGGGCGGACGATCAAGAA 416
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
16 GlyThrHisAlaGlnValGlnleuValGlnSerGlyAlaGlnVallyslY 32
417 GCGAGGGGCTCAGTCAAGTGTCTGTAAGCTACGCGGTATATTTT 466
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
32 sProGlyAlaSerValIlyValSerGlyValSerGlyTyThrleuTr 49
467 CTAAATTATGATTCATAGGGTGGTCCAGGCGCCGCGGAGGCGCTGGAA 516
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
49 hrcGluIleuProValHisTrpValGlyGlnAlaProGlyIlyGlyleuGln 65

```

```

517 TGGATGGGTGATCTTACCGGGCTCTGTGACACCGAATATACCGAAA 566
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
66 TrpValGlySerPheAspProGlnSerGlyGlnSerIleTyrAlaArgI 82
567 TTTTAAAGACCGTGTACTATAGACCGGTGACTGACTAGTACTAT 616
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
82 uphelinGlnSerValThrMetThrAlaAspThrSerThrAspIleAla 99
617 ACATGAGCTCTCCAGCCGTCGATCGAGACACGCGCTCTTATATGC 666
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
99 YrmeGlnLeuSerSerLeuArgSerAspAspThrAlaValTyrTyrCys 115
667 GCGCCTTATTTTGTGTTCTAGCCCGAATGTGATTTGATGTTGGG 716
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
116 Ala.....ValProAspProAsp...AlaPheAspIleTrpGl 127
717 TCAGGAACCCGTGTCACGTCTCGAGC 744
|||||:|||||:|||||:|||||:|||||:|||||:
127 YGlnGlnYThrMetValThrValSerSer 136

```

seq_name: sp_rudent:Q9QXF0

seq_documentation_block:

```

ID Q9QXF0 PRELIMINARY; PRT; 117 AA.
AC Q9QXF0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE TM00NGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademakers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ225171; CAB65236.1; -.
DR InterPro: IPR003596; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; 1g; 1.
DR SMART: SM00406; Igv; 1.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13060 MM; DB16AD0858A47E4C CRC64;

```

alignment_scores:

```

Quality: 389.50 Length: 122
Ratio: 3.745 Gaps: 1
Percent Similarity: 85.246 Percent Identity: 58.197

```

alignment_block:

US-08-487-283A-8 x Q9QXF0 ..

Align seg 1/1 to: Q9QXF0 from: 1 to: 117

```

379 CAGATCCAACTGTCATCGCGCCGAGTCACAGACCGACGCGCTC 428
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 GluValGlnLeuGlnGlnSerGlyProGlnLeuValSerProGlyAla 17
429 AGTCAAGTCTCTGTAAGCTAGCGCGCTATATTTTCTAATATATGCA 478
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17 TrpValGlnSerCysLysAlaSerGlyTyrThrPheThrAspTyrTyrM 34
479 TTCATGGGTGCGTCAGCGCCCGGCGAGGCTCGAATGATGGGTGAG 528
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34 eLysTyrValGlnSerHisGlyLysSerLeuGlnIleTyrPheGlyAsp 50
529 ATCTTACCGGGCTGTGTAGACACCGAATATACGAAATTTTAAAGAC 578
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51 IleAsnProAsnAsnGlnGlyThrSerTyrAsnGlnLysPheLysGly 67

```

```

579 TGTACTATGACCGGTGACACTTGACTAGTACATATATGAGCTCT 628
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
67 AlaThrLeuThrValAspLysSerSerSerThrAlaTyrMetGlnLeu 84
629 CCAGCGTCGATCGGAGACACGCGCTCTATTTATGCGCGCTATTTT 678
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
84 snSerLeuThrSerGlnAspSerAlaValTyrTyrCysAlaArg..... 98
679 TTGCTTCTGACCCGGAATGTGATTTGATGTTGGGTCAAGAACCT 728
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
99 .....AspLysAspTyrTyrPheAspTyrTrpGlnGlnGlyThr 112
729 GGTCACTGTCGAGC 744
|||||:|||||:|||||:|||||:|||||:|||||:
112 rLeuThrValSerSer 117

```

seq_name: sp_rudent:Q9RLA5

seq_documentation_block:

```

ID Q9RLA5 PRELIMINARY; PRT; 214 AA.
AC Q9RLA5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RL Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF152371; AAD40242.1; -.
DR HSP: P01789; IMCP.
DR InterPro: IPR003606; -.
DR InterPro: IPR003606; -.
DR Pfam: PF00047; 1g; 2.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR SMART: SM00410; IG_Like; 1.
FT NON_TER 1
FT NON_TER 214
SQ SEQUENCE 214 AA; 23922 MM; 52BA205FDE995E2A CRC64;

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alignment_scores:

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Quality: 379.00 Length: 221
Ratio: 2.596 Gaps: 5
Percent Similarity: 66.063 Percent Identity: 41.629

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alignment_block:

US-08-487-283A-8 x Q9RLA5 ..

Align seg 1/1 to: Q9RLA5 from: 1 to: 214

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7 GATATCCAGATGACCCAGTCCCGTCTCCCTGTCGCGCTGTGGGGA 56
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 AspIleGlnLeuThrGlnSerProSerSerMetTyrAlaSerLeuGly 17
57 TAGGGTACCATCATCCTGCGCGCGCAGGAAACATCTATGCGCGCTGA 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17 uArgValThrIlePheThrCysLysAlaSerGlnAspIleAsnSerTyr 34
107 ACTGCTTCAACGTAACCTCGGAAAGCTCGAAGCTTCGATTATACGCT 156
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34 eTrpPheGlnGlnLysProGlyLysSerProLysTyrLeuIleTyrArg 50
157 GCGACGACCTGCGCAGATGAGATCCCTCTCTCTCTGATCCGCGCTC 206
|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```


[illegible]

OM bf: US-08-487-283A-8 to: A_Geneseq_0601.* out_format : pfs
Date: Jul 19, 2001 8:14 AM

About: Results were produced by the Gencore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL=framed_nzp.model -DEV=xlp
-O=/cgn2_1/USPTO_spool/US08487283/funat_19072001_075936_3807/app-query.fasta_1.817
-DB=A_Geneseq_0601 -OFMT=fasta -SUFFIX=tra.rag -GAPOP=12.000
-GAPEXT=4.000 -MIMATCH=0.100 -LOOPCL=0.000 -LDOPEXT=0.000
-CGAPOP=4.500 -CGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -START=1 -MATRIX=blissum62
-DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -MINLEN=0 -MAXLEN=200000000
-USR=US08487283_6CGN1_1100 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPX
-WAIT -THRAIDS=1

Search information block:

Query: US-08-487-283A-8
Query length: 747
Database: A_Geneseq_0601.*
Database sequences: 412676
Database length: 60623988
Search time (sec): 45.140000

score_list:

Sequence	Strd Orig	ZScore	EScore	Len	Documentation	
/SID88/gcgdata/geneseq/geneseqp/AA1995.DAT:AA77607			1312.00	2073.37	5.3e-108	248
/SID88/gcgdata/geneseq/geneseqp/AA1995.DAT:AA77607			1279.00	2021.02	4.4e-105	248
/SID88/gcgdata/geneseq/geneseqp/AA1995.DAT:AA77606			1122.00	1771.97	3.3e-91	248
/SID88/gcgdata/geneseq/geneseqp/AA1997.DAT:AA76651			949.50	1494.36	6.2e-76	382
/SID88/gcgdata/geneseq/geneseqp/AA1997.DAT:AA76648			949.50	1493.87	6.2e-76	403
/SID88/gcgdata/geneseq/geneseqp/AA1997.DAT:AA76647			949.50	1492.40	6.4e-76	473
/SID88/gcgdata/geneseq/geneseqp/AA1997.DAT:AA76647			949.50	1491.64	6.5e-76	514
/SID88/gcgdata/geneseq/geneseqp/AA1997.DAT:AA76649			949.50	1489.48	6.8e-76	651
/SID88/gcgdata/geneseq/geneseqp/AA1997.DAT:AA76650			949.50	1488.92	6.9e-76	692
/SID88/gcgdata/geneseq/geneseqp/AA2001.DAT:AA30633			928.50	1459.94	4.5e-74	431
/SID88/gcgdata/geneseq/geneseqp/AA1999.DAT:AA94269			858.50	1345.99	7.3e-68	592
/SID88/gcgdata/geneseq/geneseqp/AA1992.DAT:AA20185			857.50	1351.57	7.8e-68	271
/SID88/gcgdata/geneseq/geneseqp/AA2000.DAT:AA91026			849.00	1333.72	4.8e-67	436
/SID88/gcgdata/geneseq/geneseqp/AA2000.DAT:AA43749			822.00	1289.09	1.2e-64	531
/SID88/gcgdata/geneseq/geneseqp/AA2000.DAT:AA59264			816.00	1284.65	3.7e-64	305
/SID88/gcgdata/geneseq/geneseqp/AA2000.DAT:AA51141			816.00	1284.65	3.7e-64	305
/SID88/gcgdata/geneseq/geneseqp/AA2000.DAT:AA50822			813.00	1274.42	7.6e-64	554
/SID88/gcgdata/geneseq/geneseqp/AA2000.DAT:AA44933			812.50	1268.67	9.2e-64	951
/SID88/gcgdata/geneseq/geneseqp/AA2000.DAT:AA78328			811.50	1272.41	1.0e-63	533
/SID88/gcgdata/geneseq/geneseqp/AA2000.DAT:AA44944			810.50	1270.98	1.2e-63	523
/SID88/gcgdata/geneseq/geneseqp/AA2000.DAT:AA44995			810.50	1270.97	1.3e-63	524
/SID88/gcgdata/geneseq/geneseqp/AA2000.DAT:AA80746			810.50	1269.85	1.3e-63	601
/SID88/gcgdata/geneseq/geneseqp/AA2000.DAT:AA84965			809.00	1266.71	1.8e-63	633
/SID88/gcgdata/geneseq/geneseqp/AA1999.DAT:AA70627			808.50	1271.44	1.8e-63	352
/SID88/gcgdata/geneseq/geneseqp/AA2000.DAT:AA82815			802.00	1264.19	6.2e-63	252
/SID88/gcgdata/geneseq/geneseqp/AA1999.DAT:AA97989			800.50	1261.42	8.5e-63	263
/SID88/gcgdata/geneseq/geneseqp/AA2000.DAT:AA82816			799.50	1260.74	1.0e-62	253
/SID88/gcgdata/geneseq/geneseqp/AA1997.DAT:AA83512			799.50	1250.19	2.5e-62	335
/SID88/gcgdata/geneseq/geneseqp/AA1997.DAT:AA83512			795.50	1250.66	2.5e-62	355
/SID88/gcgdata/geneseq/geneseqp/AA1997.DAT:AA83512			795.50	1250.66	2.5e-62	358
/SID88/gcgdata/geneseq/geneseqp/AA1997.DAT:AA83513			795.50	1250.66	2.5e-62	358
/SID88/gcgdata/geneseq/geneseqp/AA1997.DAT:AA83512			795.50	1250.61	2.5e-62	360
/SID88/gcgdata/geneseq/geneseqp/AA1997.DAT:AA83512			795.50	1250.14	2.5e-62	379
/SID88/gcgdata/geneseq/geneseqp/AA1994.DAT:AA86026			793.00	1247.46	4.4e-62	302
/SID88/gcgdata/geneseq/geneseqp/AA1994.DAT:AA85074			783.00	1226.96	3.4e-61	546
/SID88/gcgdata/geneseq/geneseqp/AA2001.DAT:AA83064			780.00	1225.79	9.0e-61	412
/SID88/gcgdata/geneseq/geneseqp/AA1994.DAT:AA86078			777.50	1225.62	2.1e-60	244
/SID88/gcgdata/geneseq/geneseqp/AA2000.DAT:AA85080			774.00	1213.15	2.1e-60	519
/SID88/gcgdata/geneseq/geneseqp/AA2000.DAT:AA85081			774.00	1211.43	2.2e-60	626
/SID88/gcgdata/geneseq/geneseqp/AA2000.DAT:AA85082			774.00	1211.23	2.2e-60	640

/SID88/gcgdata/geneseq/geneseqp/AA1998.DAT:AA40070	771.50	1214.09	3.2e-60	304
/SID88/gcgdata/geneseq/geneseqp/AA2001.DAT:AA83142	765.00	1205.87	1.1e-59	242
/SID88/gcgdata/geneseq/geneseqp/AA1994.DAT:AA86078	764.00	1204.24	1.4e-59	243
/SID88/gcgdata/geneseq/geneseqp/AA1997.DAT:AA83561	763.50	1203.60	1.5e-59	239
/SID88/gcgdata/geneseq/geneseqp/AA1997.DAT:AA80981	763.50	1203.60	1.5e-59	239

seq_name: /SID88/gcgdata/geneseq/geneseqp/AA1995.DAT:AA77607

seq_documentation_block:

ID AAR77607 standard; Protein: 248 AA.

AC AAR77607;

DT 15-MAR-1996 (first entry)

DE Humanised CDR-grafted 5G1.1 scfv CB.

KW Complement C5; haemolysis; kidney; glomerulonephritis;
KW monoclonal antibody; antiinflammatory; antibody engineering;
KW humanised antibody; complementarity determining region; CDR;
KW single chain antibody; scfv.

OS Synthetic.

FX Key Location/Qualifiers

FT Region /label- CDR-L1

FT Region /label- CDR-L2

FT Region /label- CDR-L3

FT Region /label- CDR-H1

FT Region /label- CDR-H2

FT Region /label- CDR-H3

MO9529697-A1.

PD 09-NOV-1995.

XX 01-MAY-1995; 95WO-US05668.

XX 02-MAY-1994; 94US-0236208.

XX (ALEX-) ALEXION PHARM INC.

PI Evans MJ, Mattis L, Mueller EE, Nye SH, Rollins S;

PI Rother RP, Springhorn J P, Squinto SP, Thomas JC;

XX Wang Y, Wilkins JA;

DR WPI: 1995-392923/50.

DR N-PSDB: AAT08480.

PT Treating glomerulonephritis with antibody against complement C5

XX component - to inhibit complement induced cell lysis

PS Example 11: Page 110-113; 181pp; English.

XX Humanised CDR-grafted 5G1.1 scfv CB (AAR77607) is the product of a

CC DNA construct (AAR0479) derived from DNA of hybridoma ATCC HB 11625,

CC the producer of anti-C5 monoclonal antibody (Mab) 5G1.1. Recombinant

CC scfv CB is obtd. by expression of this DNA in Escherichia coli using

CC vector pET Trc SO5/NI. The light and/or heavy chain CDRs of

CC scfv CB can be combined with CDRs from other 5G1.1-derived antibodies,

CC fids and light chains (AAR77606-16) in the prodn. of recombinant,

CC including humanised, antibodies that retain the ability of Mab 5G1.1

CC to block human complement C5a generation and thus to reduce glomerular

CC inflammation and kidney dysfunction associated with glomerulonephritis.

XX Sequence 248 AA;

SQ

alignment_scores: length: 248
Quality: 1312.00
Ratio: 5.290
Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-487-283A-8 x AAR77607 ..

Align seg 1/1 to: AAR77607 from: 1 to: 248

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1 ATGGCGCATATCCAGATGACCCAGTCCCTCCCTGCTCCGCTCTGT 50
|||||
1 MetAlaAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerVa 17
51 GGGCGATAGGGTACACATCACCCTGGCGGCGGCAAGAAACATCTATGGCG 100
|||||
17 IGLYsPArYValThrlleThrcYsGLyAlaSerGlnAsnIleTYrGLY 34
101 CGCTGACTGTATCAGCTAAACCTGGGAAAGCTCCGAGCTTGTGATT 150
|||||
34 IAlEuAsnTrPYrGlnArGLysProGLYsAlaProLYsLeuLeuIle 50
151 TACGCTGGGAGACACTGGCAGATGAGTCCCTTCGCTTCTCTGATC 200
|||||
51 TYrGLYAlaThrAsnLeuAlaAspGLYValProSerArGPhsSerGLYse 67
201 CGGCTCCGGAACGGATTTCACCTCTGACATGACAGCTGACGCGCTGAG 250
|||||
67 rGLYserGLYThrAspPheThrLeuThrIleSerSerLeuGlnProGLY 84
251 ACTTCGCTACGTATTACTGTCTCAGAACGTTTAAATCTCCGTGACTTTC 300
|||||
84 sPPhAlAlThrTYrTYrCYsGlnAsnValLeuAsnThrProLeuThrPhe 100
301 GGACAGGGTACCAAGCTGGAATAAAGCTACTGCGGCTGCTGTCTGG 350
|||||
101 GLYGLnGLYThrLYsValGLYIleLYsArGThnGLYGLYserGL 117
351 TGGCGGTGGATGTGGTGGCGGCTTCAATCCCAACGTGTCATCCG 400
|||||
117 YGLYGLYserGLYserGLYGLYserGlnValGlnLeuValGlnSerC 134
401 GCGCGGAGTCAAGAACCGGCGCTCAGTCAAAAGTGTCTGTAAAGCT 450
|||||
134 YAlaGLYValLYsLYsProGLYAlaSerValLYsValSerCYsLYsAla 150
451 AGCGGCTATATTTTCTAATTATTGGATTCAATGGGCTCGTCAGCCCC 500
|||||
151 SerGLYTYrIlePheSerAsnTYrTrPleGlnTrPValAlArgGlnAlaPr 167
501 CGGCGAGGGCCCTGGAAATGATGGTGAGATCTTACCGGGCTCGGTAGCA 550
|||||
167 oGLYGLnGLYLeuGlnTYrPMeGLYGLYIleLeuProGLYserGLYser 184
551 CCGATATACGGAATAATTTAAAGCCGTTACTACTGACGCGCTGACACT 600
|||||
184 hrgLUrTYrThrGlnAsnPhelysAspArYValThrMetThrArGAspThr 200
601 TCGACTACTACAGTATACATGAGAGCTCTCCAGCTCGATCGAGAGACAC 650
|||||
201 SerThrSerThrValTYrMetGLYLeuSerSerLeuArgSerClnAspTh 217
651 GGGCGTCTATATTCGCGCGCTTATTTTGGTTCTACCCGGAATTGGT 700
|||||
217 rAlaValTYrTYrCYsAlaArGLYrPhhehGLYserSerProAsnTrP 234
701 ATTTCGATGTTGGGTCAGAGACCCCTGCTACCTCTCGAGC 744
|||||
234 YrPhAspValTrPGLYGLnGLYThrLeuValThrValSerSer 248
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seq_name: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT: AAR77616

seq_documentation_block:

ID AAR77616 standard; protein: 248 AA.

XX AAR77616;

XX 15-MAR-1996 (first entry)

DE Humanised CDR-grafted 5G1.1 scFv DO12.

XX Complement C5; haemolysis; kidney; glomerulonephritis;

KW monoclonal antibody; anti-inflammatory; antibody engineering;

KW humanised antibody; complementarity determining region; CDR;

XX single chain antibody; scFv.

OS Synthetic.

FT Key Location/Qualifiers

FT Region /label= CDR-L1

FT Region /label= CDR-L2

FT Region /label= CDR-L3

FT Region /label= CDR-H1

FT Region /label= CDR-H2

FT Region /label= CDR-H3

XX WO9529697-A1.

PD 09-NOV-1995.

XX 01-MAY-1995; 95WO-US05688.

XX 02-MAY-1994; 94US-0236208.

PA (ALEX-) ALEXION PHARM INC.

XX Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;

PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;

PI Wang Y, Wilkins JA;

XX MPI: 1995-392923/50.

DR N-PSDB; AAT08488.

XX Treating glomerulonephritis with antibody against complement C5

PT component - to inhibit complement induced cell lysis

XX Example 11; Page 138-140; 181pp; English.

PS A humanised CDR-grafted scFv, designated 5G1.1 scFv DO12 (AAR77616),

XX includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1.

CC The scFv can be expressed in Escherichia coli ME1 cells by subcloning

CC of encoding DNA (AAR08488) into vector pET Trc S05/Tr1. This

CC humanised, recombinant antibody retained the ability of Mab 5G1.1 to

CC block human complement C5a generation and thus to reduce glomerular

CC inflammation and kidney dysfunction associated with

CC glomerulonephritis.

SO Sequence 248 AA;

alignment_scores: length: 248
Quality: 1279.00
Ratio: 5.178
Gaps: 0
Percent Similarity: 99.597 Percent Identity: 97.177

alignment_block:

US-08-487-283A-8 x AAR77616 ..

Align seg 1/1 to: AAR77616 from: 1 to: 248


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seq_name: /SID8/gcgdata/geneseq/geneseqp/AA1997.DAT:AAW26651
seq_documentation_block:
ID   AAW26651 standard; Protein; 382 AA.
XX
XX   AAC      AAW26651;
XX
XX   DT       12-FEB-1998    (first entry)
XX
DE   Chimeric receptor hCTMO1/h/zeta.
```

```

alignment_scores:
    Quality: 949.50
    Ratio: 4.220
    Percent Similarity: 84.906
    Percent Identity: 70.189

alignment_block:
    US-08-487-283A-8 x AAW26651 ..

Align seg 1/1 to: AAW26651 from: 1 to: 382

7 GATATTCAGATGACCCAGCTCCCGTCTCCCTGTCCGCGCTGTGGGCGA 56
  |||.....|.....|.....|.....|.....|.....|.....|.....|
21 AspliegImetHrGlnserProserHrleuSerAlaSerValGlyas 37
  |||.....|.....|.....|.....|.....|.....|.....|.....|
57 TAGGGTCACCATCACCCTCGGGCGGCAGGAAACATCATATGCGCGC... 104
  |||.....|.....|.....|.....|.....|.....|.....|.....|
37 pargvalHrIrlleHrnyCysArgSerSerLysSerleuHuhIserang 54
  |||.....|.....|.....|.....|.....|.....|.....|.....|
103 .....CTGAACGTGATATCAACGTAAACCTGGGAAAGCTCCGAG 141

```

```

54  lyasphrphleuetyrtrpheelnglnlyserglyalalprolys 70
142 CTCTGATTTAGCGTGGACGACAGTGGACAGATGAGTCCCTTCGCTT 191
71  leuleuetyrargmetserasnlleualaserglyalproserarph 87
192 CTGTGATCCGGCTCCGGAACGATTTCACTGTGACATCAGCAGTGGC 241
87  eserglyserglyserglythrghlupherleuthrilleserleug 104
242 AGCCTGAGACTTCGCTACGATTTACTGTCAGACGTTTAAATCTCCG 291
104 lnprospasphnealahrtyrtyrcysmetglnhslenglutypro 120
292 TTGACTTTCCGACAGGTACCAAGGTGGAATAAAGCTACT..... 333
121 Phethrhehglynglnlythrlyvalglvalylsargthrnglygl 137
334 .....GGCGGTGGTGGTTCGTGGTGGCGGTGCAT 361
137 ygllyserglygllyserglygllyserglygllygllys 154
362 CTGTGTGGTGGGTTTCAGTCCAGTGGTGCATCCGGGGCGGAGGTC 411
154 erglygllygllyserglnleuvalglnserglyalalval 170
412 AAGAGCCAGGCGCTCAGTCAGATGCTCGTAAAGCTACCGCTATAT 461
171 lysalysprogllyserlvalylvalsercysylsalaserglytyr 187
462 TTTTCTAATTAATGATTCAGTGGTGGTGGTGGTGGTGGTGGTGGT 511
187 rphethrasptryrtyrileasnrtpmetarglnalaproglnglnly 204
512 TGGATGATGAGGTGAGATCTTACCGGCTGTGGTACCGCAATATACC 561
204 englurpilleglytrpilleasprogllyserglyasnthrlysrasn 220
562 GAAATTTTAAAGACGCTTACTATGACGCGTGCACCTTGACAGATAC 611
221 Glulysheylsglyaralathrleuthrvalasphrserthrlnsth 237
612 AGTATACATGAGCTTCACAGCTGCATCGAGAGACAGCGCTGTATTT 661
237 ralatymerglunuserserleuargsergluasphrhalapheyrp 254
662 ATTGCGGCGGT.....TATTTTGTGTTCTAGCCCAATTTGG 699
254 hecysalaarglulysthrthryrtyrala..... 265
700 TATTTGATGTTGGGTCAGAAACCTGCTCACTGTCTGAGC 744
266 ...MetasprtyrtrpilynglnlythrleuvalthrvalserSer 279

seq_name: /SID8/gcgdata/geneseq/AA1997.DAT.AAM26648
seq_documentation_block:
ID AAM26648 standard; Protein; 403 AA.
XX
XX AAM26648;
AC
XX
XX
DT 12-FEB-1998 (first entry)
DE
XX
XX Chimeric receptor hCTMO1/CD8/CD28.
KM Cell activation; chimeric receptor; DNA delivery; CTMO1; scFv; CD8;
KM CD28; cell proliferation; cytokine; inflammation; effector;
KM cell differentiation; antibody secretion; phagocytosis;
KM tumor infiltration; adhesion; infection; cancer; allergy;
KM rheumatoid arthritis; osteoarthritis; asthma; eczema;
KM inflammatory bowel disease; cystic fibrosis; sickle cell anaemia;
KM psoriasis; multiple sclerosis; transplant rejection; diabetes;

```

```

KM graft versus host disease; human; therapy.
XX
XX Chimeric - Homo sapiens.
OS
XX WO9723613-A2.
XX
XX 03-JUL-1997.
PD
XX
XX 23-DEC-1996; 96WO-GB03209.
PF
XX
XX 21-DEC-1995; 95GB-0026131.
PR
XX
XX (CLIT ) CELLTech THERAPEUTICS LTD.
PA
XX Bebbington CR, Finney HM, Lawson ADG, Weir ANC;
PI
XX
XX WPI: 1997-351052/32.
XX N-PSDB; AAT90511.
DR
XX
XX New DNA systems for activating cells - comprising DNA coding for a
PT chimeric receptor comprising 2 or more different cytoplasmic
PT signalling components.
PS
XX Disclosure: Fig 6; 90pp; English.
XX
XX This protein comprises a chimeric receptor consisting of an scFv
CC engineered from anti-CD3 human antibody CTMO1 linked to an
CC extracellular spacer from part of human CD8 hinge, linked to the
CC extracellular and intracellular components of human CD28. It can
CC be expressed in host cells using a chimeric receptor gene (see
CC AAT90511) constructed from DNA cassettes of each component. In a
CC claimed cell activation process an effector cell is transformed with
CC DNA encoding a chimeric receptor containing 2 or more different
CC cytoplasmic signalling components. Also claimed is use of DNA
CC encoding a recombinant chimeric receptor in a DNA delivery system.
CC The DNA delivery systems can be used for the activation of cells to
CC provide e.g. an increase in cell proliferation, expression of
CC cytokines with e.g. pro- or anti-inflammatory responses, stimulation
CC of cytolytic activity, differentiation or other effector functions,
CC antibody secretion, phagocytosis, tumour infiltration and/or
CC increased adhesion. They can be used in the treatment of e.g.
CC infectious disease, inflammatory disease, cancer, allergic/atopic
CC disease, congenital disease, dermatologic disease, neurologic
CC disease, transplant and metabolic/idiopathic disease (claimed).
CC In particular, they can be used in the treatment of rheumatoid
CC arthritis, osteoarthritis, inflammatory bowel disease, asthma,
CC eczema, cystic fibrosis, sickle cell anaemia, psoriasis, multiple
CC sclerosis, organ or tissue transplant rejection, graft-versus-host
CC disease or diabetes (claimed).
XX
XX Sequence 403 AA:

alignment_scores:
Quality: 949.50 Length: 265
Ratio: 4.220 Gaps: 4
Percent Similarity: 84.906 Percent Identity: 70.189

alignment_block:
US-08-487-283A-8 x AAM26648 ..
Align seg 1/1 to: AAM26648 from: 1 to: 403

7 GATATCCAGATGACCCAGTCCCGTCCCTGTCGCGCTGTGGGCGA 56
|||||
21 AsplleGlmethrhglInserProserThrleuSerlaserValgllys 37
|||||
57 TAGGTCACATGACCTCGCGCGCGCGGAAACATCTATGGGCGG... 102
|||||
37 ragValThrThrCysargserSerlySerleuSerleuSerleuSer 54
103 .....CTGACCTGTATCAAGCTAAACCTGGGAAGCTCGAAG 141
||| |||

```

```

54  lYAspThrPheLeuTyrTrpPheGlnGlnLysProGlyLysAlaProLys 70
142 CTTTCATTTATTCAGTGCAGAACCTGGAGATGAGTCCCTTCGCTT 191
    |||||.....:|||||.....:|||||.....:|||||.....:
71  LeuLeuMetTyrArgMetSerAsnLeuAlaSerGlyValProSerAsp 87
192 CTTCTGATCCGGCTCCGGAACGATTTCACTCTACCATCAGACTGC 241
    |||||.....:|||||.....:|||||.....:|||||.....:
87  eSerGlySerGlySerGlyThrGlnPheThrLeuThrIleSerSerLeu 104
242 ACCCTGAACACTTCGCTACGATTTACTGTCAGAACGTTTAACTCCG 291
    |||||.....:|||||.....:|||||.....:|||||.....:
104 lnpRaspaSpasPheAlaThrTyrTyrCysMetGlnHisLeuGluTyrPro 120
292 TTGACTTTGGACAGGCTGACCAAGTGGAATAAAGCTACT..... 333
    |||||.....:|||||.....:|||||.....:|||||.....:
121 PheThrPheGlnGlnGlyThrLysValGluValLysArgThrGlyGly 137
334 .....:GGCGTGCTGCTTCGTGCGGCTGCAT 361
    |||||.....:|||||.....:|||||.....:|||||.....:
137 yGlySerGlyGlyGlyGlySerGlyGlyGlyGlySerGlyGlyGly 154
362 CTTGCTGCTGGCGCTTCTCAAGTCAACTGTCGATCCGCGCGAGCTC 411
    |||||.....:|||||.....:|||||.....:|||||.....:
154 eGlyGlyGlyGlySerGlnIleGlnLeuValGlnSerGlyAlaGluVal 170
412 AAGAACCCAGGGGCTCAGTCAAGTGCTCTTAAGCTAGCGGCTATAT 461
    |||||.....:|||||.....:|||||.....:|||||.....:
171 LysLysProGlySerSerValLysValSerCysLysAlaSerGlyTyr 187
462 TTTTCTAATATTTGATTCATATGATGCGTCAGCGCCCGGCGAGGCC 511
    |||||.....:|||||.....:|||||.....:|||||.....:
187 rPheThrAspTyrTyrIleAsnTrpMetArgGlnAlaProGlyGlnGly 204
512 TGGAAATGATGGCTGAGATCTTACCGGCTCTGTAGCACCGATATACC 561
    |||||.....:|||||.....:|||||.....:|||||.....:
204 eGlnLysPheGlyTyrIleAspProGlySerGlyAsnTrpLysTyrAsn 220
562 GAAATATTTAAAGCCGTGTACTATAGCCGCTGACTGCTACTATAC 611
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221 GluLysPheLysGlyArgAlaThrLeuThrValAspThrSerThrAsn 237
612 ACTATATGATGAGCTCTCCAGCTCGCATGCGAGACACGCGCTATAT 661
    |||||.....:|||||.....:|||||.....:|||||.....:
237 rAlaTyrMetGlnLeuSerSerLeuArgSerGluAspThrAlaPheTyr 254
662 ATTTGCGCGCT.....TATTTTGGCTTACCGCGAATTTGG 699
    |||||.....:|||||.....:|||||.....:|||||.....:
254 hEcysAlaArgGluLysThrThrTyrTyrAla..... 265
700 TATTTGATGTTGGGTCAGAGAACCTGGTCACTGTCGAGC 744
    |||||.....:|||||.....:|||||.....:|||||.....:
266 ...MetAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 279

```

seq_name: /SIDS8/gcdata/geneseq/AA1997.DAT:AAW26646

seq_documentation_block:

ID AAW26646 standard; Protein: 473 AA.

AC AAW26646;

DT 12-FEB-1998 (first entry)

DE Chimeric receptor hCTM01/CD8/zeta.

KW Cell activation; chimeric receptor; DNA delivery; CTM01; scfv; CD8;
 KW T cell receptor zeta chain; cell proliferation; cytokine;
 KW inflammation; effector; cell differentiation; antibody secretion;
 KW phagocytosis; tumour infiltration; adhesion; infection; cancer;
 KW allergy; rheumatoid arthritis; osteoarthritis; asthma; eczema;
 KW inflammatory bowel disease; cystic fibrosis; sickle cell anaemia;
 KW psoriasis; multiple sclerosis; transplant rejection; diabetes;
 KW graft-versus host disease; human; therapy.

```

XX OS Chimeric - Homo sapiens.
XX PN WO9723613-A2.
XX PD 03-JUL-1997.
XX PF 23-DEC-1996; 96WO-GH03209.
XX PR 21-DEC-1995; 95GB-0026131.
XX PA (CLLT ) CELLTECH THERAPEUTICS LTD.
XX PI Bebbington CR, Flinney HM, Lawson ADG, Weir ANC;
XX DR WP1; 1997-351052/32.
XX DR N-PSDB: AAT90509.
XX PT New DNA systems for activating cells - comprising DNA coding for a
XX PT chimeric receptor comprising 2 or more different cytoplasmic
XX PT signalling components.
XX PS Disclosure; Fig 4; 90pp; English.
XX CC This protein comprises a chimeric receptor consisting of an scfv
XX CC engineered from anti-CD3 human antibody CTM01 linked to an
XX CC extracellular spacer in the form of part of human CD8 hinge, linked
XX CC to the extracellular, transmembrane and intracellular components of
XX CC the human T cell receptor zeta chain. It can be expressed in host
XX CC cells (e.g. Jurkat) using a chimeric receptor gene (see AAT90509)
XX CC constructed from DNA cassettes of each component. In a claimed
XX CC cell activation process an effector cell is transformed with DNA
XX CC encoding a chimeric receptor containing 2 or more different
XX CC cytoplasmic signalling components. Also claimed is use of DNA
XX CC encoding a recombinant chimeric receptor in a DNA delivery system.
XX CC The DNA delivery systems can be used for the activation of cells to
XX CC provide e.g. an increase in cell proliferation, expression of
XX CC cytokines with e.g. pro- or anti-inflammatory responses, stimulation
XX CC of cytolytic activity, differentiation or other effector functions,
XX CC antibody secretion, phagocytosis, tumour infiltration and/or
XX CC increased adhesion. They can be used in the treatment of e.g.
XX CC infectious disease, inflammatory disease, cancer, allergic/atopic
XX CC disease, congenital disease, dermatologic disease, neurologic
XX CC disease, transplant and metabolic/diopathic disease (claimed).
XX CC In particular, they can be used in the treatment of rheumatoid
XX CC arthritis, osteoarthritis, inflammatory bowel disease, asthma,
XX CC eczema, cystic fibrosis, sickle cell anaemia, psoriasis, multiple
XX CC sclerosis, organ or tissue transplant rejection, graft-versus-host
XX CC disease or diabetes (claimed).
XX SQ Sequence 473 AA;

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alignment_scores:

Quality: 949.50 Length: 265

Ratio: 4.220 Gaps: 4

Percent Similarity: 84.906 Percent Identity: 70.189

alignment_block:

US-08-487-283a-8 x AAW26646 ..

Align seg 1/1 to: AAW26646 from: 1 to: 473

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7 GATATCCAGATGACCCAGTCCCGCTCCCTGCTGCGCTGTGGGCGA 56
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21 A||l||e||g||i||m||e||t||h||r||G||l||n||S||e||r||P||r||o||S||e||r||T||h||r||L||e||u||S||e||r||A||l||a||S||e||r||V||a||l||G||y||S 37
  |||||.....:|||||.....:|||||.....:|||||.....:
57 TAGGGTCAACATACCTGCGGCGCCAGGAAACATCTATGGCGGG.... 102
  |||||.....:|||||.....:|||||.....:|||||.....:
37 pArgValThrIleThrCysArgSerSerLysSerLeuLeuHisSerAng 54
  |||||.....:|||||.....:|||||.....:|||||.....:
103 .....CTGAACGTGATCAACCTAAACCGGGAAGCTCGAAG 141
  |||||.....:|||||.....:|||||.....:|||||.....:

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54  LysPThrPheLeuTyrTrpPheGlnGlnLysProGlyLysAlaProLys 70
142 CTTTGATTTACGGTCGACGACCACTGGCAGATGAGTCCTTCGCTT 191
    |||||
71  LeuLeuMetTyrArgMetSerAlaLeuAlaSerGlyValProSerArgPh 87
192 CTCTGATTCGGCTCCGAGACGATTTACGTCCTGACCACTGACGATCTC 241
    |||||
87  eSerGlySerGlySerGlyThrGluPheThrLeuThrIleSerSerLeuG 104
242 AGCCTGAAGACTTCGCTACGATTTACTGTGACAGACGTTTAAATACCTCG 291
    |||||
104 InProAspArgPheAlaThrTyrTyrCysMetGlnHisLeuGluTyrPro 120
292 TTGACTTTGGACAGGAGTACCAGGTGGAATAAAGCTACT..... 333
    :|||
121 PheThrPheGlyGlnGlyThrLysValGluValLysArgThrGlyGlyG 137
334 .....GGCGGTGGTGGTCTGTCGGCGGTGGAT 361
137 yGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyGlyGly 154
362 CTGCTGGTGGCGGTTCTCAACGTCACAGTGGTCATCCGGCGCGAGGTC 411
    |||||
154 erGlyGlyGlyGlySerGlnIleGlnLeuValGlnSerGlyAlaGluVal 170
412 AAGAGCCAGGCGGCTCAGTCAAGTGTCTGTAAAGCTAGCGGCTATAT 461
    |||||
171 LysLysProGlySerSerValLysValSerCysLysAlaSerGlyTyrTrh 187
462 TTTTCTTAATATTGATTCATATGGGTCGTCAGGCCCCGGGCGAGGGC 511
    |||||
187 rPheThrAspTyrTyrIleAsnTrpMetArgGlnAlaProGlyGlnGlyL 204
512 TGGATGGATGGTGAAGATCTTACCGGCTCTGAGACCAACCAATATACC 561
    |||||
204 euGluTrpIleGlyTyrIleAspProGlySerGlyAsnThrLysTyrAsn 220
562 GAAATTTTAAAGACCGTGTACTATGACGCGTGCACCTTCGACAGATAC 611
    |||||
221 GluLysPheLysGlyArgAlaThrLeuThrValAspThrSerThrAsnTh 237
612 AGTATACATGAGCTCTCCAGCTCGCATCGAGAGACGGCGCTGTATAT 661
    |||||
237 rAlaTyrMetGluLeuSerSerLeuArgSerGlnAspThrAlaPheTyrP 254
662 ATTCCGGCGCT.....TATTTTTCGTCAGCCCGGAATGG 699
    :|||
254 heCysAlaAlaArgGluLysThrThrTyrTyrAla..... 265
700 TATTTGATGTTGGGTCACAGAACCTGGTCACTGTCGAGC 744
    :|||
266 ...MetAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 279

seq_name: /SID8/gcgcdata/geneseq/geneseq/AA1997.DAT:AAW26647
seq_documentation_block:
ID   AAW26647 standard; protein; 514 AA.
XX
XX   AAW26647;
XX
XX   12-FEB-1998 (first entry)
XX
DE   Chimeric receptor hCTMO1/CD8/zeta-CD28.
XX
KW   Cell activation; chimeric receptor; DNA delivery; CTMO1; scFv; CD8;
KW   CD28; T cell receptor zeta chain; cell proliferation; cytokine;
KW   inflammation; effector; cell differentiation; antibody secretion;
KW   phagocytosis; tumor infiltration; adhesion; infection; cancer;
KW   allergy; rheumatoid arthritis; osteoarthritis; asthma; eczema;
KW   inflammatory bowel disease; cystic fibrosis; sickle cell anaemia;
KW   psoriasis; multiple sclerosis; transplant rejection; diabetes;
KW   graft versus host disease; human; therapy.

```

```

XX OS Chimeric - Homo sapiens.
XX
XX PN WO9723613-A2.
XX
XX PD 03-JUL-1997.
XX
XX PE 23-DEC-1996; 96WO-GB03209.
XX
XX PR 21-DEC-1995; 95GB-0026131.
XX
XX PA (CLUT ) CELLTECH THERAPEUTICS LTD.
XX
XX PI Beddington CR, Finney HM, Lawson ADG, Weir ANC;
XX
XX WP1: 1997-351052/32.
XX
XX DR N-PSDB; AAT90510.
XX
XX PT New DNA systems for activating cells - comprising DNA coding for a
XX PT chimeric receptor comprising 2 or more different cytoplasmic
XX PT signalling components.
XX
XX PS Disclosure; Fig 5; 90pp; English.
XX
CC This protein comprises a chimeric receptor consisting of an scFv
CC engineered from anti-CD3 human antibody CTMO1 linked to an
CC extracellular spacer in the form of part of human CD8 hinge, linked
CC to the extracellular, transmembrane and intracellular components of
CC the human T cell receptor zeta chain, fused to the intracellular
CC component of human CD28. It can be expressed in host cells (e.g.
CC Jurkat) using a chimeric receptor gene (see AAT90510) constructed
CC from DNA cassettes of each component of the receptor. In a claimed
CC cell activation process an effector cell is transformed with DNA
CC encoding a chimeric receptor containing 2 or more different
CC cytoplasmic signalling components. Also claimed is use of DNA
CC encoding a recombinant chimeric receptor in a DNA delivery system.
CC The DNA delivery systems can be used for the activation of cells to
CC provide e.g. an increase in cell proliferation, expression of
CC cytokines with e.g. pro- or anti-inflammatory responses, stimulation
CC of cytolytic activity, differentiation or other effector functions,
CC antibody secretion, phagocytosis, tumour infiltration and/or
CC increased adhesion. They can be used in the treatment of e.g.
CC infectious disease, inflammatory disease, cancer, allergic/atopic
CC disease, congenital disease, dermatologic disease, neurologic
CC disease, transplant and metabolic/idiopathic disease (claimed).
CC In particular, they can be used in the treatment of rheumatoid
CC arthritis, osteoarthritis, inflammatory bowel disease, asthma,
CC eczema, cystic fibrosis, sickle cell anaemia, psoriasis, multiple
CC sclerosis, organ or tissue transplant rejection, graft-versus-host
CC disease or diabetes (claimed).
XX
XX SO Sequence 514 AA:

alignment_scores:
Quality: 949.50 Length: 265
Ratio: 4.220 Gaps: 4
Percent Similarity: 84.906 Percent Identity: 70.189

alignment_block:
US-08-487-283A-8 x AAW26647 ..
Align seg 1/1 to: AAW26647 from: 1 to: 514

7 GATATCCAGATGACCCAGTCCCGTCTCCCTGTCCGCGCTGTGGGCGA 56
|||||
21 AspIleGlnMetThrGlnSerProSerThrLeuSerAlaSerValGlyAs 37
57 TAGGGTCACATCACCCTGGCGGCGGACGAGAAACATCTATGAGCGCG... 102
|||||
37 PargValThrIleThrCysArgSerSerLysSerLeuLeuHisSerGng 54
103 .....CTGAAGTGTATCAACGTAACGTAACCTGGGAAAGTCGAGAG 141

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54  lYAspThrPheLeuTyrTrpPheGlnGlnLysProGlyLysAlaProLys 70
142 CTTCTGATTTACGGTCGACGACCTGCAGATCGAGAGTCCCTTCGCTT 191
71  LeuLeuMetCysTrpArgMetSerAsnLeuAlaSerGlyValProSerAlaGph 87
192 CTCCTGATCCGGCTCCGGAACGATTTCACCTGCATCATCAGCATCTGC 241
87  eSerGlySerGlySerGlyThrGlnPheThrLeuThrLisSerSerLeug 104
242 AGCCTAAGACTTCGCTACGATTTACTGTCAGAACGTTTAAATACTCGC 291
104 lnpRoAspAspPheAlaThrTrpCysMetGlnHisLeuGlnTyrPro 120
292 TTGACTTTGCGACAGGGTACCAAGGTGAATAAAGTACT..... 333
121 PheThrPheGlyGlnGlnLysValGlnValLysArgThrGlyGlyGly 137
334 .....GGCGGTGGTGGTTCGTGTCGGCGGTGAT 361
137 yGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyGlyGly 154
362 CTGCTGTGGCGGCTTCTCAAGTCCAACTGTCGAATCCGGCGCGAGTGC 411
154 eGlyGlyGlyGlySerGlnLeuValGlnSerGlyAlaGlnVal 170
412 AAGAACCCAGGGCGCTCAGTCAAGTGCCTGTAAGCTAGCGGCTAT 461
171 LysLysProGlySerValLysValSerCysLysAlaSerGlyTrp 187
462 TTTTCTAATATATGATTCATGCGTGCCTCAGGCCCGCGGCGAGGCC 511
187 rPheThrAspTyrTyrLisAsnTrpMetArgGlnAlaProGlyGlnGly 204
512 TGGAAATGATGGTGAATCTTACCGGCTCTGTGACACCGAATATACC 561
204 eudLurPrlieGlyTrpLysProGlySerGlyAsnTrpLysTyrAsn 220
562 GAAATTTTAAAGACCGTGTACTAGTCCGACACTCGACTGATAC 611
221 GluLysPheLysGlnAlaThrLeuThrValAspThrSerThrAsnTh 237
612 AGTATACATGAGCTCTCCAGCTGCAGTCGAGACAGCGCGCTATAT 661
237 rAlaTrpMetGlnLeuSerSerLeuArgSerGlnAspThrAlaPheYrP 254
662 ATTCGCGCGCT.....TATTTTGGTGTCTACCCCGAATGG 699
254 heCysAlaArgGlnLysThrThrTyrTyrAla..... 265
700 TATTTGATGTTTGGGTGCAAGACCCGTGCTACTGTCGAGAC 744
266 ...MeLAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 279

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seq_name: /SID58/gcdata/geneseq/geneseq/AA1997.DAT:AAW26649

seq_documentation_block:

ID: AAW26649 standard; Protein: 651 AA.

AAW26649;

12-FEB-1998 (first entry)

Chimeric receptor hCTMO1/G1/zeta.

Cell activation; chimeric receptor; DNA delivery; CTMO1; scFv; IgG1; T cell receptor zeta chain; cell proliferation; cytokine; inflammation; effector; cell differentiation; antibody secretion; phagocytosis; tumour infiltration; adhesion; infection; cancer; allergy; rheumatoid arthritis; osteoarthritis; asthma; eczema; inflammatory bowel disease; cystic fibrosis; sickle cell anaemia; psoriasis; multiple sclerosis; transplant rejection; diabetes;

KW graft versus host disease; human; therapy.
 XX
 OS Chimeric - Homo sapiens.
 PN W09723613-A2.
 XX
 PD 03-JUL-1997.
 XX
 PF 23-DEC-1996; 96MO-GB03209.
 XX
 PR 21-DEC-1995; 95GB-0026131.
 XX
 PI (CLLT) CELLTECH THERAPEUTICS LTD.
 XX Bebbington CR, Flinney HM, Lawson ADG, Weir ANC;
 DR WPI; 1997-351052/32.
 XX N-PSDB; AAT90512.
 XX
 PT New DNA systems for activating cells - comprising DNA coding for a
 PT chimeric receptor comprising 2 or more different cytoplasmic
 PT signalling components.
 XX
 PS disclosure; Fig 7; 90pp; English.
 XX
 CC This protein comprises a chimeric receptor consisting of an scFv
 CC engineered from anti-CD3 human antibody CTMO1 linked to an
 CC extracellular spacer comprising the human IgG1 hinge, CH2 and CH3,
 CC linked to transmembrane and intracellular regions of the human T
 CC cell receptor zeta chain. It can be expressed in host cells (e.g.
 CC Jurkat) using a chimeric receptor gene (see AAT90512) constructed
 CC from DNA cassettes encoding each receptor component. In a claimed
 CC cell activation process an effector cell is transformed with DNA
 CC encoding a chimeric receptor containing 2 or more different
 CC cytoplasmic signalling components. Also claimed is use of DNA
 CC encoding a recombinant chimeric receptor in a DNA delivery system.
 CC The DNA delivery systems can be used for the activation of cells to
 CC provide e.g. an increase in cell proliferation, expression of
 CC cytokines with e.g. pro- or anti-inflammatory responses, stimulation
 CC of cytolytic activity, differentiation or other effector functions,
 CC antibody secretion, phagocytosis, tumour infiltration and/or
 CC increased adhesion. They can be used in the treatment of e.g.
 CC infectious disease, inflammatory disease, cancer, allergic/atopic
 CC disease, congenital disease, dermatologic disease, neurologic
 CC disease, transplants and metabolic/diopathic disease (claimed).
 CC In particular, they can be used in the treatment of rheumatoid
 CC arthritis, osteoarthritis, inflammatory bowel disease, asthma,
 CC eczema, cystic fibrosis, sickle cell anaemia, psoriasis, multiple
 CC sclerosis, organ or tissue transplant rejection, graft-versus-host
 CC disease or diabetes (claimed).
 XX
 SQ Sequence 651 AA;

alignment_scores:

Quality: 949.50 Length: 265

Ratio: 4.220 Gaps: 4

Percent Similarity: 84.906 Percent Identity: 70.189

alignment_block:

US-08-487-283A-8 x AAW26649 ..

Align seg 1/1 to: AAW26649 from: 1 to: 651

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11  |||||||
21  AspliegImetThglnSerProSerThrLeuSerAlaSerValGlyAs 37
57  TAGGTCACCATCCTCGGGCGCGAGGAAACATCTATGCGCGG.... 102
37  pArgValThrIleThrCysArgSerSerLysSerLeuHisAsnG 54
103  .....CTGAACGTGATCAACGTAAACCTGGGAAAGCTCGAAG 141

```

```

54  lysphrphleuetytrpneinglnlyserproglylsalaprolys 70
142 CTTCTGATTTTCAGTGGCGAAGCAATGCGATGAGTCCCTTCGCTT 191
71  LeuLeuMetYrArGMeTSeRAsnLeuAlaSerGlyValProSerArgph 87
192 CTCTGGATCCGGCTCCGGAACGATTTCCTGACCATCAGCAGTCTGC 241
87  eSerGlySerGlySerGlyThrGluPheThrLeuThrLeuSerLeug 104
242 AGCCTGAGAGCTCGTACGATATCTACGTCGAGACGTTTAAATACTCG 291
104 InProSpAspPheAlaThrTyTrpCysMetGlnHisLeuGluTyrPro 120
292 TTGACTTTTCGACAGGCGTACCAAGGTGGAATAAACGACT..... 333
121 PheThrPheGlyGlnGlyThrLysValGluValLysArgThrGlyGly 137
334 .....GGCGGTGTGTCTGTGGTGGCGGTGAT 361
137 yGlySerGlyGlyGlySerGlyGlyGlySerGlyGlyGlyGlyGly 154
362 CTGTGGTGGCGGTCTTCAGTCCCACTGTGCAATCGCGGCGCGAGTGC 411
154 eRgLyGlyGlySerGlnLeuValGlnSerGlyAlaGluVal 170
412 AAGACGACAGGCGCTCAGTCAAGTCCCTGTAAGCTACGCGCTATAT 461
171 LysLysProGlySerValLysValSerCysLysAlaSerGlyTyrTh 187
462 TTTTCTAATTAATGATTCATGCGTGTGCGTACGCCCGCGGAGGCC 511
187 rPheThrAspTyrTrpLysAsnTrpMetArgGlnAlaProGlyGlnGly 204
512 TGAATGAGAGGCGTGAATCTTACCGGCTGTGTAGCAGCAGATATACC 561
204 euGluTrpIleGlyTrpLysAsnProGlySerGlyAsnThrLysTyrAsn 220
562 GAAATTTTAAAGACGCTGTACATGACGCGGTGACACTTGACTAGTAC 611
221 GluLysPheLysGlyArgAlaThrLeuThrValAspThrSerThrAspTh 237
612 AGTAACATGAGCTCTCCAGCTGCGATCGAGACAGCGCGCTTATTT 661
237 rAlaTyrMetGluLeuSerSerLeuArgSerGluAspThrAlaPheTyrP 254
662 ATTCGCGCGCT.....TATTTTGTGCTTACGCCCGCAATTGG 699
254 heCysAlaArgGluLysThrThrTyrTyrAla..... 265
700 TATTTGATGTTGGGTCAGGAAACCTGCTACTGCTCTGAGC 744
266 ...MetAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 279

seq_name: /SID58/gcdata/geneseq/geneseqp/AA1997.DAT:AAW26650
seq_documentation_block:
ID AAW26650 standard: Protein: 692 AA.
XX
XX AAW26650:
XX
XX 12-FEB-1998 (first entry)
XX
XX Chimeric receptor hCTMO1/GI/zeta-CD28.
XX
XX Cell activation; chimeric receptor; DNA delivery; CTMO1; scFv;
KW IgG1; CD28; T cell receptor zeta chain; proliferation; cytokine;
KW inflammation; effector; cell differentiation; antibody secretion;
KW phagocytosis; tumour infiltration; adhesion; infection; cancer;
KW allergy; rheumatoid arthritis; osteoarthritis; asthma; eczema;
KW inflammatory bowel disease; cystic fibrosis; sickle cell anaemia;
KW psoriasis; multiple sclerosis; transplant rejection; diabetes;

```

```

KW graft versus host disease; human; therapy.
XX
XX Chimeric - Homo sapiens.
XX
XX WO9723613-A2.
XX
XX 03-JUL-1997.
XX
XX 23-DEC-1996; 96WO-GB03209.
XX
XX 21-DEC-1995; 95GB-0026131.
XX
XX (CLLT ) CELLTech THERAPEUTICS LTD.
XX
XX Bebbington CR, Finney HM, Lawson ADG, Weir ANC;
XX
XX WPI: 1997-351052/32.
XX
XX N-PSDB: AAT90513.
XX
XX New DNA systems for activating cells - comprising DNA coding for a
XX chimeric receptor comprising 2 or more different cytoplasmic
XX signalling components.
XX
XX Disclosure: Fig 8; 90pp: English.
XX
XX This protein comprises a chimeric receptor consisting of an scFv
XX engineered from anti-CD3 human antibody CTMO1 linked to an
XX extracellular spacer comprising the Human IgG1 hinge, CH2 and CH3,
XX linked to the transmembrane and intracellular components of the
XX human T cell receptor zeta chain, fused to the intracellular region
XX of human CD28. It can be expressed in host cells (e.g. Jurkat)
XX using a chimeric receptor gene (see AAT90513) constructed from DNA
XX cassettes encoding each component of the receptor. In a claimed
XX cell activation process an effector cell is transformed with DNA
XX encoding a chimeric receptor containing 2 or more different
XX cytoplasmic signalling components. Also claimed is use of DNA
XX encoding a recombinant chimeric receptor in a DNA delivery system.
XX The DNA delivery systems can be used for the activation of cells to
XX provide e.g. an increase in cell proliferation, expression of
XX cytokines with e.g. pro- or anti-inflammatory responses, stimulation
XX of cytolytic activity, differentiation or other effector functions,
XX antibody secretion, phagocytosis, tumour infiltration and/or
XX increased adhesion. They can be used in the treatment of e.g.
XX infectious disease, inflammatory disease, cancer, allergic/atopic
XX disease, congenital disease, dermatologic disease, neurologic
XX disease, transplant and metabolic/idiopathic disease (claimed).
XX In particular, they can be used in the treatment of rheumatoid
XX arthritis, osteoarthritis, inflammatory bowel disease, asthma,
XX eczema, cystic fibrosis, sickle cell anaemia, psoriasis, multiple
XX sclerosis, organ or tissue transplant rejection, graft-versus-host
XX disease or diabetes (claimed).
XX
XX Sequence 692 AA:
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alignment_scores:
Quality: 949.50 Length: 265
Ratio: 4.220 Gaps: 4
Percent Similarity: 84.906 Percent Identity: 70.189

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alignment_block:
US-08-487-283A-8 x AAW26650 ..

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Align seg 1/1 to: AAW26650 from: 1 to: 692

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57 TAGGTCACATCAGCTCGCGCGCCGAGCAAAACATCTAAGCGCG... 102
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37 pArgValThrIleThrCysArgSerSerLysSerLeuLeuHisSerAsnG 54

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103 .....CTAAGTCGTATCAACGTAACCTGGGAAGCTCCGAG 141
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54 LysphtrPheLeuTyrTrpPheGlnGlnLysProGlyLysAlaProLys 70
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142 CTTCGTGATTACGGTGCGACGAACTGGCAGATGGAGTCCCTTCGCTT 194
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71 LeuLeuMetYrArgMetSerAsnLeuAlaSerGlyValProSerArghp 87
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192 CTTGGATCCGGCTCCGGAACGATTTCACCTGACATCAGCAGTCTGC 241
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87 eSerGlySerGlySerGlyThrGluPheThrLeuThrIleSerSerLeug 104
      ||| |:::|:::|:::|:::|:::|:::|:::|:::|:::|
242 AGCGTGAAGACTTCGCTACGATATTACCTGCAACAGCTTTAAATACTCCG 291
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104 InProSapSpPhalathrYrTrpCySmeGlnHisLeuGluTrypro 120
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121 PheThrPheGlyGlnGlyThrLysValGluValLysArgThnGlyGly 137
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334 .....GGCGGTGGTGCTCTGGTGGCGGTGAT 361
      ||| |:::|:::|:::|:::|:::|:::|:::|:::|:::|
137 yGlyserGlyyGlyLysSerGlyGlyGlyLysSerGlyGlyGlyLys 154
      ||| |:::|:::|:::|:::|:::|:::|:::|:::|:::|
362 CTGGTGGTGGCGGTTTCACAATCCAATCGTGCATACCGCGCGGAGTGC 411
      ||| |:::|:::|:::|:::|:::|:::|:::|:::|:::|
154 erGlyGlyGlyGlySerGlnGlnLeuValGlnSerGlyAlaGluVal 170
      ||| |:::|:::|:::|:::|:::|:::|:::|:::|:::|
412 AAGAAGCCAGGGGCCCTCAGTCAAAGTGTCTGTAAAGTAGCGGTATAT 461
      ||| |:::|:::|:::|:::|:::|:::|:::|:::|:::|
171 LysLysProGlySerSerValLysValSerGlyLysLysSerGlyTrh 187
      ||| |:::|:::|:::|:::|:::|:::|:::|:::|:::|
462 TTTTCTAATTATTGATTCAATGGGTGTCAGGCCCCCGGACAGGCC 511
      ||| |:::|:::|:::|:::|:::|:::|:::|:::|:::|
187 rPheThrAspTyrrylLeasnTrpMeLarglInAlaProGlyGlnGlyL 204
      ||| |:::|:::|:::|:::|:::|:::|:::|:::|:::|
512 TGGAATGAGATGGGTGAGATCTTACCGGGCTCTGGTAGCACCAATATAC 561
      ||| |:::|:::|:::|:::|:::|:::|:::|:::|:::|
204 euGIurPrIleGlyTriPlasProGlySerGlyAsnThrLysTyraSn 220
      ||| |:::|:::|:::|:::|:::|:::|:::|:::|:::|
562 GAAATTTTAAAGACCGGTACTACTATGAGCGGCTGACACTTCGCTGTAC 611
      ||| |:::|:::|:::|:::|:::|:::|:::|:::|:::|
221 GluLysPheLysGlyArgAlaThrLeuThrValAspThrSerThrSnth 237
      ||| |:::|:::|:::|:::|:::|:::|:::|:::|:::|
612 AGTATCATGAGAGCTCTCCACCTTCGATCGAGAGACAGCGCGTCTATT 661
      ||| |:::|:::|:::|:::|:::|:::|:::|:::|:::|
237 rAlaTyMeGlInuSerSerLeuArgSerLusPthrAlaPheTyrrp 254
      ||| |:::|:::|:::|:::|:::|:::|:::|:::|:::|
662 ATTCGCCGCGT.....TATTTTTTTGGTTCAGCCGAATTGG 699
      ||| |:::|:::|:::|:::|:::|:::|:::|:::|:::|
254 hecyAlaIarGluLysThrThrTrpTyrTala..... 265
      ||| |:::|:::|:::|:::|:::|:::|:::|:::|:::|
700 TATTTGATGTTGGGGTCAAGAACCTCGTCACGTCGTCGAGC 744
      ||| |:::|:::|:::|:::|:::|:::|:::|:::|:::|
266 ...MetaspTyrrIpGlyGlnGlyThrLeuValThrValSerSer 279
      ||| |:::|:::|:::|:::|:::|:::|:::|:::|:::|
seq_name: /SID8/gc9data/geneseq/geneseqp/AA2001.DAT: AAB30693
seq_documentation_block:
ID AAB30693 standard; Protein; 431 AA.
XX AAB30693;
XX AC
XX DT
XX 02-APR-2001 (first entry)
XX DE
XX A fusion of single chain antibody/screptavidin.
XX KW
XX Streptavidin; tumour cell; cancer; adenocarcinoma;
XX hematological malignancy; huNR-LU-10; EGP40; EPCAM.
XX OS
XX Synthetic.
OS Streptomycetes avidinii.
OS Homo sapiens.
```

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XX  W0200075333-A1.
PN
XX
XX  14-DEC-2000.
PD
XX
XX  05-JUN-2000; 2000WO-US15595.
PF
XX
XX  07-JUN-1999; 99US-0137900.
PR
XX  03-DEC-1999; 99US-0168976.
PA
XX  (NEOR-) NEORX CORP.
XX
XX  Goshorn SC, Graves SS, Schultz JE, Lin Y, Sanderson JA, Reno JM;
XX
XX  WPI: 2001-091213/10.
DR
XX  N-PSDB: AAC86562.
XX
XX  New vector constructs for expressing genomic streptavidin fusion
XX  proteins which are useful for targeting tumour cells associated with
XX  cancer, e.g. adenocarcinomas -
XX
XX  Example 1; Fig 10; 100pp: English.
XX
XX  The present sequence encodes a fusion of the single chain antibody
XX  EPNM-1U-10 and streptavidin. The antibody binds the antigen EGP40 or
XX  EPCAM. The fusion protein is expressed using vectors of the invention.
XX
XX  The specification describes vector constructs for expressing streptavidin
XX  fusion proteins. The vector comprises a first nucleic acid encoding
XX  streptavidin or its functional variant operatively linked to a promoter,
XX  and a cloning site for insertion of a second nucleic acid sequence
XX  encoding a polypeptide to be fused with streptavidin, intersposed between
XX  the promoter and the first nucleic acid sequence. Alternatively, the
XX  vector construct comprises a first nucleic acid, operatively linked to a
XX  promoter, encoding a polypeptide to be fused with streptavidin, and a
XX  cloning site for insertion of a second nucleic acid encoding at least
XX  129 amino acids of streptavidin or its functional variant. The fusion
XX  proteins are useful for targeting tumour cells, particularly tumour cells
XX  associated with cancer, e.g. adenocarcinomas or hematological
XX  malignancies. The vector construct is useful for expressing of
XX  streptavidin fusion proteins. In particular, these are useful as tools
XX  for medical diagnostics and therapeutic purposes, e.g. for detecting the
XX  presence or absence of, or treating, a target site within a mammalian
XX  host.
XX
XX  SQ      Sequence      431 AA:
XX
XX
XX  alignment_scores:
XX      Quality: 928.50      Length: 249
XX      Ratio: 4.201      Gaps: 2
XX  Percent Similarity: 88.755      Percent Identity: 73.494
XX
XX  alignment_block:
XX  US-08-487-283A-8 x AAB30693 ..
XX
XX  Align seg 1/1 to: AAB30693 from: 1 to: 431
XX
XX      1  ATGGCCGATATCCAGATGACCCGTCGCCGTCGCGCCTGTGT  50
XX      ||||||||||||||||||||||||||||||||||||||||
XX  21  MetAlaSplIleGlnMetThGlnSerProSerLeuSerAlaIleSerVa  37
XX
XX      51  GGGCGATAGGGGTCCACATCACTCGGCGCCAGCGAAACATCTATGCG  100
XX      ||||||||||||||||||||||||||||||||||||
XX  37  IGIYAspArgValThrIleThrIleThyGATGAlaSerGlnGlyIleArgGlyA  54
XX
XX      101 CGCTGAACCTGTATCAACGTAAACCTGGGAAAGCTCCGACACTTGTGAT  150
XX      ||||||||||||||||||||||||||||||||||||
XX  54  snleuAspTrpTyrGlnGlnIleProGlyIleProGlyLeuIleuIle  70
XX
XX      151 TAGGGTCGCGAAGCACTGGGCGATGAGTGCTCCCTGCTCTCTGGATC  200
XX      ||||||||||||||||||||||||||||||||||||
XX  71  TySerThrSerAsnIleAsnSerGlyValProSerArgPheSerGlySe  87

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|||||
137 yglglyserglglyglglyserglvalglnglinserspa 154
404 CCGAGGTCAAGAACCCGAGGCTCACTCAAGTCTCTTAAAGTACG 453
154 lacluleuValysProglYAlaserValysIleserCyslyAlaser 170
454 GGGTATATTTTCTATATTTGATTCATGGGCGGTGAGCCCGG 503
171 GYTYThrPheThrAspHisAlaIleHisThrAlaLysGlnLysProgl 187
504 GCGGGCTGAGTGGATGGATGATTCACCGGCTCGGTGATGACCG 553
187 uGlnGlyLeuGlnTrrIleGlyTrrIleSerProglYAsnAspIleL 204
554 AATATACCGAAATTTTAAAGACCGTGTACTATAGCCGCTGACACTTCG 603
204 ystrAsnGlnLysPheLysGlyLysAlaThrLeuThrAlaAspLysSer 220
604 ACTAGTACAGTATACATGAGCTCTCCAGCTCGATCGAGACACGGC 653
221 SerSerThrAlaTyrMetGlnLeuAsnSerLeuThrSerGlnAspSerAl 237
654 CGTCTATTATGGCGGTATTTTGGTGTCTAGCCCGAATGGTAT 703
237 ValTyrPheCysLysArgSerTyrTyrGlyHis..... 248
704 TTGATGTTGGGTCAAGAACCTGCTGACCTGTCTGACG 744
249TrrGlyGlnGlyThrThrLeuThrValSerSer 259
seq_name: /SID58/gcgdata/geneseq/geneseq/AA2000.DAT:AA91026
seq_documentation_block:
ID AA91026 standard; Protein; 436 AA.
XX
AC AA91026;
XX
DT 05-SEP-2000 (first entry)
XX
DE Apoptobody3sc fusion protein SEQ ID NO:8.
XX
XX Human; Fas antigen; apoptosis; apoptobody3sc; antibody; fusion gene;
KW medical; pharmaceutical; pharmacological; biochemical.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
PN JP2000102389-A.
XX
PD 11-APR-2000.
XX
PE 29-SEP-1998; 98JP-0291441.
XX
PR 29-SEP-1998; 98JP-0291441.
XX
PA (HAGI/) HAGIMARA Y.
XX (HAGI/) HAGIMARA H.
XX
DR WPI; 2000-332086/29.
XX
DR N-PSDB; AAA39167.
XX
PT Causing apoptosis comprises transfecting fused gene to cell and
PT reacting cell with idiotype antibody -
XX
PS Disclosure: Page 8-9; 10pp; Japanese.
XX
CC The present invention describes a method for causing apoptosis in which
CC a fused gene consisting of a gene participating to apoptosis and a gene
CC encoding at least the variable region of anti-idiotype antibody is
CC transfected to a cell to express the fused gene and then an idiotype
CC antibody is reacted with the expressed cell. The method is useful in
CC medical, pharmaceutical, pharmacological and biochemical fields. The

CC present sequence represents a fusion protein designated apoptobody3sc.
CC which is used in the exemplification of the present invention.
XX
SQ Sequence 436 AA;
alignment_scores:
Quality: 849.00 Length: 256
Ratio: 4.082 Gaps: 3
Percent Similarity: 81.250 Percent Identity: 64.844
alignment_block:
US-08-487-283a-8 x AA91026 ..
Align seg 1/1 to: AA91026 from: 1 to: 436
7 GATATCCAGATGACCCAGTCCGCTCCCTGCTGCGGCGCA 56
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21 AspIleGlnMetAsnIleSerProSerSerLeuSerAlaSerLeuLys 37
57 TAGGGTCAACATCACCTCGCGGCGCCAGCAAAACATGTATGGCGCGCTGA 106
37 PrrIleThrIleThrCysHisAlaSerGlnAsnIleAspValTrrPleus 54
107 ACTGATATGACGTAACTCGGAAAGCTCCGAACTGTGATTTACGT 156
54 ErrTrrGlnGlnLysProGlnAsnValPrrLysLeuLeuIleTrrLys 70
157 GCGAGAACCTGGCAGATGAGTCCCTGCTGCTGCTGATCCGCGGC 206
71 AlaSerAsnLeuHisThrGlyAlaPrrSerArgPrrSerGlySerIys 87
207 CGGAACGATTTTCACCTGACCATGACAGTCTGACGCTGAAAGACTTCG 256
87 rGlyThrGlyPrrLeuThrIleSerSerLeuGlnProGlnAspIleAla 104
257 CTACGATATTCGTGCAGAACGTTTAAATACCTCCGTGACTTTCGACAG 306
104 laThrTrrTrrCysGlnGlnGlnIleSerTrrPrrArgTrrPrrGlyGly 120
307 GGTACCAAGCTGGAAATAAAGTACT..... 333
121 GylThrLysLeuGlnIleLysArgAlaAspAlaAlaPrrThrValSerLe 137
334 ...GCGGTGGTGGTCTGCTGCGGCTGATCTGCTGCGGCTTC 379
137 uGlnGlyGlyGlySerGlyGlyGlySerGlyGlyGlySerG 154
380 AAGTCCAACTGGTGCATCCGCGCGGAGTCAAGAACCCAGGCGCTCA 429
154 luValGlnLeuGlnIleSerGlyThrValLeuAlaArgProGlyAlaSer 170
430 GTCAAGTGTCTGTAAAGTACGCGGTATATTTTCTTAATTTATTTGAT 479
171 ValLysMetSerCysLysAlaSerGlyTrrPrrAsnSerTrrTrrPrr 187
480 TCAATGGTGGCTGACGCGCGCGGCGAGGCTGCAATGAGTGGTGAA 529
187 HisTrrValLysGlnArgProGlnIleGlnIleGlnIleGlnIle 204
530 TCTTACCGGCTCTGTAGCACCGCAATATACGAAATTTTAAAGCTC 579
204 leryTrProGlnAsnSerAspIleSerTrrSerGlnAsnPrrLysAspArg 220
580 GTTACTATGACCGCTGACACTTCGACTAGTACAGTATACATGAGCTTC 629
221 AlaLysLeuThrAlaValThrSerThrSerThrAlaTyrMetGlnLeuThr 237
630 CAGCTCGCATCGAGAGACACGCGCTATATTATTCGCGCGCT.....T 673
237 gserLeuThrAsnGlnAspSerAlaValTrrPrrCysTrrLysGlnGln 254
674 ATTTTTCGTTCTAGCCCGAATGGTATTTTATGATTTTGGGCTCAAGCA 723

RA Hartmann L., Schroeder W., Luebke-Becker A.;
 RT "Isolation of the major outer-membrane protein of *Actinobacillus*
 RL *pleuropneumoniae* and *Haemophilus parvus*.";
 CC J. Vet. Med. B 42:59-63(1995).
 CC -1- FUNCTION: STRUCTURAL RIGIDITY OF THE OUTER MEMBRANE OF ELEMENTARY
 CC BODIES AND PORIN FORMING, PERMITTING DIFFUSION OF SOLUTES THROUGH
 CC THE INTRACELLULAR RETICULATE BODY MEMBRANE.
 CC -1- SUBUNIT: DISULFIDE BONDS INTERACTIONS WITHIN AND BETWEEN MONO
 CC MOLECULES & OTHER COMPONENTS FORM HIGH MOLECULAR-WEIGHT OLIGOMERS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
 KM Outer membrane; Transmembrane; Porin.
 FT NON_TER 21 21
 SQ SEQUENCE 21 AA: 2396 MW: 690385CEA907A637 CRC64;

Query Match 22.4%; Score 24; DB 1; Length 21;
 Best Local Similarity 50.0%; Pred. No. 7.1e+02;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 VIDROGTR 8
 Db 3 YVENGGTR 10

RESULT 3
 RS19_PMPBP STANDARD; PRT; 14 AA.
 AC 052093;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 30S RIBOSOMAL PROTEIN S19 (FRAGMENT).
 GN RPS19 OR RPS19.
 OS Pigeon pea witches'-broom phytoplasma.
 CC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 CC Acholoplasmataceae; Phytoplasma.
 OC NCBI_TaxID=37700;
 RX MEDLINE=94350802; PubMed=8071198;
 RP SEQUENCE FROM N.A.
 RA Gunderson D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
 RT "Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for
 RT their classification.";
 RL J. Bacteriol. 176:5244-5254(1994).
 CC -1- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY
 CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
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 CC -----
 CC EMBL: L27036; AAA83946.1; -
 CC InterPro: IPR002222; -
 DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
 KM Ribosomal protein; rRNA-binding.
 FT NON_TER 1 1
 SQ SEQUENCE 14 AA: 1668 MW: 8FDA6FB830DFBBA CRC64;

Query Match 21.5%; Score 23; DB 1; Length 14;
 Best Local Similarity 62.5%; Pred. No. 6.8e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 WGTKSSK 11
 Db 2 HGRTKSK 9

RESULT 4
 LPTP_BACST STANDARD; PRT; 20 AA.
 AC P05658;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE TETRACYCLINE RESISTANCE LEADER PEPTIDE.
 GN TETL.
 OS *Bacillus stearothermophilus*, *Bacillus cereus*, and
 OS *Staphylococcus hyicus*.
 OG Plasmid pTH15, Plasmid pBC16, and Plasmid pSTEL.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC *Bacillus/Staphylococcus* group; *Bacillus*.
 OC NCBI_TaxID=1422, 1396, 1284;
 OX [1]
 RP SEQUENCE FROM N.A.
 RA PLASMID-pTH15;
 RC MEDLINE=86031344; PubMed=2996983;
 RX Hoshino T., Ikeda T., Tomizuka N., Furukawa K.;
 RT "Nucleotide sequence of the tetracycline resistance gene of pTH15, a
 RT thermophilic *Bacillus* plasmid: comparison with *Staphylococcus* TCR
 RT controls.";
 RT Gene 37:131-138(1985).
 RL [2]
 RP SEQUENCE FROM N.A.
 RA PLASMID-pBC16;
 RC MEDLINE=90221899; PubMed=2109312;
 RX Palva A., Vidgren G., Simonen M., Rintala H., Laamanen P.;
 RT "Nucleotide sequence of the tetracycline resistance gene of pBC16
 RT from *Bacillus cereus*.";
 RL Nucleic Acids Res. 18:1635-1635(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES-S.*hyicus*; PLASMID-pSTEL;
 RX MEDLINE=92321725; PubMed=1622166;
 RA Schwarz S., Cardoso M., Wegener H.C.;
 RT "Nucleotide sequence and phylogeny of the tet(L) tetracycline
 RT resistance determinant encoded by plasmid pSTEL from *Staphylococcus*
 RT *hyicus*.";
 RL Antimicrob. Agents Chemother. 36:580-588(1992).
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 CC -----
 CC EMBL: D00006; BAA00004.1; -
 CC EMBL: M11036; AAA22850.1; -
 DR EMBL; X51366; CAA35750.1; -
 DR EMBL; X60828; CAA43219.1; -
 DR PIR; S09233; LFBSTU.
 DR PIR; S23742; S23742.
 KM leader peptide; Antibiotic resistance; Plasmid.
 SQ SEQUENCE 20 AA: 2253 MW: 18D0FA6CA231CA1 CRC64;

Query Match 21.0%; Score 22.5; DB 1; Length 20;
 Best Local Similarity 50.0%; Pred. No. 1.2e+03;
 Matches 7; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

OY 8 KSKCYR-QKEGGS 20
 Db 2 KCNECNRYOLKEGS 15

RESULT 5
 UN15_CLOPA STANDARD; PRT; 17 AA.
 AC P81354;

DT 15-JUL-1998 (Rel. 36, Last Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE UNKNOWN PROTEIN CP 15 FROM 2D-PAGE (FRAGMENT).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
CC Clostridium.
OX NCBI_TaxID=1501;
RN (1)
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed-9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -I- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 5.1, ITS MW IS: 38.9 KDA.
FT NON TER 17
SO SEQUENCE 17 AA; 2015 MW; 46F8D8DC14A1CB4A CRC64;

Query Match 20.6%; Score 22; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 OKVEG 19
Db 4 OKLEG 8

RESULT 6
NO40_LOTJA STANDARD; PRT; 12 AA.
AC 022426;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE EARLY NODULIN 40.
GN ENOD40.
OS Lotus japonicus.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
CC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Fabales; Fabaceae; Papilionoideae; Lotus.
OX NCBI_TaxID=34305;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=CV. GIFU;
RA Chian R.-J., Gresshoff P.M.;
RT "Isolation and Primary Characterization of genomic Enod40 gene from
Lotus japonicus cultivar 'Gifu.'";
RL (In) Plant Gene Register PGR97-142.
CC -I- FUNCTION: MODULATES THE ACTION OF AUXIN, AND MAY FUNCTION AS PLANT
GROWTH REGULATOR THAT ALTERS PHYTOHORMONE RESPONSES (BY
SIMILARITY).
CC -I- DEVELOPMENTAL STAGE: EXPRESSED IN THE EARLY STAGES OF THE NODULE
DEVELOPMENT.
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CC -----
DR EMBL; AF013594; AAB82785.1; -
KW Nodulation.
SO SEQUENCE 12 AA; 1480 MW; 3C61E8257CB326C3 CRC64;

Query Match 19.6%; Score 21; DB 1; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 12 CVROKVEGS 20
Db 4 CWRKSHGS 12

RESULT 7
NO40_SESRO STANDARD; PRT; 12 AA.
AC 024369;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE EARLY NODULIN 40.
GN ENOD40.
OS Sesbania rostrata.
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
CC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Fabales; Fabaceae; Papilionoideae; Sesbania.
OX NCBI_TaxID=3895;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Stem nodules;
RX MEDLINE=98281575; PubMed-9620265.
RA Corich V., Goormachtig S., Lievens S., van Montagu M., Holsters M.;
RT "Patterns of ENOD40 gene expression in stem-borne nodules of Sesbania
rostrata.";
RL Plant Mol. Biol. 37:67-76(1998).
CC -I- FUNCTION: MODULATES THE ACTION OF AUXIN, AND MAY FUNCTION AS PLANT
GROWTH REGULATOR THAT ALTERS PHYTOHORMONE RESPONSES (BY
SIMILARITY).
CC -I- DEVELOPMENTAL STAGE: EXPRESSED IN THE EARLY STAGES OF THE NODULE
DEVELOPMENT.
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CC -----
DR EMBL; Y12714; CAA73252.1; -
KW Nodulation.
SO SEQUENCE 12 AA; 1418 MW; 3C6955187CB326C3 CRC64;

Query Match 19.6%; Score 21; DB 1; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.2e+03;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 12 CVROKVEGS 20
Db 4 CWRKSHGS 12

RESULT 8
NO40_PEA STANDARD; PRT; 13 AA.
AC P55959;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE EARLY NODULIN 40.
GN ENOD40.
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
CC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Fabales; Fabaceae; Papilionoideae; Pisum.
OX NCBI_TaxID=3888;
RN (1)
RP SEQUENCE FROM N.A.

RC STRAIN-CV. SPARKLE; TISSUE-Root nodules;
 RX MEDLINE=95036021; PubMed=7948896;
 RA Matvienko M., Van de Sande K., Yang W.C., van Kammen A., Bisseling T.,
 RA Franssen H.J.;
 RT "Comparison of soybean and pea ENOD40 cDNA clones representing genes
 expressed during both early and late stages of nodule development.";
 RL Plant Mol. Biol. 26:487-493(1994).
 CC -1- FUNCTION: MODULATES THE ACTION OF AUXIN, AND MAY FUNCTION AS PLANT
 CC GROWTH REGULATOR THAT ALTERS PHYTOHORMONE RESPONSES (BY
 CC SIMILARITY).
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN THE EARLY STAGES OF THE NODULE
 CC DEVELOPMENT.
 CC -----
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 CC -----
 CC EMBL: X81064; -; NOT_ANNOTATED_CDS.
 CC Nucleotide
 CC DR Modulation.
 CC KW SEQUENCE 13 AA; 1565 MW; 3C695B66BD8A26C3 CRC64;
 SQ
 Query Match 19.6%; Score 21; DB 1; Length 13;
 Best Local Similarity 33.3%; Pred. No. 1.3e+03;
 Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 12 CVRQKVEGS 20
 1 : : : : :
 5 CWQKSTHGS 13
 Db
 RESULT 9
 NO40_VICSA STANDARD; PRT; 13 AA.
 ID NO40_VICSA
 AC P55961;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE EARLY NODULIN 40.
 GN ENOD40.
 OS Vicia sativa (Spring vetch) (Tare).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
 OC Fabales; Fabaceae; Papilionoideae; Vicia.
 OX NCBI_TaxID=3908;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. NIGRA; TISSUE-Root nodules;
 RX MEDLINE=96011756; PubMed=7548828;
 RA Vijn I., Yang W.-C., Pallsgaard N., Oostergaard Jensen E.,
 RA van Kammen A., Bisseling T.;
 RT "VENOD5, VENOD12 and VENOD40 expression during Rhizobium-induced
 RT nodule formation on Vicia sativa roots.";
 RL Plant Mol. Biol. 28:1111-1119(1995).
 CC -1- FUNCTION: MODULATES THE ACTION OF AUXIN, AND MAY FUNCTION AS PLANT
 CC GROWTH REGULATOR THAT ALTERS PHYTOHORMONE RESPONSES (BY
 CC SIMILARITY).
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING RHIZOBIUM-INDUCED NODULE
 CC FORMATION. IN 4-DAY OLD NODULES IT IS FOUND IN ALL THE CELLS OF
 CC THE CENTRE OF THE NODULE PRIMORDIUM AND ALSO OCCURS IN THE REGION
 CC OF THE ROOT PERICYCLE FACING THE NODULE CENTRAL TISSUE. AT DAY 5,
 CC EXPRESSION IS SEEN IN THE COMPLETE CENTRAL TISSUE. AT DAY 20
 CC EXPRESSED IN THE COMPLETE PREFIXATION ZONE II, AND IN THE PROXIMAL
 CC PART OF THIS ZONE IT IS FOUND ONLY IN THE INFECTED CELLS BUT NOT
 CC IN THE UNINFECTED CELLS. AT THE TRANSITION OF PREFIXATION ZONE II
 CC INTO INTERZONE II-III EXPRESSION DECREASES IN THE INFECTED CELLS.
 CC IN THE FIXATION ZONE III, EXPRESSION IS INDUCED IN THE UNINFECTED
 CC CELLS AND IN THE PROXIMAL PART OF THIS ZONE IT IS UNDETECTABLE.
 CC PRESENT AT HIGH LEVELS IN THE PERICYCLE OF THE NODULE VASCULAR

CC BUNDLE.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X83683; -; NOT_ANNOTATED_CDS.
 CC Nucleotide
 CC DR Modulation.
 CC KW SEQUENCE 13 AA; 1531 MW; 3C6953C4BD8A26C3 CRC64;
 SQ
 Query Match 19.6%; Score 21; DB 1; Length 13;
 Best Local Similarity 33.3%; Pred. No. 1.3e+03;
 Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 12 CVRQKVEGS 20
 1 : : : : :
 5 CWQKSTHGS 13
 Db
 RESULT 10
 SCK3_LEIOU STANDARD; PRT; 14 AA.
 ID SCK3_LEIOU
 AC P45661;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE LEIURTOXIN III (FRAGMENT).
 OS Leiurus quinquestriatus quinquestriatus (Egyptian scorpion).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Butioidae; Butiidae; Leiurus.
 OX NCBI_TaxID=6885;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Venom;
 RX MEDLINE=93075256; PubMed=1280139;
 RA Valdivia H.H., Martin B.M., Escobar L., Possani L.D.;
 RA "Noxiustoxin and leiurotoxin III, two homologous peptide toxins with
 RT binding properties to synaptic membrane K⁺ channels.";
 RL Biochem. Int. 27:953-962(1992).
 CC -1- FUNCTION: BLOCKER OF POTASSIUM CHANNELS.
 CC -1- SIMILARITY: BELONGS TO THE SHORT SCORPION TOXIN FAMILY. POTASSIUM
 CC CHANNEL INHIBITORS SUBFAMILY.
 CC InterPro: IPR001947;
 DR PROSITE: PS01138; SCOP: SHORT_TOXIN; PARTIAL.
 KW Neurotoxin; Potassium channel inhibitor.
 FT NON_TER 14
 SQ SEQUENCE 14 AA; 1588 MW; 83C67CCBD691205E CRC64;
 QY 1 VIDHOGTKSSKC 12
 1 : : : : :
 2 LIDVRCYDSSQC 13
 Db
 RESULT 11
 UN37_CLOPA STANDARD; PRT; 14 AA.
 ID UN37_CLOPA
 AC P81358;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE UNKNOWN PROTEIN CP 37 FROM 2D-PAGE (FRAGMENT).
 OS Clostridium pasteurianum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;

```

OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=M5;
RA MEDLINE=98291870; PubMed=9629918;
RA Flensburg R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5."
RL Electrophoresis 19:802-806(1998).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.8, ITS MW IS: 44.7 KDA.
FT NON TER
SO SEQUENCE 14 AA; 1579 MW; 05384662DEF89210 CRC64;

Query Match
Best Local Similarity 19.6%; Score 21; DB 1; Length 14;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IDHOGTK 8
   1 : 111
Db 7 IEDOGVK 13

RESULT 12
ALIT_OLEEU
ID ALIT_OLEEU STANDARD; PRT; 19 AA.
AC P81430;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE POLLEN ALLERGEN OLE E 7 (OLE E VII) (FRAGMENT).
OC Olea europaea (Common olive).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
OC Lamiales; Oleaceae; Olea.
OX NCBI_TaxID=4146;
RN [1]
RP SEQUENCE.
RC TISSUE=Pollen;
RA Tejera M.L., Villalba M., Rodriguez R.;
RT "Isolation and characterization of Ole e 7, a new allergen from olive
RT tree pollen."
RL Submitted (JUL-1998) to the SWISS-PROT data bank.
KW Allergen.
FT NON TER
SO SEQUENCE 19 AA; 1986 MW; 999A5008C41A67E CRC64;

Query Match
Best Local Similarity 19.6%; Score 21; DB 1; Length 19;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 OGFKSSK 11
   111 : 11
Db 4 OCTVTAK 10

RESULT 13
MISG_MISAN
ID MISG_MISAN STANDARD; PRT; 21 AA.
AC P81474;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE MISGURIN.
OS Misgurnus anguillicaudatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cobitidae; Misgurnus.
OX NCBI_TaxID=75329;
RN [1]

```

```

RP SEQUENCE.
RX MEDLINE=97415401; PubMed=9271200;
RA Park C.B., Lee H.J., Park I.Y., Kim M.S., Kim S.C.;
RT "A novel antimicrobial peptide from the loach, Misgurnus
RT anguillicaudatus."
RL FBS Lett. 411:173-178(1997).
CC -1- FUNCTION: STRONG ANTIMICROBIAL ACTIVITY AGAINST SEVERAL
CC GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA AND FUNGI.
CC -1- MASS SPECTROMETRY: MW=2502; METHOD=MALDI.
KW Antibiotic; Fungicide.
SO SEQUENCE 21 AA; 2502 MW; 4A6E9D0AB391BCF1 CRC64;

Query Match
Best Local Similarity 19.6%; Score 21; DB 1; Length 21;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 RORVE 18
   111 : 11
Db 1 RORVE 5

RESULT 14
OMPA_PASHA
ID OMP4_PASHA STANDARD; PRT; 21 AA.
AC P80228;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE MAJOR OUTER MEMBRANE PROTEIN P44 (OMP) (FRAGMENT).
OC Pasteurella haemolytica.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Mannheimia.
OX NCBI_TaxID=75985;
RN [1]
RP SEQUENCE.
RC STRAIN=BIOVAR A / SEROVAR 1 129;
RX MEDLINE=95102227; PubMed=7803929;
RA Luebke A., Hartmann L., Schroeder W., Hellmann E.;
RT "Isolation and partial characterization of the major protein of the
RT outer membrane of Pasteurella haemolytica and Pasteurella
RT multocida."
RL Int. J. Med. Microbiol. Virol. Parasitol. Infect. Dis. 281:45-54(1994).
CC -1- SUBUNIT: MONOMER (PROBABLE).
KW Outer membrane; Porin.
FT NON TER
SO SEQUENCE 21 AA; 2286 MW; E6EF82BEACT7BB63B CRC64;

Query Match
Best Local Similarity 19.6%; Score 21; DB 1; Length 21;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VIDHOGTK 8
   111 : 11
Db 3 VYDAEGSK 10

RESULT 15
OSMB_SALTY
ID OSMB_SALTY STANDARD; PRT; 20 AA.
AC P37723;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE OSMOTICALLY INDUCIBLE LIPOPROTEIN B (FRAGMENT).
OS OSMB.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.

```

RX MEDLINE=87190435; PubMed=2436909;
 RA Theisen M., Keilin R.A., Neuhard J.;
 RT "Cloning and characterization of the pyrF operon of Salmonella
 RT typhimurium.";
 RL Eur. J. Biochem. 164:613-619(1987).
 RN [2]
 RP IDENTIFICATION.
 RX MEDLINE=95004589; PubMed=7920643;
 RA Robison K., Gilbert W., Church G.M.;
 RT "Large scale bacterial gene discovery by similarity search.";
 RL Nat. Genet. 7:205-214(1994).
 CC -1- FUNCTION: PROVIDES RESISTANCE TO OSMOTIC STRESS. MAY BE IMPORTANT
 CC FOR STATIONARY-PHASE SURVIVAL.
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A LIPID
 CC ANCHOR (PROBABLE).
 CC -1- INDUCTION: BY ELEVATED OSMOTIC PRESSURE IN THE GROWTH MEDIUM.
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 CC -----
 CC EMBL: X05382; -; NOT_ANNOTATED_CDS.
 DR STyGene; SG10272; osmb.
 DR InterPro: IPR000437; -;
 DR PROSITE: PS00013; PROKAR_LIPOPROTEIN; PARTIAL.
 KW Membrane; Lipoprotein.
 FT NON_TER 1
 SQ SEQUENCE 20 AA; 1792 MW; FCCID85EC27ABC87 CRC64;

Query Match 18.7%; Score 20; DB 1; Length 20;
 Best Local Similarity 80.0%; Pred. No. 3e+03; 1; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 1;
 QY 1 VIDHO 5
 DB 13 VIGHQ 17

Search completed: July 19, 2001, 07:50:21
 Job time: 162 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 19, 2001, 07:46:49 ; Search time 12.72 Seconds

(without alignments)
125.760 Million cell updates/sec

Title: us-08-487-283a-1

Perfect score: 107

Sequence: 1 VIDHGTSSKSCYRQKVEGSS 21

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 4046

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	28.0	16	2	PH1589
2	25	23.4	15	2	PH1582
3	25	23.4	18	2	S45373
4	23	23.4	19	2	S02808
5	23	21.5	12	2	PH1675
6	23	21.5	13	2	PH1676
7	23	21.5	14	2	PH1677
8	23	21.5	15	2	I67525
9	23	21.5	16	2	D45193
10	23	21.5	17	2	B86323
11	23	21.5	18	2	PH1621
12	23	21.5	19	2	T50329
13	23	21.5	20	2	A44927
14	23	21.5	20	2	S19618
15	23	21.5	21	2	PH1688
16	22.5	21.0	20	1	LEBSTU
17	22.5	21.0	20	1	S23742
18	22	20.6	11	2	A33917
19	22	20.6	14	2	S11074
20	22	20.6	14	2	PH1311
21	22	20.6	15	2	PH0753
22	22	20.6	16	2	F57789
23	22	20.6	16	2	JQ2306
24	22	20.6	16	2	JQ2316
25	22	20.6	16	2	I51879
26	21	19.6	13	2	S60046
27	21	19.6	13	2	S52356
28	21	19.6	13	2	S23638
29	21	19.6	14	2	A48389

ALIGNMENTS

30	21	19.6	14	2	S23639	Ig kappa chain J s
31	21	19.6	15	2	PH1320	Ig heavy chain DJ
32	21	19.6	16	2	S28433	major outer membra
33	21	19.6	17	2	S48655	glutathione dehydr
34	21	19.6	17	2	I57941	beta 3-adrenergic
35	21	19.6	20	2	C44907	manganese peroxida
36	21	19.6	21	2	S03506	T-cell receptor al
37	20	18.7	9	4	I73804	hypothetical E2 pr
38	20	18.7	13	2	A26999	carboxylesterase (
39	20	18.7	14	2	C44823	synaptosomal-assoc
40	20	18.7	15	2	F29501	fibrinopeptide A -
41	20	18.7	15	2	PA0036	glycine cleavage s
42	20	18.7	16	2	A49226	major outer membra
43	20	18.7	16	2	B48406	annexin VI homolog
44	20	18.7	17	2	I49425	mitogen regulated
45	20	18.7	17	2	C37396	pollen allergen Fe

RESULT 1
PH1589
Ig H chain V-D-J region (wild-type clone 140) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C/Accession: PH1589
R/Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less m
A/Reference number: PH1580; MUID:93301609
A/Accession: PH1589
A/Molecule type: DNA
A/Residues: 1-16 <LEV>
A/Experimental source: bone marrow pre-B lymphocyte
C/Keywords: Immunoglobulin

Query Match 28.0%; Score 30; DB 2; Length 16;
Best Local Similarity 55.6%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 CVRQKVEGS 20
DB 1 CARQSYDGS 9
RESULT 2
PH1582
Ig H chain V-D-J region (wild-type clone 5) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
R/Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less m
A/Reference number: PH1580; MUID:93301609
A/Accession: PH1582
A/Molecule type: DNA
A/Residues: 1-15 <LEV>
A/Experimental source: bone marrow pre-B lymphocyte
C/Keywords: immunoglobulin

Query Match 23.4%; Score 25; DB 2; Length 15;
Best Local Similarity 44.4%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 12 CVRQKVEGS 20
DB 1 CARQSYDGS 9

RESULT 3
S45373
translation elongation factor EF-1a - common tobacco
C:Species: Nicotiana glauca (common tobacco)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jul-2000
C:Accession: S45373
R:Marty, I.; Brugidou, C.; Chartier, Y.; Meyer, Y.
Plant J. 4, 265-278, 1993
A:Title: Growth-related gene expression in Nicotiana tabacum mesophyll protoplasts
A:Reference number: S45372; MUID:94035181
A:Accession: S45373
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-18 <MAR>
A:Cross-references: EMBL:Z14080; NID:g443955; PIDN:CAA78458.1; PID:g443956

Query Match	23.4%	Score 25:	DB 2:	Length 18:
Best Local Similarity	35.7%	Pred. No.	1.3e+03:	
Matches	5;	Conservative	3;	Mismatches 6;
				Indels 0;
				Gaps 0;

```

QY      3 DHQGTSSKCVROK 16
          | | | : | :: |
Db      3 DPTGAKVTKAQKK 16

```

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RESULT      4
S02808
nucleolin - bovine (fragment)
C/Species: Bos primigenius taurus (cattle)
C/Date: 28-Feb-1990 #sequence_revision 28-Feb-1993
C/Accession: S02808
R/Sapp, M.; Richter, A.; Weissbart, K.; Calzergues-Ferrer, M.; Amarlic, F.; Wallace, M.C.
Eur. J. Biochem. 179, 541-548, 1989
A/Title: Characterization of a 46-kDa nucleic-acid-binding fragment of nucleolin.
A/Reference number: S02808; MUID:89153087
A/Accession: S02808
A:Molecule type: protein
A:Residues: 1-19 <SAP>

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Query Match	23.4%	Score 25;	DB 2;	Length 19;
Best Local Similarity	100.0%	Pred. No. 1.4e+03;		
Matches	5;	Conservative 0;	Mismatches 0;	Indels 0;
				Gaps 0;

QY	15	QKVEG	19
Db	15	QKVEG	19

RESULT 5
PH1675
Ig heavy chain V region (clone NP-6-7) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C:Accession: PH1675
R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A:Title: Antigen-driven B cell differentiation in vivo.
A:Reference number: PH1675; MUID:93301607
A:Accession: PH1675
A:Molecule type: mRNA
A:Residues: 1-12 <MCH>
C:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match	21.5%	Score 23;	DB 2;	Length 12;
Best Local Similarity	57.1%;	-Pred. No.	1.9e+03;	
Matches	4;	Conservative	3;	Mismatches 0; Gaps 0;

QY 5 QGTKSSK 11

```
Db      6 RGTKSTE 12
```

RESULT 6
PH1676
Ig heavy chain V region (clone NP-6-5) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999

R;McHeyzer Williams, M.G.; McLean, M.J.; Lator, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993

A;Title: Antigen-driven B cell differentiation in vivo.
A;Reference number: PH1675; MUID:93301607

A;Accession: PH1676
A;Molecule type: mRNA

A;Residues: 1-13 <MCH>
A;Experimental source: B cell
C:Superfamily: Immunoglobulin

C;superfamily: immunoglobulin V region; immunoglobulin homology
C;keywords: heterotetramer; immunoglobulin

Query Match	21.5%	Score 23;	DB 2;	Length 13;
Best Local Similarity	57.1%	Pred	No. 2b+03;	
Matches 4;	Conservative	3;	Mismatches	0;
			Indels	0;
			Gaps	0;

QY	5	QGTSKSSK	11
		: :	
Db	6	RGTSKSTE	12

RESULT 7
PH1677
Ig heavy chain V region (clone NP-6-6) - mouse (fragment)
This was a mouse (clone NP-6-6) Ig heavy chain V region (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C:Accession: m1677

C/Accession: PH16//
R/McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
Eryd Mod 178 205-207 1002

U. Exp. Med. 176, 295-307, 1993

A: Molecule type: mRNA

A:Experimental source: B cell

C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin

Query Match	21.5%	Score 23	DB 2	Length 14
Best Local Similarity	57.1%	Pred. No. 2.2e+03		
Matches 4	Conservative	3	Mismatches 0	Indels 0
			Gaps	0

QY	5	QGTSKSK	11
		:1111::	
Db	6	RGTKSTE	12

RESULT	8
I67525	
CD33 antigen homolog - mouse (fragment)	

C:Species: Mus sp. (mouse)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Jun-1998

C/Accession: I67525
R/Chies, J.A.; Lembezat, M.P.; Freitas, A.A.
Eur. J. Immunol. 34: 1657-1664 2004

A: Title: Entry of B lymphocytes into the persistent cell pool in non-immunized mice
 Eur. J. Immunol. 24, 1657-1664, 1994
 Reference number: 153303, PMID: 9408870

A; Accession: 167525

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA

A;Residues: 1-15 <RES>
A;Cross-references: GB:S71349; NID:g550037

C:Genetics:
A:Gene: Ig VH7183

Query Match 21.5%; Score 23; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 12 CVRQKVGSS 21
| | | | |
Db 2 CARRDHGSS 11

RESULT 9
D45193
zinc finger protein ZNF60 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 01-Jan-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: D45193
R:Lichter, P.; Bray, P.; Ried, T.; David, I.B.; Ward, D.C.
Genomics 13, 999-1007, 1992
A:Title: Clustering of C2-H2 zinc finger motif sequences within telomeric and fragile site
A:Reference number: A43284; MUID:92372070
A:Accession: D45193
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-16 <LIG>
A:Cross-references: GB:M8369; NID:9340475; PIDN:AAA61327.1; PID:9340476
A:Note: sequence extracted from NCBI backbone (NCBIN:111662, NCBI:P:111664)

Query Match 21.5%; Score 23; DB 2; Length 16;
Best Local Similarity 44.4%; Pred. No. 2.5e+03;
Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 4 HOGTKSSKC 12
| | | | |
Db 2 HTGKPFSC 10

RESULT 10
B86323
protein F14D16.5 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: B86323
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizart, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, G.; Yraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: B86323
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-17 <STO>
A:Cross-references: GB:AE05172; NID:98778270; PIDN:AAF79279.1; GSPDB:GN00141
C:Genetics:
A:Gene: F14D16.5
A:Map position: 1

Query Match 21.5%; Score 23; DB 2; Length 17;
Best Local Similarity 44.4%; Pred. No. 2.6e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 4 HOGTKSSKC 12
| | | | |

Db 8 HHLSPSSRC 16

RESULT 11
PH1621
Ig H chain V-D-J region (clone B-less 41) - mouse (fragment)

C:Species: Mus musculus (house mouse)
C>Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1621
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993

A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less m
A:Reference number: PH1580; MUID:93301609
A:Accession: PH1621
A:Molecule type: DNA
A:Residues: 1-18 <LEV>
A:Experimental source: bone marrow pre-B lymphocyte
C:Keywords: immunoglobulin

Query Match 21.5%; Score 23; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 CVRQ 15
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Db 1 CVRQ 4

RESULT 12
T50329
wd-repeat protein popl. [imported] - fission yeast (Schizosaccharomyces pombe) (fragm
C:Species: Schizosaccharomyces pombe
C>Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
C:Accession: T50329
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Harris, D.
submitted to the EMBL Data Library, February 2000
A:Reference number: Z25062
A:Accession: T50329
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-19 <LYN>
A:Cross-references: EMBL:AL157874; PIDN:CA875991.1; GSPDB:GN00067; SPDB:SPBC1718.01
A:Experimental source: strain 972h(-); cosmid c1718
C:Genetics:
A:Gene: SPBC262.18; SPDB:SPBC1718.01
A:Map position: 2

Query Match 21.5%; Score 23; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 2.9e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 VIDHGTSS 10
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Db 10 VLEFGSTKSS 19

RESULT 13
A44927
major outer membrane protein 28k chain - Legionella pneumophila (fragment)
N:Alternate names: major outer membrane protein 31k chain
C:Species: Legionella pneumophila
C>Date: 01-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Mar-1996
C:Accession: A44927; B44927
R:Hoffman, P.S.; Seyer, J.H.; Butler, C.A.
J. Bacteriol. 174, 908-913, 1992
A:Title: Molecular characterization of the 28- and 31-kilodalton subunits of the LegI
A:Reference number: A44927; MUID:92121130
A:Accession: A44927
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <HOF>

A:Experimental source: SVIR Philadelphia 1, serogroup 1
 A:Note: sequence extracted from NCBI backbone (NCBIP:77834)
 A:Accession: B44927
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 4-17 <HO2>
 A:Experimental source: SVIR Philadelphia 1, serogroup 1
 A:Note: sequence extracted from NCBI backbone (NCBIP:77837)

Query Match 21.5%; Score 23; DB 2; Length 20;

Best Local Similarity 50.0%; Pred. No. 3e+03; Mismatches 1; Indels 0; Gaps 0;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 IDHOGT 7

Db 14 VPHGT 19

RESULT 14

SI9618 globin - polychaete (Eudistylia vancouveri) (fragment)

N:Alternate names: chlorocortin

C:Species: Eudistylia vancouveri

C>Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 05-Dec-1998

C:Accession: SI9618

R:Qabar, A.N.; Stern, M.S.; Walz, D.A.; Chiu, J.T.; Timkovich, R.; Wall, J.S.; Kapp, O.H.

J. Mol. Biol. 222, 1109-1129, 1991

A:Title: Hierarchy of globin complexes. The quaternary structure of the extracellular ch

A:Reference number: SI9532; MUID:92106333

A:Accession: SI9618

A:Molecule type: protein

A:Residues: 1-20 <QAB>

A:Experimental source: plume

C:Keywords: calcium; dodecamer; each consisting of a trimer of tetramers of globin chains; dodeca

Query Match 21.5%; Score 23; DB 2; Length 20;

Best Local Similarity 50.0%; Pred. No. 3e+03; Mismatches 5; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 2 IDHOGTSSK 11

Db 10 IDANGKKDK 19

RESULT 15

PH1688 Ig heavy chain V region (clone NP-7-1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999

C:Accession: PH1688

R:McHeyzer-Williams, M.G.; McLean, M.J.; Lajor, P.A.; Nossal, G.J.V.

J. Exp. Med. 178, 295-307, 1993

A:Title: Antigen-driven B cell differentiation in vivo.

A:Reference number: PH1675; MUID:93301607

A:Accession: PH1688

A:Molecule type: mRNA

A:Residues: 1-21 <MCH>

A:Experimental source: B cell

Search completed: July 19, 2001, 07:47:53

Job time: 64 sec

Query Match 21.5%; Score 23; DB 2; Length 21;

Best Local Similarity 57.1%; Pred. No. 3.2e+03; Mismatches 3; Conservative 0; Indels 0; Gaps 0;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 5 QGTSSK 11

Db 6 RGTSSK 12

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34 eTrrpHeGlnGlnLysProGlyLysAlaProLysThrLeuIleTyrArg 50
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207 CGGAACGATTTCTACTCTGACATCAGACATGTCAGACCTGAGACTTCG 256
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67 rGlyThrAspTyrThrIleThrIleSerSerLeuGlnTyrGlnAspPheG 84
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507 GGGCCCTGAGATGATGGTGGATCTTACCGGGCTCGTGGAGACCGCAAT 556
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557 ATACCGAAATTTTAAAGACCGCTGTTACTATGACGCGCTGACACTTCGACT 606
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seq_name: /cgn2_6/plodata/2/iaa/5A_COMB.pep:US-08-477-484B-147

seq_documentation_block:

; Sequence 147, Application US/08477484B

; Patent No. 5756599

; GENERAL INFORMATION:

; APPLICANT: Better, Marc D.

; APPLICANT: Carroll, Stephen F.

; APPLICANT: Studnika, Gary M.

; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

```

? TITLE OF INVENTION: Proteins
? NUMBER OF SEQUENCES: 169
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Mcandrews, Held & Malloy, Ltd.
? STREET: 500 West Madison Street, 34th floor
? CITY: Chicago
? STATE: Illinois
? COUNTRY: USA
? ZIP: 60661
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/477,484B
? FILING DATE: 07-JUN-1995
? CLASSIFICATION: 530
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/425,336
? FILING DATE: 18-APR-1995
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/064,691
? FILING DATE: 12-MAY-1993
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/988,430
? FILING DATE: 09-DEC-1992
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/901,707
? FILING DATE: 19-JUN-1992
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/787,567
? FILING DATE: 04-NOV-1991
? ATTORNEY/AGENT INFORMATION:
? NAME: McNicholas, Janet M.
? REGISTRATION NUMBER: 32,918
? REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312/707-8889
? TELEFAX: 312/707-9155
? TELEX: 650 388-1248
? INFORMATION FOR SEQ ID NO: 147:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 240 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-477-484B-147

alignment_scores:
  Quality: 858.00 Length: 246
  Ratio: 4.105 Gaps: 2
  Percent Similarity: 84.959 Percent Identity: 66.667

alignment_block:
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Align seg 1/1 to: US-08-477-484B-147 from: 1 to: 240

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57 TAGGTCACCATCACCCTGGCGCCGAGGAAACATCTATGCGCGCTGA 106
|||||
17 pArgValThrIleThrCysArgAlaSerGlnAspIleAsnSerTyrLeuS 34
ACTGATATCAAGCTAAACCTGGGAAAGCTCCGAAAGCTTCTGATTTACGCT 156
:::
34 eTrrpHeGlnGlnLysProGlyLysAlaProLysThrLeuIleTyrArg 50
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215 lYrPheCysThrArgArgGlyTyr.....AspTyrPhe 228
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seq_documentation_block:
Sequence 147, Application US/08839765
Patent No. 6146631
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studlika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567

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FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-9155
TELEFAX: 312/707-8889
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 147:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-839-765-147

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alignment_scores:
Quality: 858.00 Length: 246
Ratio: 4.105 Gaps: 2
Percent Similarity: 84.959 Percent Identity: 66.667

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alignment_block:

US-08-487-283A-8 x US-08-839-765-147 ..

Align seg 1/1 to: US-08-839-765-147 from: 1 to: 240

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67 rGlyThrAspTyrThrLeuThrIleSerSerLeuGlnIlyrGlnAspPheG 84
257 CTACGTATTAATGTCAGACGTTTAAATACCTCGTTACTTTCGACAG 306
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Sequence 147, Application US/09136389
Patent No. 6146850
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESSES:
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STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70..P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 147:
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LENGTH: 240 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-136-389-147
Alignment_scores:
Quality: 858.00 Length: 246
Ratio: 4.105 Gaps: 2
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Alignment_block:
US-08-487-283A-8 x US-09-136-389-147 ..
Align seg 1/1 to: US-09-136-389-147 from: 1 to: 240
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seq_documentation_block:
; Sequence 41, Application US/08400115
; Patent No. 5864019
; GENERAL INFORMATION:
; APPLICANT: KING, David John
; APPLICANT: MOUNTAIN, Andrew
; APPLICANT: OWENS, Raymond John
; APPLICANT: YARRANTON, Geoffrey Thomas
; TITLE OF INVENTION: Multivalent Antigen-Binding Proteins
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/400,115
; FILING DATE: 06-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,136
; FILING DATE: 27-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/842,193
; FILING DATE: 17-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/00935
; FILING DATE: 11-JUN-1991
; APPLICATION NUMBER: GB 9012995.8
; FILING DATE: 11-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: ISACSON, John P.
; REGISTRATION NUMBER: 33,715
; REFERENCE/DOCKET NUMBER: 040283/0106 CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-400-115-4

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Quality: 857.50 Length: 247
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seq_documentation_block:
; Sequence 41, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Bogue, Luis
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:

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154 IagIleValIlyProGlyAlaSerValIlySerCysIlyAlaSer 170
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: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/875,811
: FILING DATE: 19-FEB-1998
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO PCT/US97/02588
: FILING DATE: 19-FEB-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/011,800
: FILING DATE: 21-FEB-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Faris, Susan K.
: REGISTRATION NUMBER: 41,739
: REFERENCE/DOCKET NUMBER: 015280-244100US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 576-0200
: TELEFAX: (415) 576-0300
: INFORMATION FOR SEQ ID NO: 41:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 355 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-875-811-41

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alignment_scores:
: Quality: 795.50      Length: 246
: Ratio: 3.938         Gaps: 2
: Percent Similarity: 82.114      Percent Identity: 62.195

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357 TGGATCTGGGTGGCGGTTCTCAAGTCAACGTAACGTAACGTAACGTAACG 406
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seq_documentation_block:

: Sequence 49, Application US/08875811

: Patent No. 6045793

: GENERAL INFORMATION:

: APPLICANT: Rybak, Susanna M.

: APPLICANT: Boque, Luis

: APPLICANT: Wlodawer, Alexander

: TITLE OF INVENTION: Recombinant Ribonuclease Proteins

: NUMBER OF SEQUENCES: 64

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Townsend and Townsend and Crew LLP

: STREET: Two Embarcadero Center, Eighth Floor

: CITY: San Francisco

: STATE: California

: COUNTRY: USA

: ZIP: 94111-3834

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS.

: SOFTWARE: Patentin Release #1.0, Version #1.30

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/08/875,811

: FILING DATE: 19-FEB-1998

: CLASSIFICATION: 435

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: WO PCT/US97/02588

: FILING DATE: 19-FEB-1997

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: US 60/011,800

: FILING DATE: 21-FEB-1996

: ATTORNEY/AGENT INFORMATION:

: NAME: Faris, Susan K.

: REGISTRATION NUMBER: 41,739

: REFERENCE/DOCKET NUMBER: 015280-244100US

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: (415) 576-0200

: TELEFAX: (415) 576-0300

: INFORMATION FOR SEQ ID NO: 49:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 355 amino acids

: TYPE: amino acid

: TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-875-811-49

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Quality: 795.50 Length: 246
Ratio: 3.938 Gaps: 2
Percent Similarity: 82.114 Percent Identity: 62.195

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; Sequence 64, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Bogue, Luis
; APPLICANT: Kiodaver, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Fatis, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
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Ratio: 3.938 Gaps: 2
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: Patent No. 6045793
: GENERAL INFORMATION:
: APPLICANT: Rybak, Susanna M.
: APPLICANT: Newton, Dianne L.
: APPLICANT: Boque, Luis
: APPLICANT: Wlodawer, Alexander
: TITLE OF INVENTION: Recombinant Ribonuclease Proteins
: NUMBER OF SEQUENCES: 64
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/875,811
: FILING DATE: 19-FEB-1998
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO PCT/US97/02388
: FILING DATE: 19-FEB-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/011,800
: FILING DATE: 21-FEB-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Faris, Susan K.
: REGISTRATION NUMBER: 41,739
: REFERENCE/DOCKET NUMBER: 015280-244100US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 576-0200
: TELEFAX: (415) 576-0300
: INFORMATION FOR SEQ ID NO: 47:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 360 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-875-811-47

alignment_scores:
: Quality: 795.50 Length: 246
: Ratio: 3.938 Gaps: 2
: Percent Similarity: 82.114 Percent Identity: 62.195

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seq_documentation_block:
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: Patent No. 6045793
: GENERAL INFORMATION:
: APPLICANT: Rybak, Susanna M.
: APPLICANT: Newton, Dianne L.
: APPLICANT: Boque, Luis
: APPLICANT: Wlodawer, Alexander
: TITLE OF INVENTION: Recombinant Ribonuclease Proteins
: NUMBER OF SEQUENCES: 64
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/875, 811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011, 800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-43

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Ratio: 3.938         Gaps: 2
Percent Similarity: 82.114   Percent Identity: 62.193

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seq_documentation_block:
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; Patent No. 5637481
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Gilliland, Lisa K.
; APPLICANT: Hayden, Martha S.
; APPLICANT: Linsley, Peter S.
; APPLICANT: Bajorath, Jurgen
; TITLE OF INVENTION: Expression Vectors Encoding Bispecific
; TITLE OF INVENTION: Fusion Proteins and Methods of Producing Biologically
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,054C
; FILING DATE: 13-SEP-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/013,420
; FILING DATE: 01-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436.18US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 302 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-121-054c-18

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2001, 02:33:26 ; Search time 2123.9 Seconds
(without alignments)
5462.033 Million cell updates/sec

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Perfect score: 750
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Scoring table: IDENTITY_MDC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 segs, 7733874588 residues
Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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C 12	467.4	62.3	3282	10	158609	158609 Sequence 16
C 13	467.4	62.3	13254	9	AR038307	AR038307 Sequence
C 14	467.4	62.3	13254	9	AR038321	AR038321 Sequence
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AUTHORS	Knick,V.C., Stimmel,J.B. and Thurmond,L.M.		
TITLE	Combination of an anti-ep-cam antibody with a chemotherapeutic agent		
JOURNAL	Patent: WO 0107082-A 4 01-FEB-2001;		
FEATURES	GLAXO GROUP LIMITED (GB)		
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[illegible]

KEYWORDS	complementarity-determining region; Constant region; immunoglobulin gamma chain; Immunoglobulin heavy chain; variable region.
SOURCE	Homo sapiens CDNA to mRNA.
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE AUTHORS	1 (bases 1 to 1599) Lewis,A.P., Lemon,S.M., Barber,K.A., Murphy,P., Parry,N.R., Peakman,T.C., Sims,M.J., Worden,J. and Crowe,J.S. Rescue, expression, and analysis of a neutralizing human anti-hepatitis A virus monoclonal antibody J. Immunol. 151 (5), 2829-2838 (1993)
JOURNAL MEDLINE FEATURES	93367243
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3'UTR	1463..1599 /note="putative"
polyA_signal	1566..1571 /note="putative"
BASE COUNT	357 a 526 c 441 g 275 t
ORIGIN	
Query Match	63.8%; Score 478.2; DB 97; Length 1599;
Best Local Similarity	78.0%; Pred. No.3.5e-103;
Matches 595; Conservative	0; Mismatches 153; Indels 15; Gaps 1;
OY	1 ATGAAGTGAGCGAGGTATTCTCTCCCTGTCAGTAACTGCGGGCTCCACTGCCAA 60 DB 35 AGACTGTGACCTGAGGTCTCTTTGTGGGGCAGCAGCATACAGGTGTCTCAAGTCCAG 94
OY	61 GTCCAACTGCTGCATTCGGGGCCGAGGTCAAGAAGCAAGGGGGCTTCAGTCAAAGTGTCC 120

Db		95	ATGCAAGTGGTCACACTCTGGGGCTGAAGTAAGAAGCCTGGGTCTCGTGACGGTCTCC	154
Oy	121	TGTAAAGTAGAGCGGCTATATTTTTCTAATTAATGATTCATGGGTGCCTGACGCCCCC	180	
Db	155	TCCAAGGCATCTGGAGGCCACTTCAGCAACATGCTATCAGCTGGGTGGAGACGGCCCCCT	214	
Oy	181	GGGCAGAGGCGCTGGAAATGGATGGGTGAGATCTTACC GGCGCTGGTAGACACCGAATATAC	240	
Db	215	GGACAAGGCGCTTGAATGGATGGAGGAGATCATCCCTCTTTTGGTAGCACCAACCTACTCA	274	
Oy	241	GAATAATTTTAAAGACCGGTCTTACTATGACCGCTGACACTTGACACTAATGATATACATG	300	
Db	275	CGAACCTTCACAGGAGAGATCAGATTACCGCGCAATTCACACGACAGACGCCACATG	334	
Oy	301	GAGCTCTCCAGCGCTCGATCGGAGACACAGGCGCGCTAATTAATGGCGCGTTAT-----	354	
Db	335	GAGCTGATCAGCGCTTGAATCTGAGATCTGAGACACAGCGCGCTGATTACTGTGCGACAGATCGTAC	394	
Oy	355	-----TTTTTGGTTCTAGCCCCGAATGGTATTTTGAATGTTTGGGGGTCAAGGAAC	405	
Db	395	AGCGAGGCAATTTTGTGACCGGGCGCGGGTTGGCTGTTCGACCCCTGGGGCCAGGGCAC	454	
Oy	406	CTGGTCACTGTCTCGAGGGCCCTCACCACAAAGGCCCATGGGTCTTCCCTGGCGCCCTCC	465	
Db	455	CTGGTCACTGTCTCGAGGGCCCTCACCACAAAGGCCCATGGGTCTTCCCTGGCGCCCTCC	514	
Oy	466	TCCAAGAGACCTCTGGGGGACACAGCGCGCTGGGCTGCTGTCGAAGACTACTTCC	525	
Db	515	TCCAAGAGACCTCTGGGGGACACAGCGCGCTGGGCTGCTGTCGAAGACTACTTCC	574	
Oy	526	GAACCGGTGACGGTGTCTGGAACACAGGCGCCCTGACCCAGCGCGTGCACACTTCCG	585	
Db	575	GAACCGGTGACGGTGTCTGGAACACAGGCGCCCTGACCCAGCGCGTGCACACTTCCG	634	
Oy	586	GCTGTCTTCACTCTCTCAGAGACTCTACCTCCCTCAGACAGTGTGTAACGTGCCCTCCACG	645	
Db	635	GCTGTCTTCACTCTCTCAGAGACTCTACCTCCCTCAGACAGTGTGTAACGTGCCCTCCACG	694	
Oy	646	ACCTTGGGACCCAGACCTACATCTGCAAACGTGATACAAAGCCAGCACACAAAGGTG	705	
Db	695	ACCTTGGGACCCAGACCTACATCTGCAAACGTGATACAAAGCCAGCACACAAAGGTG	754	
Oy	706	GACAAAGAAAGTTGAGCCCAATCTTGTGACAAACCTCACACAT	748	
Db	755	GACAAAGAAAGTTGAGCCCAATCTTGTGACAAACCTCACACAT	797	
RESULT	3			
AR000007	AR000007	9209 bp	DNA	PAT
LOCUS	Sequence	3 from patent US 5736137.		04-DEC-1998
DEFINITION	AR000007			
ACCESSION	AR000007			
VERSION	AR000007.1	GI:3962538		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1 (bases 1 to 9209)			
AUTHORS	Anderson,D.R., Hanna,N., Leonard,J.E., Newman,R.A., Reff,M.E. and Rasletter,W.H.			
TITLE	Therapeutic application of chimeric and radiolabeled antibodies to human B lymphocyte restricted differentiation antigen for treatment of B cell lymphoma			
JOURNAL	Patent: US 5736137-A 3 07-APR-1998;			
FEATURES	Location/Qualifiers			
source	1..9209			
BASE COUNT	2239 a 2397 c 2390 g 2183 t			
ORIGIN	/organism="unknown"			
Query Match	63.5%; Score476; DB 9; Length 9209;			

Best Local Similarity 78.2%; Pred. No. 9.1e-103;
Matches 585; Conservative 0; Mismatches 160; Indels 3; Gaps 1;

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QY 1 ATGAAGTGGAGCTGGTATTCCTTCCTCCGTCAGTAACGCGGGCTCCACATCCCA 60
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Db 2401 ATGGGTGGAGCTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2460
QY 61 GTCCACTGTGTCAATCCGCGCGAGGTCAAGAACGCCAGGCTCCAGTCAAGTGTCC 120
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2461 GTACAACTGCAGACGCGCGGGGTGAGCTGGAGCCTGGGGCCTCACTGTAAGATGTC 2520
QY 121 TGTAAAGCTAGCGGCTATATTTTCTAATTAATGGAATCAATGGGCGGTACAGCCCCC 180
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2521 TGCAGAGCTTCCTGCTACACATTAACAGTATACATGACATGAGGTAAACAGACACT 2580
QY 181 GGGGAGGGCCCTGGAATGATGAGATCTTACCGGGCTCTGAGTACCAACCAATATACC 240
    ||| ||||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2581 GGTGCGGGCTGGAATGATGAGATCTTATTAATCCGGAATGATGATCTTCTACAT 2640
QY 241 GAAATTTTAAAGACCGCTGTACTATGACGGGTGACACTGTGACTAGTATACATG 300
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2641 CAGAACTTCAAGGCAAGGCCACATTTGACTGACAGCAATCTCCAGACACACTATAG 2700
QY 301 GAGCTCTCAGCTTGCATCGAGACAGCGGCTCTATTAATGGCGGCTATTTT 360
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2701 CAGCTCAGACGCTGACATCTGAGGACTCTGCGGTCTATTAATGAGTCAAGATCGACT 2758
QY 361 GGTCTAGCCCGAATTTGATTTGATTTGGGTCAAGAACCTGTCTGCTCTG 420
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2759 -ACTAGCGCGGTGACTGTACTTCAATCTGCGGGCGAGGACACAGGCTCCCTCT 2817
QY 421 AGCGCTCCACCAAGGGCCCATCGGCTTCCCTCGCGGCTCCCTCCAGACACTCT 480
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2818 GCAGCTAGCACCAAGGGCCCATCGGCTTCCCTCGCGGCTCCCTCCAGACACTCT 2877
QY 481 GGGGGCACAGCGGCTGCGGTGCTGCTCAAGACTCTCCCGAACCAGGTGACGGTG 540
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2878 GGGGGCACAGCGGCTGCGGTGCTGCTCAAGACTCTCCCGAACCAGGTGACGGTG 2937
QY 541 TCGTGAACCTAGGCGGCTGACAGCGGGCGTGCACACTTCCGGCTGCTTACAGTTC 600
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2938 TCGTGAACCTAGGCGGCTGACAGCGGGCGTGCACACTTCCGGCTGCTTACAGTTC 2997
QY 601 TCAGACTCTACTCCTCAGCAGCGGTGTAACCTGCTCCAGCAGGTTGGGCAACCCAG 660
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Db 2998 TCAGACTCTACTCCTCAGCAGCGGTGTAACCTGCTCCAGCAGGTTGGGCAACCCAG 3057
QY 661 ACCTACATCTGCAACGTGAATCACAAGCCCAAGCAACCAAGGTGACAAAGTTGAG 720
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3058 ACCTACATCTGCAACGTGAATCACAAGCCCAAGCAACCAAGGTGACAAAGTTGAG 3117
QY 721 CCCAAATCTTGTGACAAACTCACACAT 748
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Db 3118 CCCAAATCTTGTGACAAACTCACACAT 3145
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RESULT 4
LOCUS AR015961 9209 bp DNA PAT 05-DEC-1998
DEFINITION Sequence 2 from patent US 5776456.
ACCESSION AR015961
VERSION AR015961.1 GI:3972238
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 9209)
AUTHORS Anderson,D.R., Hanna,N., Leonard,J.E., Newman,R.A., Reff,M.E. and
TITLE Therapeutic application of chimeric and radiolabeled antibodies to
human B lymphocyte restricted differentiation for treatment
of B cell lymphoma
JOURNAL Patent: US 5776456-A 2 07-JUL-1998;

FEATURES
source Location/Qualifiers
BASE COUNT 2238 a 2395 c 2394 g 2182 t
ORIGIN

Query Match 63.5%; Score 476; DB 9; Length 9209;
Best Local Similarity 78.2%; Pred. No. 9.1e-103;
Matches 585; Conservative 0; Mismatches 160; Indels 3; Gaps 1;

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QY 1 ATGAAGTGGAGCTGGTATTCCTTCCTCCGTCAGTAACGCGGGCTCCACATCCCA 60
    ||| ||||| ||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2401 ATGGGTGGAGCTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2460
QY 61 GTCCACTGTGTCAATCCGCGCGAGGTCAAGAACGCCAGGCTCCAGTCAAGTGTCC 120
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2461 GTACAACTGCAGACGCGCGGGGTGAGCTGGAGCCTGGGGCCTCACTGTAAGATGTC 2520
QY 121 TGTAAAGCTAGCGGCTATATTTTCTAATTAATGGAATCAATGGGCGGTACAGCCCCC 180
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2521 TGCAGAGCTTCCTGCTACACATTAACAGTATACATGACATGAGGTAAACAGACACT 2580
QY 181 GGGCAGGGCCCTGGAATGATGAGATCTTACCGGGCTCTGAGTACCAACCAATATACC 240
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2581 GGTGCGGGCTGGAATGATGAGATCTTATTAATCCGGAATGATGATCTTCTACAT 2640
QY 241 GAAATTTTAAAGACCGCTGTACTATGACGGGTGACACTGTGACTAGTATACATG 300
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2641 CAGAACTTCAAGGCAAGGCCACATTTGACTGACAGCAATCTCCAGACACACTATAG 2700
QY 301 GAGCTCTCAGCTTGCATCGAGACAGCGGCTCTATTAATGGCGGCTATTTT 360
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Db 2701 CAGCTCAGACGCTGACATCTGAGGACTCTGCGGTCTATTAATGAGTCAAGATCGACT 2758
QY 361 GGTCTAGCCCGAATTTGATTTGATTTGGGTCAAGAACCTGTCTGCTCTG 420
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Db 2759 -ACTAGCGCGGTGACTGTACTTCAATGCTGCGGGCGAGGACACAGGCTCCCTCT 2817
QY 421 AGCGCTCCACCAAGGGCCCATCGGCTTCCCTCGCGGCTCCCTCCAGACACTCT 480
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2818 GCAGCTAGCACCAAGGGCCCATCGGCTTCCCTCGCGGCTCCCTCCAGACACTCT 2877
QY 481 GGGGGCACAGCGGCTGCGGTGCTGCTCAAGACTCTCCCGAACCAGGTGACGGTG 540
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2878 GGGGGCACAGCGGCTGCGGTGCTGCTCAAGACTCTCCCGAACCAGGTGACGGTG 2937
QY 541 TCGTGAACCTAGGCGGCTGACAGCGGGCGTGCACACTTCCGGCTGCTTACAGTTC 600
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2938 TCGTGAACCTAGGCGGCTGACAGCGGGCGTGCACACTTCCGGCTGCTTACAGTTC 2997
QY 601 TCAGACTCTACTCCTCAGCAGCGGTGTAACCTGCTCCAGCAGGTTGGGCAACCCAG 660
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2998 TCAGACTCTACTCCTCAGCAGCGGTGTAACCTGCTCCAGCAGGTTGGGCAACCCAG 3057
QY 661 ACCTACATCTGCAACGTGAATCACAAGCCCAAGCAACCAAGGTGACAAAGTTGAG 720
    ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3058 ACCTACATCTGCAACGTGAATCACAAGCCCAAGCAACCAAGGTGACAAAGTTGAG 3117
QY 721 CCCAAATCTTGTGACAAACTCACACAT 748
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Db 3118 CCCAAATCTTGTGACAAACTCACACAT 3145
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RESULT 5
LOCUS AR060920 9209 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5843439.
ACCESSION AR060920
VERSION AR060920.1 GI:5988611
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.


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OY 481 GGGGGCAGCGCGCCCTGGCTGCTGCTCAAGACTACTTCCCGAACCAGCGTGAGCGTG 540
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Db 9910 GGGGGCAGCGCGCCCTGGCTGCTGCTGCTCAAGACTACTTCCCGAACCAGCGTGAGCGTG 9969
OY 541 TCGTGAAGTCAAGCGCGCCCTGACAGCGCGCTGACACACTTCCCGCTGCTCCACAGTCC 600
    |||||||
Db 9970 TCGTGAAGTCAAGCGCGCCCTGACAGCGCGCTGACACACTTCCCGCTGCTCCACAGTCC 10029
OY 601 TCAGACTCTACTCTCCCTGACAGCGCGCTGACCGCTGCTCCACAGCTTGGGACCCAG 660
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Db 10030 TCAGACTCTACTCTCCCTGACAGCGCGCTGACCGCTGCTCCACAGCTTGGGACCCAG 10089
OY 661 ACCTCATCTGCAAGTGAATACAAAGCCGACACACCAAGGTGACAGAAAGTTGAG 720
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Db 10090 ACCTCATCTGCAAGTGAATACAAAGCCGACACCAAGGTGACAGAAAGTTGAG 10149
OY 721 CCCAATCTTGTGACAAACTCACACAT 748
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Db 10150 CCCAATCTTGTGACAAACTCACACAT 10177

RESULT 9
LOCUS AR038306 3282 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 154 from patent US 5804440.
ACCESSION AR038306
VERSION AR038306.1 GI:5957023
KEYWORDS
SOURCE .
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3282)
AUTHORS Burton,D.R., Barbats,C.F. and Lerner,R.A.
TITLE Human neutralizing monoclonal antibodies to human immunodeficiency
virus
JOURNAL Patent: US 5804440-A 154 08-SEP-1998;
FEATURES
source Location/Qualifiers
BASE COUNT 710 a 1109 c 864 g 599 t
ORIGIN

Query Match 62.3%; Score 467.4; DB 9; Length 3282;
Best Local Similarity 78.7%; Pred. No. 1.2e-100;
Matches 577; Conservative 0; Mismatches 141; Indels 15; Gaps 1;

OY 1 ATGAAGTGGAGCTGGGTATTTCTTCTCTCTGTCAGTACTGCGCGCTCCACCTCCAA 60
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Db 15 ATGGAATGGAGCTGGGTATTTCTTCTCTCTCTGTCAGTACTGCGCGCTCCACCTCCAG 74
OY 61 GTCCAACTGGTCATTCGGCGCGCGCGGTCAAGAGCCAGGGGCTCCAGTCAAGTGTCC 120
    |||||||
Db 75 GTTCAGCTGGTTCATTCGGCGCGCGGTCAAGAGCCAGGGGCTCCAGTCAAGTGTTC 134
OY 121 TGTAAAGCTAGCGGCTATATTTTCTTATTAATTAATGATTCATAGGCTGCGTCCAGCC 180
    |||||||
Db 135 TGTGAGGCTTCTGATACAGATTCAGTACTTGTATTCATTTGGGTGCGCCAGCGCC 194
OY 181 GGGCAGGCGCTGGAATGATGGGTGAGATCTTACCGGGCTCGTGAAGCAACGAATATAC 240
    |||||||
Db 195 GGACAGAGTGTGAGTGGATGATGATCAATCCTTACAGGAAACAAAGAAATTTTCA 254
OY 241 GAAATTTTAAAGACCGGTCTTACTATGACGCGTGCACACTTCGACTAGTACAGTATACATG 300
    |||||||
Db 255 GCGAAGTTCACAGACAGATGACCTTTACCGCGGACACATCCGCGAACAAGCCTCATG 314
OY 301 GAGCTCTCCAGCTCGCATCGAGGACAGCGCGCTATATTATTTGGCGC----- 348
    |||||||
Db 315 GAGTTGAGAGGCTCAGGCTGTCAGACAGCGGCTGTTATTTATTTGTCGAGAGTGGGCCA 374
OY 349 ---CGTTATTTTGTGTTCTTACCGGAATTTGATTTTGGGCTCAAGGAACC 405
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Db 375 TATAGTTGGATGATTTCTCCCGACACATATTATATGACAGCTCTGGGGCAAGGAACC 434
OY 406 CTGTGCACTGTTCTGAGCGCTCCACCAAGGGCCATCGTCTTCCCTGGCGCCCTCC 465
    |||||||
Db 435 ACGGTCACTGAGCTGAGCTTCCACCAAGGGCCATCGTCTTCCCTGGCACCCCTCC 494
OY 466 TCCAAAGACACCTTGGGGGACAGCGGCTGGGCTGCTGCTGCTCAAGACTACTTCC 525
    |||||||
Db 495 TCCAAAGACACCTTGGGGGACAGCGGCTGGGCTGCTGCTGCTCAAGACTACTTCC 554
OY 526 GAACGGGTGACGGTGTGGAATCAAGCGCCCTGACACAGCGGCTGACACCTTCCG 585
    |||||||
Db 555 GAACGGGTGACGGTGTGGAATCAAGCGCCCTGACACAGCGGCTGACACCTTCCG 614
OY 586 GCTGTCTTACAGTCTCAGACTACTCTCCACAGCGGCTGAGACGCTGCTCCAGC 645
    |||||||
Db 615 GCTGTCTTACAGTCTCAGACTACTCTCCACAGCGGCTGAGACGCTGCTCCAGC 674
OY 646 AGCTTGGGACCCAGACCTTACATCTGCAAGTGAATCAAGCCAGCAACCAAGGTG 705
    |||||||
Db 675 AGCTTGGGACCCAGACCTTACATCTGCAAGTGAATCAAGCCAGCAACCAAGGTG 734
OY 706 GACAAGAAAGTTG 718
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Db 735 GACAAGAAAGTTG 747

RESULT 10
LOCUS AR038320/c 3282 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 169 from patent US 5804440.
ACCESSION AR038320
VERSION AR038320.1 GI:5957037
KEYWORDS
SOURCE .
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3282)
AUTHORS Burton,D.R., Barbats,C.F. and Lerner,R.A.
TITLE Human neutralizing monoclonal antibodies to human immunodeficiency
virus
JOURNAL Patent: US 5804440-A 169 08-SEP-1998;
FEATURES
source Location/Qualifiers
BASE COUNT 599 a 864 c 1109 g 710 t
ORIGIN

Query Match 62.3%; Score 467.4; DB 9; Length 3282;
Best Local Similarity 78.7%; Pred. No. 1.2e-100;
Matches 577; Conservative 0; Mismatches 141; Indels 15; Gaps 1;

OY 1 ATGAAGTGGAGCTGGGTATTTCTTCTCTCTGTCAGTACTGCGCGCTCCACCTCCAA 60
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Db 3268 ATGGAATGGAGCTGGGTATTTCTTCTCTCTGTCAGTACTGCGCGCTCCACCTCCAG 3209
OY 61 GTCCAACTGGTCAATTCGGCGCGCGGTCAAGAGCCAGGGGCTCCAGTCAAGTGTCC 120
    |||||||
Db 3208 GTTCAGCTGGTTCATTCGGCGCGGTCAAGAGCCAGGGGCTCCAGTCAAGTGTTC 3149
OY 121 TGTAAAGCTAGCGGCTATATTTTCTTATTAATTAATGATTCATAGGCTGCGTCCAGCC 180
    |||||||
Db 3148 TGTAGGCTTCTGATACAGATTCAGTACTTGTATTCATTTGGGTGCGCCAGCGCC 3089
OY 181 GGGCAGGCGCTGGAATGATGGGTGAGATCTTACCGGGCTCGTGAAGCAACGAATATAC 240
    |||||||
Db 3088 GCGAAGTTCACAGACAGATGACCTTTACCGCGGACACATCCGCGAACAAGCCTCATG 3029
OY 241 GAAATTTTAAAGACCGGTCTTACTATGACGCGTGCACACTTCGACTAGTACGATATACATG 300
    |||||||
Db 3028 GCGAAGTTCACAGACAGATGACCTTTACCGCGGACACATCCGCGAACAAGCCTCATG 2969

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QY 301 GAGCTCCAGCCCTGCATGGAGACAGCGCCCTCATATTATTCGCG----- 348
 Db 2968 GAGTTGAGAGCCCTCAGCTGCAGACAGCGCTTATTATTTGGCAGAGTGGGGCA 2909
 QY 349 ---CGTATTATTTTGGTCTAGCCCAATTTGATTTTGTGGGGTCAAGAAC 405
 Db 2908 TATAGTTGGGATGATTTTCCCGAGACAAATTATATGAGCTGTGGGGAAGAAC 2849
 QY 406 CTGCTACCTGCTCCAGCGCCCTCCACCAAGGGCCATCGATTCCTCCCGGCGCC 465
 Db 2848 ACGTCTACCTGCTAGCTACGCTTCCACCAAGGGCCATCGATTCCTCCCGGCGCC 2789
 QY 466 TCCAGAGCACCTCTGGGGGACACAGCGCCCTGGGCTGCTGTCAGAGCTATTTCCC 525
 Db 2788 TCCAGAGCACCTCTGGGGGACACAGCGCCCTGGGCTGCTGTCAGAGCTATTTCCC 2729
 QY 526 GAACCGGTGACGGTGTGTGGAATCAGAGCGCCCTGACACAGCGGCTGACACCTTCCC 585
 Db 2728 GAACCGGTGACGGTGTGTGGAATCAGAGCGCCCTGACACAGCGGCTGACACCTTCCC 2669
 QY 586 GCTGTCTACAGTCTCTAGAGCTACTCTCCCTCAGCAGCGGCTGACCGGCTCCAGC 645
 Db 2668 GCTGTCTACAGTCTCTAGAGCTACTCTCCCTCAGCAGCGGCTGACCGGCTCCAGC 2609
 QY 646 AGCTTGGGACCCAGACCTACATCTGCAACGTGATCAACAAGCCAGACACCAAGGTG 705
 Db 2608 AGCTTGGGACCCAGACCTACATCTGCAACGTGATCAACAAGCCAGACACCAAGGTG 2549
 QY 706 GACAGAAAGTTG 718
 Db 2548 GACAGAAAGTTG 2536

RESULT 11
 LOCUS 158595 3282 bp DNA PAT 07-OCT-1997
 DEFINITION Sequence 154 from patent US 5652138.
 ACCESSION 158595
 VERSION 158595.1 GI:2477893
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 3282)
 AUTHORS Burton,D.R., Barbas,C.F. and Lerner,R.A.
 TITLE Human neutralizing monoclonal antibodies to human immunodeficiency virus
 JOURNAL Patent: US 5652138-A 154-29-JUL-1997;
 FEATURES
 source Location/Qualifiers
 1..3282
 BASE COUNT 710 a 1109 c 864 g 599 t
 ORIGIN

Query Match 62.3%; Score 467.4; DB 10; Length 3282;
 Best Local Similarity 78.7%; Pred. No. 1.2e-100;
 Matches 577; Conservative 0; Mismatches 141; Indels 15; Gaps 1;
 QY 1 ATGAAGTGAAGCTGGGTATTTCTTCCTCTCTGTCAGTAAGTGGCGGCTCCACTCCCA 60
 Db 15 ATGAATGAGAGCTGGGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 74
 QY 61 GTCCAACTGCTGCAATCCGGCCGAGGTCAAGAAGCCAGGGGCTCAGTAAAGTCTC 120
 Db 75 GTTCACGCTGTGCTTACGTCCGGGGCTGAGGTGAAGAGCTGGGGCTCAGTAAAGTCT 134
 QY 121 TGTAAAGCTAGCGGTATTTTCTTATTTATGATGATCAATGGTCCGTCAGGCCCC 180
 Db 135 TGTCAAGCTTCTGATTAACAAATTCAGTAACCTTTTATTCATTTGGGTGCGCAGGCC 194
 QY 181 GGCAGGGGCTGGAATGATGGGTGAAGATCTTACGGGCTGTGTAGACCGAATATACC 240

Db 195 GGACAGAGGTTTGGATGGATGATGATCAATCTTACACGGAACAAAGATTTC 254
 QY 241 GAAATTTAAAGACCGGTACTATGAGCGGTGACACTTCGACTGTACAGTATACATG 300
 Db 255 GCGAAGTTCAGAGACAGATCACTTACCGGGACACATCCGCGAACACAGCTACATG 314
 QY 301 GAGCTCTCCAGCTCGATCGAGAGACAGCGGCTGTATTTATTTGCGCG----- 348
 Db 315 GAGTTGAGAGGCTCAGGCTCTGAGACAGCGGCTGTATTTATTTATTTGTCAGAGTGGGGCCA 374
 QY 349 ---CGTATTATTTTGGTCTTACCCGAAATTTGATTTTGTGGGTCAAGAAC 405
 Db 375 TATAGTTGGGATGATTTCTCCAGACAAATTTATATGAGACCTGTGGGCAAGAAC 424
 QY 406 CTGCTACCTGCTCAGAGCGCTCCACCAAGGGCCATCGATTCCTCCCGGCGCCCTCC 465
 Db 435 ACGGTATCTGTAGCTACACTTCCACCAAGGGCCATCGATTCCTCCCGGCGCCCTCC 494
 QY 466 TCCAGAGCACCTCTGGGGGACACAGCGCCCTGGGCTGCTCAAGAGCTACTTCCC 525
 Db 495 TCCAGAGCACCTCTGGGGGACACAGCGCCCTGGGCTGCTCAAGAGCTACTTCCC 554
 QY 526 GAACCGGTGACGGTGTGTGGAATCAGAGCGCCCTGACACAGCGGCTGACACCTTCCC 585
 Db 555 GAACCGGTGACGGTGTGTGGAATCAGAGCGCCCTGACACAGCGGCTGACACCTTCCC 614
 QY 586 GCTGTCTACAGTCTCTAGAGCTACTCTCCCTCAGCAGCGGCTGACCGGCTCCAGC 645
 Db 615 GCTGTCTACAGTCTCTAGAGCTACTCTCCCTCAGCAGCGGCTGACCGGCTCCAGC 674
 QY 646 AGCTTGGGACCCAGACCTACATCTGCAACGTGATCAACAAGCCAGACCAAGGTG 705
 Db 675 AGCTTGGGACCCAGACCTACATCTGCAACGTGATCAACAAGCCAGACCAAGGTG 734
 QY 706 GACAGAAAGTTG 718
 Db 735 GACAGAAAGTTG 747

RESULT 12
 LOCUS 158609/c 3282 bp DNA PAT 07-OCT-1997
 DEFINITION Sequence 169 from patent US 5652138.
 ACCESSION 158609
 VERSION 158609.1 GI:2477847
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 3282)
 AUTHORS Burton,D.R., Barbas,C.F. and Lerner,R.A.
 TITLE Human neutralizing monoclonal antibodies to human immunodeficiency virus
 JOURNAL Patent: US 5652138-A 169-29-JUL-1997;
 FEATURES
 source Location/Qualifiers
 1..3282
 BASE COUNT 599 a 864 c 1109 g 710 t
 ORIGIN

Query Match 62.3%; Score 467.4; DB 10; Length 3282;
 Best Local Similarity 78.7%; Pred. No. 1.2e-100;
 Matches 577; Conservative 0; Mismatches 141; Indels 15; Gaps 1;
 QY 1 ATGAAGTGAAGCTGGGTATTTCTTCCTCTCTGTCAGTAAGTGGCGGCTCCACTCCCA 60
 Db 3268 ATGAATGAGAGCTGGGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3209
 QY 61 GTCCAACTGCTGCAATCCGGCCGAGGTCAAGAAGCCAGGGGCTCAGTAAAGTCTC 120
 Db 3208 GTTCACGCTGTGCTTACGTCCGGGGCTGAGGTGAAGAGAGCTGGGGCTCAGTAAAGTCT 3149

OY	121	TGTAAAGCTACGCGGCTATATTTTTTTTCTAATTATTTGGATTGCATTTGGTGTCAGGGCCCC	180
Db	3148	TOTCAGGCTTCGTGGATTACAGATTCCAGTAACCTTTGTATTATTCATTTGGGTGCGCCAGGGCCCC	3089
OY	181	GCGCAGGGCCCTGGGAATGATGGGTGAGATCTTTACC GG GCTGTGGTAGCACCAATATATACC	240
Db	3088	GGACAGAGAGTTTGAATGGATGGATGGATGATCATCTTACAAACGGAAACAAGAAATTTTCA	3029
OY	241	GAATAATTTTAAAAGACCGGTACTATATGACGCGTGACACTTCGACTATATGTAACATATACATG	300
Db	3028	GCGAAGTTCACAGGACAGAGATCTACCTTTACCGGGACACATCCGCCAACACAGCCTACATG	2969
OY	301	GAGCTCCAGCCTCGATCGGAGACACGGCGCTATATTTATTTGGCGCG-----	348
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OY	406	CTGCTCACTGTCTCGAGCGCCCTCCACCAAAGGGCCATGGGTCTTCCCCTGGCGCCCTCC	465
Db	2848	ACGGTCATCGTAGCTCAGCTCAGCTTCCACCAAGGGCCCATGGTCTTCCCTCCGACACCTCC	2789
OY	466	TCCAGAGACACCTCTGGGGGGGCACAGCGGCCCTGGGCTCGCTGTCGAAGGACTACTTTCC	525
Db	2788	TCCAAAGACACCTCTGGGGGGGCACAGCGGCCCTGGGCTCGCTGTCGAAGGACTACTTTCC	2729
OY	526	GAACCGGTGACGGTGTCTGTGAACACAGGCGCCCTGACACAGCGCGGTGCACACCTTCCG	585
Db	2728	GAACCGGTGACGGTGTCTGTGAACACAGGCGCCCTGACACAGCGCGGTGCACACCTTCCG	2669
OY	586	GCTGTCTACAGTCTCAGAGACTACTTCCCTCAGACAGCGGTGTAACCGTGCCTCCACG	645
Db	2668	GCTGTCTACAGTCTCAGAGACTACTTCCCTCAGACAGCGGTGTAACCGTGCCTCCACG	2609
OY	646	AGCTTGGGCACCCCAACACTACATCTGCGCAACGTGAATCACAAAGCCCAACACAAAGGTG	705
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OY	706	GACAGAAAAAGTTG 718	
Db	2548	GACAGAAAAAGTTG 2536	
RESULT	13		
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DEFINITION	Sequence 156 from patent US 5804440.	PAT	29-SEP-1999
ACCESSION	AR038307		
VERSION	AR038307.1	GI:5957024	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 13254)		
AUTHORS	Burton,D.R., Barbadas,C.F. and Lerner,R.A.		
TITLE	Human neutralizing monoclonal antibodies to human Immunodeficiency virus		
JOURNAL	Patent: US 5804440-A 156 08-SEP-1998;		
FEATURES	Location/Qualifiers		
SOURCE	1..13254		
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ORIGIN	/organism="unknown"		
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Matches 577; Conservative	0; Mismatches 141; Indels 15; Gaps 1.		
OY	1	ATGAAGTGGACCTGGGCTATCTCTTCTCTCTGCTAGTAACTACCGGGCTCACACTGCCAA	60

Db	2450	ATGGAAATGAGACTGGGTCCTTTCTCTTCTCTGTCAGTAACCTACAGGTGCTCCACCTCCAG	2509
Qy	61	GTCCACACTGGTGTGCAATCCGGCGCCGAGAGGTAAAGAACCCAGGGGCTCATCAAAATGTCC	120
Db	2510	GTTCAGCGTGTTCAGTGTCCGGGGCTGAGAGTAAGAACGCTGGGGCTTCAGTGAAGGTTTCT	2569
Qy	121	TGTAAAGCTTACGGCTATATTTTTCATTTATTTGATTTCAATGGGTTGAGGCTAGCCCCC	180
Db	2570	TGTCAAGCTTTGTGATATACAGATTCTAGTAACCTTTGTTATTCTATTGGTGGCCAGGCCCC	2629
Qy	181	GGCGAGGGCCCTGGAATGGATGGGTGAGATCTTACCGGGGCTCTGGTAGCACCGAATATACC	240
Db	2630	GGACAGAGAGTTTGATGGATGGATGGATGATCAATCTTACAAAGGAAACAAAGAAATTTTCA	2689
Qy	241	GAATAATTTTAAAGACCGTGTACTATGACCGCTGACACTTTCAGTCTAGTACAGTATACATG	300
Db	2690	GCGAAGTTCACGAGCAGAGTGTACCTTTACCGGAGACATCCCGCAACAGCTTACATG	2749
Qy	301	GAGCTCTCCACCCTCGCATCGGAGAGAACGGCCGCTCATATATGGCCG-----	348
Db	2750	GAGTTGAGAGACCCCTCAGGTGTGACAGACAGCGCTGTTATTTGTCGAGAGTGGGGCCA	2809
Qy	349	---CGTTATTTTTTTTGGTCTAGCCCCCAATTTGGATTTTATTTTGGGTGTCAGAAAC	405
Db	2810	TATAGTTGGGATGATTTCTCCCGAGACAAATTTATATATGACAGTCTGGGGCAAGGAACC	2869
Qy	406	CTGTGCTACTGTCTGTGAGCGCCTCCACCAAGGGCCCATCGGTCTTCCCGCTGGCGCCCTCC	465
Db	2870	AAGCGATACGTGAGACTCAGCTTCACCAAGGGCCCATCGGTCTTCCCGCTGGCGCCCTCC	2929
Qy	466	TCCAAAGACACCTCTGGGGGACACAGCGGCCCTGGGCTGCTGTCAAGACTATCTTCCC	525
Db	2930	TCCAAGACACCTCTGGGGGACACAGCGGCCCTGGGCTGCTGTCAAGACTATCTTCCC	2989
Qy	526	GAACCGTGAGCGTGTGTGAACTCAGAGGGCCCTGACCAAGGGCGGTGACACACTTCCG	585
Db	2990	GAACCGTGAGCGTGTGTGAACTCAGAGGGCCCTGACCAAGGGCGGTGACACACTTCCG	3049
Qy	586	GCTGCTCACAGTCTCCTCAGACTTACTCCCTCAGCAGCGTGTGACCGTGCCTCCAGC	645
Db	3050	GCTGCTCACAGTCTCCTCAGACTTACTCCCTCAGCAGCGTGTGACCGTGCCTCCAGC	3109
Qy	646	AGCTTGGGACCCAGACCTACATCTGCAACGTGAATCACAAGCCACAGCAACAGGTG	705
Db	3110	AGCTTGGGACCCAGACCTACATCTGCAACGTGAATCACAAGCCACAGCAACAGGTG	3169
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Db	3170	GACAGAAGAGTTG 3182	
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DEFINITION	AR038321	13254 bp	DNA
ACCESSION	AR038321	Sequence 170 from patent US 5804440.	PAT
VERSION	AR038321.1	GI:5957038	29-SEP-1999
KEYWORDS			
SOURCE			
ORGANISM		Unknown.	
REFERENCE		Unclassified.	
AUTHORS		1 (bases 1 to 13254)	
TITLE		Burton, D.R., Barbas, C.F. and Lerner, R.A.	
JOURNAL		Human neutralizing monoclonal antibodies to human immunodeficiency	
FEATURES		Patent: US 5804440-A 170 08-SEP-1998;	
BASE COUNT		location/Qualifiers	
ORIGIN		1..13254	
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		3238 a 3251 c 3559 g 3206 t	

Query Match						62.3%;	Score 467.4;	DB 9.4;	Length 13254;
Best Local Similarity						78.7%;	Pred. No. 9.4e-101;		
Matches 577;						Conservative	0;	Mismatches 141;	Indels 15; Gaps 1
OY	1	ATGAAGTGAGCTGGGTTATTCTCTTTCCTCCTGTCAAGTAACGCCGCGCTCCACTCCAA	60						
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OY	61	GTCCAACTGGTGTCAATTCGGCGCGCCGACGTCAAGAAGCCAGGGGCCTCACTCAAAGTCCG	120						
Db	10745	GTTCCAGCTGGTTCACTCCGGGGCTGAGGTGAAGAAGCCGTGGGGCCTCATGTGAAGGTTTCT	10686						
OY	121	TGTAAAGTAGCGGGCTATATTATTTTTTCTAATTATTTGGATTCAATGGGTGGGTGAGGGCCCC	180						
Db	10685	TGTCAAGCTCTTCGATTCACAGATTCAAGTACTTGTATTATTCATTTGGGTGGGCCAGGGCCCC	10626						
OY	181	GGCGAGGGCCCTGGAATGAGATGGGTAGATCTTACC GGCGCTGTGTAGACACCGAATATACC	240						
Db	10625	GGACAGAGGTTTGAATGGATGGGATGAGATCAATFCTTACAAGGAAACAAAGATTTTCA	10566						
OY	241	GAAAATTTTAAAGACCGGTATTACTATFGACGGGTGACACTTGCAGTACTAGTACATATACATG	300						
Db	10565	GGCAAGTTCACAGACAGAGATCACCTTACCGGGGACACATCCGCGAACACAGCTCTACATG	10506						
OY	301	GAGCTCTCCAGCCTCGAATCGGAGACACGGCGGCTATATTGGGCG-----	348						
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OY	349	--CGTTATTTTTTGTGTCTAGCCCGAATTTGATATTTTGATGTTTGGGTGACAGGAMCC	405						
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OY	406	CTGTGCTACTGTCTCGAGCGCCTCCACCAAGGGCCCATGTGGTTTCCCCTGGCGCCTCC	465						
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OY	466	TCCAGAGACACCTCGGGGGGACACGGGCGTGGGGCTGCTGTGTAAGAGTACTTCCCC	525						
Db	10325	TCCAGAGACACCTCTGGGGGGACACGGGCGCTGGGGCTGCTGTGTAAGAGTACTTCCCC	10266						
OY	526	GAACCGGTGACGGTGTGCTGTAAGTCAAGCGCCCTGACAGCGGGGTGCACACCTTCCCG	585						
Db	10265	GAACCGGTGACGGTGTGCTGTAAGTCAAGCGCCCTGACAGCGGGGTGCACACCTTCCCG	10206						
OY	586	GCTGTCTACAGTCTCTCAGAGTACTTCTCCCTCAGACAGCGGTGTGACCGCTGCCCTCCAGC	645						
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OY	646	AGCTTGGGCAACCAACCTACATCTGCAACGTGATACAAACCCAGCAACACAAAGGTG	705						
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OY	706	GACAGAAAAAGTTG 718							
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ACCESSION	158596								
VERSION	158596.1	GI:2477834							
KEYWORDS									
SOURCE	Unknown.								
ORGANISM	Unknown.								
REFERENCE	Unclassified.								
AUTHORS	1 (bases 1 to 13254)								
TITLE	Burton,D.R.,Barbas,C.F. and Lerner,R.A.								
JOURNAL	Human neutralizing monoclonal antibodies to human immunodeficiency								
FEATURES	virus .Patent: US 5652138-A 156 29-JUL-1997;								
	Location/Qualifiers								

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source              1..13254
                    /organism="unknown"
BASE COUNT          3206 a   3559 c   3251 g   3238 t
ORIGIN
Query Match        62.3% Score 467.4; DB 10; Length 13254;
Best Local Similarity 78.7%; Pred No.9.4e-101;
Matches 577; Conservative 0; Mismatches 141; Indels 15; Gaps
OY      1 ATGAAGTGAGCGTGGGTATTTCTCTTCCTCCTGCTACGTACTGCCGGCGTCCACTCCAA 60
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Db       2450 ATGAGTAGAGCATGGGTCTTCTCTCTCTCTCTCACTGTAATAAAGTGTCCACTCCAG 2509
OY      61 GTCCAACGTGCCTCANATTCGGGGCCGAGGTCACAAGAACCCAGGGGCCCCACTCAAAGTCCC 120
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Db       2690 GCGAAGTTCAGAGACAGAGATCACTTACCAGGGGACACATCCGCCAACAACAGGCTACATG 2749
OY      301 CAGCTCTCCAGCCTCGATCGAGACACAGCGGCTATATTATGCGCG----- 348
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Search completed: July 20, 2001, 02:34:00
Job time: 6268 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2001, 01:57:44 ; Search time 1948.2 Seconds
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Title: US-08-487-283A-12
Perfect score: 750
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Scoring table: IDENTITY_NUC
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Searched: 10228115 seqs, 4726426750 residues
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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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				Gaps	5;
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61	GTCCAACTGGTGCAATCCGCGCCGAGGCTCAAGAACGAGGGGCTCACTCAAGTGTCC	120			
101	GTCCAGCTGTGACAGCTCGGGGCTGAGGTGAAGAGCTCGGGGCTCACTGAAAGTCTCC	160			
121	TGTAAAGCTACCGCTATATTTTCTTCAATATTTGGATTCAATGGGTTGGTCAAGTCCC	180			
161	TGCAAGGTTTCCCGCTTACACCTCACTCAATATTCATGCACTGGGTTGGAGAGGCTCT	220			
181	GGGAGGAGCTGGAAATGATGGGTAGATCTTACCGGGCTGGTGAAGCAGCAATATACC	240			
221	GGAAAGGGCTTGAAGTGGATGGAGGTTTGTATCTGAAAGCTGGTGGAAAGATCTACGA	280			
241	GAATATTTTAAAGACCGTGTACTATGACGCGCTGACACTTGCAGTACATATATACATG	300			
281	CAGAAGTTCAGAGGAGAGTCAACATGACAGACACATATACAGAGAGCAGCTACATG	340			
301	GAGCTCTCAGCTGCGATCGAGAGACAGCGCGCTATATATTTGGCGCGCTATTTT	360			
341	GAGCTGAGCAGCTGAGATCTGACGACACAGCGCGCTATATTTGCTGCAACCTACATGAT	400			
361	GGTCTTACCCGGAATGATATTTTGTATTTTGGGTCAAGAAACCTGGTCACTGTCTCG	420			
401	-----ATTAGGGGCTGTGACTACTGAGGGGACAGGAAACCTGGTCACTGTCTCG	448			
421	AGGCGCTCAGCAGAGGAGGCAATGGTCTTCCCGCTGGGAGCCCTCTCCAGAGCACTCT	480			
449	TCAAGCTTCCACCAAGAGGCGCATCGGTCTTCCCGCTGGAGACCTCTCTCCAGAGCACTCT	508			
481	GGGGGACAGGCGGCTGGGCTGCTGTGTCAGAGCACTATTTCCCGGAACCGGTGACGGTG	540			
509	GGGGGACAGGCGGCTGGGCTGCTGTGTCAGAGCACTATTTCCCGGAACCGGTGACGGTG	568			
541	TCTGTGAATCAGGCGGCTTACAGCGGCGGTGACACCTTCCGGGCTGTCTTACAGTCC	600			

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Db 569 TCGTGAACACGAGCGCCCTGACCAAGGCGGTGACACACCTTCCGGCTGCTCTACAGTC 628
QY 601 TCAGACTCTACTCCCTCAGCAGGCGGTGTGACCGTCCCTCAGCAGGTGGGACCCAG 660
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 629 TCAGACTCTACTCCCTCAGCAGGCGGTGTGACCGTCCCTCAGCAGGTGGGAC-CCAG 687
QY 661 ACCTACATCTGCAACGTGAATCAGAACGCCAGCAACACCAAGTGAGACAGAAAGTTGAG 720
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 688 AACTACATCTGCAACGTGAATCAGAAC-CCAGCAACACCAAG--GGACAGAAAGTTGAG 744
QY 721 CCCAAATCTGTGACAAA 739
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Db 745 -AATCTGTGTGACAAA 761

RESULT 2
BF342599 783 bp mRNA EST 22-NOV-2000
LOCUS DEFINITION 602013731F1 NCI.CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4149679
ACCESSION BF342599
VERSION BF342599.1 GI:11289621
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 783)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM6411 row: m column: 08
High quality sequence stop: 744.
Location/Qualifiers
1. 783
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4149679"
/tissue_type="glioblastoma with EGFR amplification"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: brain; Vector: PCMV-SPORT6; Site: 1; NotI;
Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 185 a 235 c 209 g 154 t
ORIGIN
Query Match 53.38; Score 399.8; DB 147; Length 783;
Best Local Similarity 76.88; Pred. No. 1.8e-102;
Matches 509; Conservative 0; Mismatches 137; Indels 17; Gaps 1;

QY 103 GCCCAGTCAAGTGTCTGTAAGCTAGCGGCTATATTTTCTTAATTATTTGATTGCA 162
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Db 6 GCGGCCAGAGACTCTCTGTGTCAGCCCTGTGATTCATTTCAAAACTATGGCATGAC 65
QY 163 TGGGTGCGTACAGCCCGGCGGAGGCGCTGGAATGATGGGTGAGATCTTACCGGGCTCT 222
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 66 .TGGGTGCGGCGGCTGTCAGGAGGCGGTGAGTGGCGAGTATATATGATATGATGA 125
QY 223 GGTAGCACCGATATACCGAAAATTTTAAGACCGGTGTACTATGACCGGTGACACTTCG 282
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 126 AGTATTCATATCTACACAGACTCCGTGAAGGCGGATTCACCGTCTCAAGAGACATGTT 185

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QY 283 ACTAGTACAGTATACATGAGACTCTCCAGCTCGATCGGAGACAGCGCGTCTATTAT 342
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Db 186 AAAAATATGTGTATCTGCATTAATGAACAGCTGAGAGCCGAGACAGCGCTGTATATAT 245
QY 343 TGGCGCG-----TTATTTTGTGTTCTACCCGAATTTGTAATTG 385
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 246 TGTGCGAGAGGCAAAAGAGAGTGTATATGCTTTCCCGCCCAAGAGAGCATGATGTTTG 305
QY 386 ATGTTGGGTGCAAGAACCTGTGCTACGTCTCGAGCGGCTCCACCAAGGCGCATCGG 445
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 306 ATATCTGGGGCCAGAGGACATGATGTCACGCTCTTCAGCCTCCACCAAGGCGCATCGG 365
QY 446 TCTTCCCTGAGCGCCCTCTCTCCAGAGACACTCTGGGGGACAGAGCGGCTGGGTGCC 505
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 366 TCTTCCCTGAGCGCCCTCTCTCCAGAGACACTCTGGGGGACAGAGCGGCTGGGTGCC 425
QY 506 TGTGCAAGGACTACTTCCCGGAACCGGTGACGGTGTGTGGAACCTCAGCGCCCTGACCA 565
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 426 TGTGCAAGGACTACTTCCCGGAACCGGTGACGGTGTGTGGAACCTCAGCGCCCTGACCA 485
QY 566 GCGGCGTGCACACCTTCCCGGCTGCTACAGTCCTCAGAGACCTACTCTCCAGACGCG 625
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 486 GCGGCGTGCACACCTTCCCGGCTGCTCCTACAGTCCTCAGAGACCTACTCTCCAGACGCG 545
QY 626 TGGTGACCGTGCCTCCAGAGAGCTGGGACCCAGACCTACTACTGCAAGTGAATCACA 685
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Db 546 TGTGACCGTGCCTCCAGAGAGCTGGGACCCAGACCTACTACTGCAAGTGAATCACA 605
QY 686 AGCCGACCAACCAAGTGTGACAGAAGAGTTAGCCCAATCTTGTGACAAAATCTCACA 745
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Db 606 AGCCGACCAACCAAGTGTGACAGAAGAGTTAGCCCAATCTTGTGACAAAATCTCACA 665
QY 746 CAT 748
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Db 666 CAT 668

RESULT 3
BG397867 860 bp mRNA EST 12-MAR-2001
LOCUS DEFINITION 602438967F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4565008 5',
ACCESSION BG397867
VERSION BG397867.1 GI:13291315
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 860)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staedt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM1281 row: f column: 17
High quality sequence stop: 846.
Location/Qualifiers
1. 860
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4565008"
/tissue_type="NIH_MGC_48"
/lab_host="DH10B (phage-resistant)"

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/note="Organ: B-cells; Vector: pORF; Site.1: XhoI; Site.2: EcoRI. cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library."

BASE COUNT 185 a 261 c 237 g 177 t

ORIGIN

Query Match 53.3%; Score 399.6; DB 153; Length 860;
Best Local Similarity 74.0%; Pred. No. 2.1e-102;
Matches 537; Conservative 0; Mismatches 179; Indels 10; Gaps 2;

23 TCTTCCTCTGCACTAAGTCCGCTCCAGTCCCACTGAGGCAATCGGGG 82
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85 TTTTCTTCTGCTATTAAAAAGTCTCAGTGTGAGCTGAGCTGGAGTCCGGG 144
|||||
83 CCGAGCTCAGAAAGCCAGGGGCTCAGTCAAGTCTCTGAAGCTAGCGCTATATT 142
|||||
145 GAGGTTAGTTCAGCGCTGGGGGATCCCTGAGACTCTCTGAGCGCTCTGGATTACCT 204
|||||
143 TTTCTATTATTGATTCAATGGTGGTCTCAGGCCCCGGGCAAGGCTGGAATGATGG 202
|||||
205 TTAGTAGTACTGATGATGACACTGGGTCCGCCAAG-CTCCAGAAAGGGGCTGGTGGCTCA 263
|||||
203 GTGAGATCTTACCGGCTCTGTACACCGCAATATACCAAAATTTAAAGACCGTCTTA 262
|||||
264 CACGATGAATAGTAGTATGAGTATACAACTAGCGGACTCCGGAAGGGCGATTTCA 323
|||||
263 CTATGACGCTGACACTTGCATAGTATACATGAGCTCTCAGCCTCGATCGG 322
|||||
324 CCATCTCCAGAGACACAGCCCAAGAACGCTGTATCTGAATGAACATCTAGAGCCG 383
|||||
323 AGACACGCGCTTATTATTGGGCGGCGTTATTTTGGTCTTACCGCAATTTGTTATT 382
|||||
384 AGGACACGCGTGTATTACTGTGCAACGAAAGAGAGT-----GGCTAGCATTT 434
|||||
383 TTGATGTTGGGGTCAAGAACCTGTGCTCTCGACCGCTTCACCAAGGGCCCAT 442
|||||
435 TAACGTACTGGGGCATGAAACCCGTGTCACCTCTCCACCTCCACCAAGGGCCCAT 494
|||||
443 CGGCTTCCCTCGCGGCTCTCCAGAGACCTCTGGGGGACAGGGGCTGGGCT 502
|||||
495 CGGCTTCCCTCGCGGCTCTCCAGAGACCTCTGGGGGACAGGGGCTGGGCT 554
|||||
503 GCGTGTCAAGGACTACTTCCCGGAACCGGTGACGCTGTCTGGAATCAAGGCGCCCTGA 562
|||||
555 GCGTGTCAAGGACTACTTCCCGGAACCGGTGACGCTGTCTGGAATCAAGGCGCCCTGA 614
|||||
563 CCAGCGGCTGACACACTTCCCGGCTGTCTACAGTCTCTCAGAGCTACTCTCTCAGCA 622
|||||
615 CCACGCGGCTGACACACTTCCCGGCTGTCTACAGTCTCTCAGAGCTACTCTCTCAGCA 674
|||||
623 GCGTGTCAAGGACTACTTCCCGGAACCGGTGACGCTGTCTGGAATCAAGGCGCCCTGA 682
|||||
675 GCGTGTCAAGGACTACTTCCCGGAACCGGTGACGCTGTCTGGAATCAAGGCGCCCTGA 734
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683 ACAAGCCAGCAACACCAAGGTGACAAAGATTGAGCCCAATCTTGTGACAAATCT 742
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735 ACAAGCCAGCAACACCAAGGTGACAAAGATTGAGCCCAATCTTGTGACAAAGATT 794
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743 ACACAT 748
|||||
795 ACACAT 800
|||||

RESULT 4
BG398464 775 bp mRNA EST 12-MAR-2001
LOCUS BG398464

DEFINITION 602439749F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4565676 5', mRNA sequence.
ACCESSION BG398464
VERSION BG398464.1 GI:13291912
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabds-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
Plate: LLCM1283 row: b column: 13
High quality sequence stop: 766.
Location/Qualifiers

FEATURES
source 1..775
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4565676"
/clone_11b="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pORF; Site.1: XhoI; Site.2: EcoRI. cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library."

BASE COUNT 174 a 245 c 216 g 140 t

ORIGIN

Query Match 53.1%; Score 398.4; DB 153; Length 775;
Best Local Similarity 80.8%; Pred. No. 4.4e-102;
Matches 483; Conservative 0; Mismatches 101; Indels 14; Gaps 1;

165 GTGCGTCAAGGCCCGCGGACAGGGCTGAAATGATGGTGAGATCTTACCGGCTCTGG 224
|||||
1 GGTGCGACAGACTGTGTGACACAGCCTTGAGTGTGATGATGATGATGATGATGATG 60
|||||
225 TAGCACCGAATATACGCAAAATTTTAAAGACCGTGTACTATGACGGCTGACACTGCAC 284
|||||
61 TAACACAAATTTACGACAGCAAACTCCAGAAAGAGTACACCTTACCGAGGACATGTCCAC 120
|||||
285 TAGTACGATATATACATGACGCTCTCCAGCTCCGATCCGAGAGACAGCGCCCTATTATTG 344
|||||
121 AGGCACAGCCTTACATGGAAGTTGAGACCGCTGATCCGAGAGACAGCGCCGTTATCTG 180
|||||
345 CCGCGCTATTATTTTGG-----TTCAGACCCGAATTTGTTATTTGATGTT 390
|||||
181 TCGCGGACAGCCTGATGGGGGAGCAGTGGGATTCCTCTACTACTAGGTTATGACGCTCT 240
|||||
391 TGGGCTCAAGGAACCTGTGCTACTGTCTGAGCGCTCCACCAAGAGGCCCATCGGCTTTC 450
|||||
241 GTTGGCCAAAGGACAGCGTCCACCGTCTCTACACCTTCACCAAGAGGCCCATCGGCTTTC 300
|||||
451 CCCCTGGCGCTCTCTCAAGAGACACTGTGGGGGACACAGCGGCCCTGGGCTGGCTGCTC 510
|||||
301 CCCCTGGCACCTCTCTCAAGAGACACTGTGGGGGACACAGCGGCCCTGGGCTGGCTGCTC 360
|||||

OY	511	AAGGACTCTCCTCCCGAAGCCGGTGCAGGTGTGTCGTGAACACTGAGGGGCCCTGACCAGCGCC	570
Db	361	AAGGACTCTCCTCCCGAAGCCGGTGCAGGTGTGTCGTGAACACTGAGGGGCCCTGACCAGCGCC	420
OY	571	GTCGACACCTTCGCGGCTGTCTCTACAGCTCTCTCAGACTCTACTCCCTCAGCAGCGTGtGtG	630
Db	421	GTCGACACCTTCGCGGCTGTCTCTACAGCTCTCTCAGACTCTACTCCCTCAGCAGCGTGtGtG	480
OY	631	ACCGTGCCTTCAGCAGCTTTGGGACACCCAGACCTTATCTGCAACGTGATACAAGCCC	690
Db	481	ACCGTGCCTTCAGCAGCTTTGGGACACCCAGACCTTATCTGCAACGTGATACAAGCCC	540
OY	691	AGCAACACCAAGGTGACAGAAGAAAGTTAGAGCCCAATCTTGACAAAACTCACACAT	748
Db	541	AGCAACACCAAGGTGACAGAAGAAAGTTAGAGCCCAATCTTGACAAAACTCACACAT	598
RESULT	5		
LOCUS	BG397847	869 bp	mRNA EST 12-MAR-2001
DEFINITION	602438939P1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4565192 5'		
ACCESSION	BG397847		
VERSION	BG397847.1	GI:13291295	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://Image.llnl.gov Plate: L16CM1281 row: n column: 09 High quality sequence stop: 805.		
FEATURES	Location/Qualifiers		
Source	1..869		
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	/db_xref="taxon:9606"		
	/clone="IMAGE:4565192"		
	/clone_lib="NIH_MGC_48"		
	/tissue_type="Primary B-cells from tonsils (cell line)"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: This is a NIH_MGC library."		
BASE COUNT	200 a 266 c 226 g 177 t		
ORIGIN			
Query Match	52.5%;	Score 393.6;	DB 153; Length 869;
Best Local Similarity	76.3%;	Pred. No. 1e-100;	
Matches 580;	Conservative 0;	Mismatches 159;	Indels 21; Gaps 7.
OY	1	ATGAAGTGGAGCTGGGCTATTCTCTCTCTCCGTCGATGAATCGCGGCGTCACATCCCAA	60
Db	44	ATGGACTGGAGCTGGAGCATCTTTCTTGTGGGACGACGACAAAGTGTCCCATCTCCAG	103

OY		61	GTTAACTGGGCAATCCGGCGCAGGTTCAGGAAGCACGGGGCTCAGTCAAAGTGTC	120
Db		104	GTTCAATTGGTGACACTGGAGCTGAGGTGAGAAGTAACCTGGGGCTTAGTAGAAGTCTCC	163
OY		121	TGTAAAGCTACCGCATATATTTTTTCTAAATATATGATATCAATGGTGCCCTCAAGCCCC	180
Db		164	TGCAGGTCTTCTGGTTACAGTATCTCCAGGCCAGGTATCAAGTTGGGTGGCAGAGCCCCT	223
OY		181	GGGCAGGGCCITGGAAATGGATGGGTGAGATCTTACC GGGGCTCTGGTAGCACCGAATATACC	240
Db		224	GGACAAGGTCTTCAGATGGATGGGATGGATCAGCCTTCCACAATAGTGTGACACAAATTGCA	283
OY		241	GAATAATTTAAAGACCGGTACTATAGACCGGTGACACTTCGATAGTACTAGTATACATG	300
Db		284	CAGAA - CGTCCAGGAGAGCTACCATGACACACAAACATCTCACAGATACAGCCTATATG	342
OY		301	GAGCTCTCAGCCCTGCGATWCGGAGAGACAGCGCCCTGATATATATGCGCG-----	348
Db		343	GACCTGAGAGACCTGACATCTGACAGACACG - CGTGTATTTATTTGTGGAGAAATAGGGCA	401
OY		349	-- CGTTATTTTTTGGTCTTACGCCCGAATWGTAATTTGATGTTTGGGGTCAAGAAC	405
Db		402	GCTCGTTCCATTTTAAATTTGGGATTTCTCTATTACTTTGATTAATTTGGGGCAGAGAAC	461
OY		406	CTGGCATGTCTGAGGGCCCTCCACCAAGGGGCCCATCGGCTTCCCTCGGGCCCTCC	465
Db		462	CTAGTCACCGTCTCTCAGCCTCCACCAAGGGGCCCATCGGCTTCCCTCGGGCACCCTCC	521
OY		466	TCCAAGAGCACCTCTGGGGGACACAGCGCCCTGGGGCTGCTGTCAGAGACTACTTCC	525
Db		522	TCCAAGAGCACCTCTGGGGGACACAGCG - CCTGGGCTGCTGTCAGAGACTACTTCC	580
OY		526	GAACCGGTGACGGTGTGTGTAAGTCAAGGGCCCTGACACAGCGCG--TGCACACTTTC	584
Db		581	GAACCGGTGACGGTGTGTGTAAGTCAAGGGCCCTGACACAGCGCGTTCGACACTTTC	640
OY		585	GGCTGTGC-TACAGTCCCTCAGAGACTCTACCTCCCTCAGAGCGTGGTAGCGTGCCTCCA	643
Db		641	GGCTGTCCCTTACAGTCCCTCAGAGACTCTACCTCCCTCAGAGCGTGGTAGCGTGCCTCCA	700
OY		644	GCAGCTTGGGACCCAGACCTACATCTGCAACGTAATCACAAAGCCAGCAACACCAAG	703
Db		701	GCAGCTTGGGACCCAGACCTACATCTGCAACGTAATCACAAAGCCAGCAACACCAAG	759
OY		704	TGGACAGAAAAGTTGAGCCCAATCTTGTGACAAAACTCA	743
Db		760	TGGACAGAAAAGTTGAGCCCAATCTTGTGACAAAAATCA	799
RESULT		6		
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LOCUS		823 bp	mRNA	EST
DEFINITION		60214596SF1 NIH_MGC_48 Homo sapiens cDNA IMAGE:4309720 5',		21-DEC-2000
VERSION		Bf664166		
KEYWORDS		Bf664166.1 GI:11938061		
SOURCE		EST.		
ORGANISM		human.		
		Homo sapiens		
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE		1 (bases 1 to 823)		
AUTHORS		NIH-MGC http://mgc.nci.nih.gov/		
FILE		National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL		Unpublished (1999)		
COMMENT		Contact: Robert Strausberg, Ph.D. Email: cgabps@email.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:		

http://image.llnl.gov
Plate: LCM1183 row: 1 column: 17
High quality sequence stop: 750.
Location/Qualifiers

FEATURES

Source

1. 823
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4309720"
/issue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(5). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 183 a 254 c 227 g 159 t
ORIGIN

Query Match 51.1%; Score 383.4; DB 151; Length 823;
Best Local Similarity 75.0%; Pred. No. 7.9e-98;
Matches 559; Conservative 0; Mismatches 176; Indels 10; Gaps 6;

1 ATGAAGTGTGAGGGGTTTCCTCTCCCTGCTGCTAGTACGCGCGGCTCCACCTCCCA 60
44 ATGGAAGTGTGAGGGGTTTCCTCTCCCTGCTGCTAGTACGCGCGGCTCCACCTCCCA 103
61 GTCAAGTGTGAGGGGTTTCCTCTCCCTGCTGCTAGTACGCGCGGCTCCACCTCCCA 120
104 GTTCAAGTGTGAGGGGTTTCCTCTCCCTGCTGCTAGTACGCGCGGCTCCACCTCCCA 163
121 GTTCAAGTGTGAGGGGTTTCCTCTCCCTGCTGCTAGTACGCGCGGCTCCACCTCCCA 180
144 GTTCAAGTGTGAGGGGTTTCCTCTCCCTGCTGCTAGTACGCGCGGCTCCACCTCCCA 223
181 GTTCAAGTGTGAGGGGTTTCCTCTCCCTGCTGCTAGTACGCGCGGCTCCACCTCCCA 240
224 GTTCAAGTGTGAGGGGTTTCCTCTCCCTGCTGCTAGTACGCGCGGCTCCACCTCCCA 281
241 GTTCAAGTGTGAGGGGTTTCCTCTCCCTGCTGCTAGTACGCGCGGCTCCACCTCCCA 300
282 GTTCAAGTGTGAGGGGTTTCCTCTCCCTGCTGCTAGTACGCGCGGCTCCACCTCCCA 341
301 GTTCAAGTGTGAGGGGTTTCCTCTCCCTGCTGCTAGTACGCGCGGCTCCACCTCCCA 360
342 GTTCAAGTGTGAGGGGTTTCCTCTCCCTGCTGCTAGTACGCGCGGCTCCACCTCCCA 400
361 GTTCAAGTGTGAGGGGTTTCCTCTCCCTGCTGCTAGTACGCGCGGCTCCACCTCCCA 418
401 GTTCAAGTGTGAGGGGTTTCCTCTCCCTGCTGCTAGTACGCGCGGCTCCACCTCCCA 460
419 GTTCAAGTGTGAGGGGTTTCCTCTCCCTGCTGCTAGTACGCGCGGCTCCACCTCCCA 478
461 GTTCAAGTGTGAGGGGTTTCCTCTCCCTGCTGCTAGTACGCGCGGCTCCACCTCCCA 519
479 GTTCAAGTGTGAGGGGTTTCCTCTCCCTGCTGCTAGTACGCGCGGCTCCACCTCCCA 538
520 GTTCAAGTGTGAGGGGTTTCCTCTCCCTGCTGCTAGTACGCGCGGCTCCACCTCCCA 577
539 GTTCAAGTGTGAGGGGTTTCCTCTCCCTGCTGCTAGTACGCGCGGCTCCACCTCCCA 598
578 GTTCAAGTGTGAGGGGTTTCCTCTCCCTGCTGCTAGTACGCGCGGCTCCACCTCCCA 637
599 GTTCAAGTGTGAGGGGTTTCCTCTCCCTGCTGCTAGTACGCGCGGCTCCACCTCCCA 658
638 GTTCAAGTGTGAGGGGTTTCCTCTCCCTGCTGCTAGTACGCGCGGCTCCACCTCCCA 697
659 GTTCAAGTGTGAGGGGTTTCCTCTCCCTGCTGCTAGTACGCGCGGCTCCACCTCCCA 718

Db 698 AGACCTACATCTGGCAGCTGTAATCAAGCCGAGACACCAAG--TGCCCAAGAGTTG 755
Qy 719 AGCCCAATCTTGTGACAAACTCA 743
Db 756 AGCCCAATCTTGTGACAAACTCA 780

RESULT 7
BG398411 796 bp mRNA EST 12-MAR-2001
LOCUS 602439885F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4566236 5',
DEFINITION mRNA sequence.
ACCESSION BG398411 GI:13291859
VERSION BG398411
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 796)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
CONTACT Robert Strausberg, Ph.D.
COMMENT Email: cgabs@remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LCM1284 row: 1 column: 21
High quality sequence stop: 774.

FEATURES

Source

Location/Qualifiers

1. 796
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4566236"
/issue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pORF7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(5). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

BASE COUNT 174 a 256 c 215 g 151 t
ORIGIN

Query Match 50.9%; Score 381.4; DB 153; Length 796;
Best Local Similarity 75.9%; Pred. No. 2.9e-97;
Matches 503; Conservative 0; Mismatches 146; Indels 14; Gaps 2;

Qy 98 CAGGGGCTCAGTCAAGTGTCTGTAAGCTAGCGGCTATATTTTCTTAATTAATGGA 157
Db 2 CTGGGGGGTCCCTGAGACTCTCTGCTGGGCTCTGAGGTTCAATCTTGAACAATGGA 61
Qy 158 TTCAATGGGTGCTAGGCCCCCGGAGGCGCTGGAATGATGGGTGAGATCTTACGG 217
Db 62 TGACCTGGGTGCTAGGCCCCCGGAGGCGCTGGAATGATGGGTGAGATCTTACGG 121
Qy 218 GCTGTGAGACACCAATATACCAAAATTTAAAGACCGTGTCTATAGAGCGTGACA 277
Db 122 ATGGCGCCAGTACATCTACAGTACCTCGTGAAGGCGCTTCAACATCTTCAAGACGA 181
Qy 278 CTTCAGTACATCTACAGTACCTCGTGAAGGCGCTTCAACATCTTCAAGACGA 337

Db	182	ATTTCAGGAACACACGTGTTCTTCAATGAACAGCCTCAGAGCCGAGGACACGGCCGTAT	241
QY	338	ATTATTCGCGCGCTATT-----TTTGGTTCTAGCCGAATTGTAATTTTG	385
Db	242	ATTACTGTGGGAAGAAGACTGTGCGGCTGACTCTGTGATTTGTGTGAGAGGGCGCTATGG	301
QY	386	ATTGTTGGGTCAGGAAGAACCTGGTCACTGTCTCGAGCGCTCCACCAAGGGCCATCGG	445
Db	302	ACGTCGTGGGGCCAGAGGACCAAGCTCACCGCTCTCTCTAGCCTCCACCAAGGGCCATCGG	361
QY	446	TCCTCCCGCTGGCGGCGCTCTCTCCAGAGACACTCTGTGGGGCCAGAGCGGCTGGGCTGCC	505
Db	362	TCCTTCCCGCTGGGACACCTCTCTCTCCAGAGACACTCTGTGGGGCCAGAGCGGCTGGGCTGCC	421
QY	506	TGCTCAAGGACTACTTCCCGGAACCGGTGACGGTGTCTGTGAACTAGCGGCCCTGACCA	565
Db	422	TGGTCAAGGACTACTTCCCGGAACCGGTGACGGTGTCTGTGAACTAGCGGCCCTGACCA	481
QY	566	GCGGCGGACACACTTCCCGGCTCTCTACAGTCTCAGACACTCTACTCCCTCAGACGGC	625
Db	482	GCGGCGGACACACTTCCCGGCTCTCTACAGTCTCAGACACTCTACTCCCTCAGACGGC	541
QY	626	TGGTGAAGCTGTCCCTCCAGAGAGCTTGGGACCCAGACCTATCTGCAAGTGAATACA	685
Db	542	TGGTGAAGCTGTCCCTCCAGAGAGCTTGGGACCCAGACCTATCTGCAAGTGAATACA	599
QY	686	AGCCCAACCAACCAAGGTGGACAAAGTTGAGCCCAATCTTGTGACAAAACCTACA	745
Db	600	AGCCCAACCAACCAAGGTGGACAAAGTTGAGCCCAATCTTGTGACAAAACCTACA	659
QY	746	CAT 748	
Db	660	CAT 662	
RESULT	8		
LOCUS	BG397667		
DEFINITION	BG397667	841 bp	mRNA EST 12-MAR-2001
ACCESSION	602438719F1	NIH_MGC_48	Homo sapiens cDNA clone IMAGE:4564973 5'
VERSION	BG397667		mRNA sequence.
KEYWORDS	BG397667.1	GI:13291115	
SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi.		
TITLE	Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo.		
JOURNAL	1 (Phases 1 to 841)		
COMMENT	NIH-MGC http://mgc.nci.nih.gov/ .		
	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgabs-remail.nih.gov		
	Tissue Procurement: Louis M. Staudt, M.D., Ph.D.		
	CDNA Library Preparation: Ling Hong/Rubin Laboratory		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNL at:		
	http://image.lnl.gov		
	Plate: LNCMI281	Row: e	Column: 06
	High quality sequence stop: 838.		

FEATURES
source

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/organism="Homo sapiens"
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/clone="IMAGE:4564973"
/clone_1b="M1H.MGC.48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: B-cells; Vector: pOT7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.

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directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-DNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC library.*

Query Match	49.1%;	Score 368.6;	DB 153;	Length 841;
Best Local Similarity	70.7%;	Pred. No. 1.2e-93;		
Matches 521;	Conservative 0;	Mismatches 209;	Indels 7;	Gaps 2;

QY	1	ATGAAGGAGGAGCTGGGGTTATTCCTCTTCCTCCCTGTAAGTAACAGCGGGGCTCACTCCCAA	60
Db	22	ATGAACACCTGTGGTTCTTCTCCTCCCTGGGTGGGACGCTCCCAATGGGTCTCTGTACG	81
QY	61	GTCCAACTGGTGCATTCGGGCGCGGAGTCAAGAAAGCCAGGGGGCTCAGTCAAAAGTCC	120
Db	82	GTACAGCTGTGAGGAGTCCGGGCCAGGACTGTAAGCCCTTGGGGAGCCCTGTCCCTCAAC	141
QY	121	TGTAAAGCTAGCGGCTATATTTTTCATTTATTTGGATTTCATGGGTGGCTCAGGCCCC	180
Db	142	TGGCGTGTCTCTGGTGGCTCCATCATGATTAATTTGGTGGAGTGGGTCCGACAGCCCCA	201
QY	181	GGGAGGGGGCTGGAAATGATATGGGTGATGACTTAACGGGGCTGGGTAGACAGGAATATAC	240
Db	202	GGGAAGGGGGCTGGAGTGGATTGGAGAAATATCTC---ATACTGGTAAACCACTACAC	258
QY	241	GAATAATTTTAAAGACGCTGTACTATGACGCGGTGACACTGTGACTAGTACATATACATG	300
Db	259	CCGTCCCTCCGGAGTGTGAGTCAACATTTTACTATAGAACATGTCGAAATGAGTCTCCCTG	318
QY	301	GAGCTCTCCAGCCTCGGATGAGAGACACGGCCGTATATTATGCGCGCTTAATTTTTTT	360
Db	319	AGGCTGACATCTGTGACCGCGCGGACACGGCCGTACTTCTGTGCGAGGCA---TAT	374
QY	361	GGTTCTACCCCGGAATGTATTTTATGTTTGGGGTCAAGAAACCCGTGCTACGTCTCG	420
Db	375	GGGACTACCTGGGACTCTGGGGATTTGACTACGTAGGGGGCAAGAACCTGTACCGTCTCC	434
QY	421	AGGCGCTCCACCAAGGGCCCATGCGTCTTCCCTCGTGGGCGCCTCTCCAAAGACACTCT	480
Db	435	TCAAGCTCCACCAAGGGCCCATGTGCTTCCCTCGTGGGCGCCTGTCCAGGAGCACTCC	494
QY	481	GGGGGACAGCGGCGCTGGGCTGCTGTCAAGAGACTTCCCGGAACGGTGAAGGTG	540
Db	495	GAGAGCAACAGCGGCGCTGGGCTGCTGTCAAGAGACTTCCCGGAACGGTGAAGGTG	554
QY	541	TTCGGGAACTCAGGGGCGCCGAGCACAGGGCGTGCACACCTTCCGGGCTGCTCAAGTCC	600
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QY	601	TCAAGACTCTACTCCCTCAGCAGCGTGTGACCGTGGCCCTCCAGCAGCTTGGGACCCAG	660
Db	615	TCAAGACTCTACTCCCTCAGCAGCGTGTGACCGTGGCCCTCCAGCAGCTTGGGACCCAG	674
QY	661	ACCTACATCTGCAACGTGAATCACAAGCCAGCAACACCAGAGGTGGACAGAAAGTTGAG	720
Db	675	ACCTACACCTGCAACGTAGATCACAAGCCAGCAACACCAGAGGTGGACAGAAAGTTGAG	734
QY	721	CCCAAAATCTGTGACAA	737
Db	735	CGCAAAATGTTGTGCA	751

RESULT	9
LOCUS	BF663151
DEFINITION	BF663151 864 bp mRNA EST 21-DEC-2000 602145073f1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4308402 5' mRNA sequence.

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ACCESSION. BF663151
VERSION     BF663151.1  GI:11937046
KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 864)
             NIH-MGC http://mgc.nci.nih.gov/.
             National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE       Unpublished (1999)
JOURNAL     Contact: Robert Strausberg, Ph.D.
             Email: cgapbs-remail.nih.gov
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             CDNA Library Preparation: Ling Hong/Rubin Laboratory
             CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
             found through the I.M.A.G.E. Consortium/LLNL at:
             http://image.llnl.gov
             Plate: L1CM1180 row: b column: 19
             High quality sequence stop: 703.
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               /clone_1lb="NIH-MGC.48"
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               Site_2: EcoRI; CDNA made by oligo-dT priming.
               directionally cloned into EcoRI/XhoI sites using the
               following 5' adaptor: GGCACGAG(G). Size-selected >500bp
               for average insert size 1.8kb. Library constructed by Ling
               Hong in the laboratory of Gerald M. Rubin (University of
               California, Berkeley) using ZAP-cDNA synthesis kit
               (Stratagene) and Superscript II RT (Life Technologies).
               Note: this is a NIH-MGC Library."
BASE COUNT   191 a      264 c      242 g      167 t
ORIGIN
Query Match      48.7%; Score 365; DB 151; Length 864;
Best Local Similarity 75.4%; Pred. No. 1.3e-92;
Matches 494; Conservative 0; Mismatches 155; Indels 6; Gaps 3;

OY 1 ATGAAGTGGAGCTGGGTTATTTCTCTCTCTGTCAGTACGCGCGCTCCACCCAA 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 47 ATGACTGGACCTGGAGTTCTCTTTGTGTGGCAGCAGCTCAGGTCCATCCCAA 106
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 61 GTCCAACTGGTCATCCGGGCGCGGAGTCAGAAAGCCGAGCGGCTCAGTCAAGTCC 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 107 GTCCAGCTGTGTCAGCTGTGGGCTGAGTGAAAGACCCTGGGGCTCAATAAAGTCTCC 166
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 121 TGTAAAGCTAGCGGCTATATTTTCTATTTATTTGATTCATAGGCTGCGTCAGGCCCC 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 167 TGCAGAGGTTCTCGAGGACCTCCATAGTATGCAATCACTAGGGCGCCACAGGCCCT 226
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 181 GGGCAGGCGCTGGAATGATGGTGGTGAATCTTACCGGGCTGTGTAGACCGAATATACC 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 227 GCACAAAGGCTTGAAGTATGGGGGATCAGCCCTTTCTTGGAGAAGCAAACTACGCA 286
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 241 GAAATTTTAAAGACCGTGTACTATGACGCGTGCACCTTCGACTAGTACAGTATACATG 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 287 CAGAAGTTTCAGGGGAGGAGGACGACGCGCTATATTATGGCGGTTATTT---T 357
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 301 GAGCTCTCAGCGCTGATCGGAGGACGCGCGTATATTATGGCGGTTATTT---T 357
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 347 GAGGTGACACGAGCTTGAATCTGAAGACACGCGCATTTATCTAGTCCGACATCTAGGCC 406
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 358 TTTGGTTTACGCCCAATTTGATTTTGTGTTTGGGTCAAGAACCCGTGCTACGTGTC 417
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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DB 407 TATAAGCCCACTGCTACGCTTCTTGTGACGACTGGGG-CCAGAAACCTGTGTCACGTC 465
OY 418 TCGAGCGCTTCCACCAAGGGCCATCGGCTTTCCCTCGGCGCCCTCTCCAGAGCACC 477
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 466 TCTTCAGCTTCCACCAAGGGCCATCGGCTTTCCCTCGGCGCCCTCTCCAGAGCACC 525
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 478 TCTGGGGGACAGGCGCCCTGGCTGCTGTCAAGGACTACTTCCCGAACCAGGTACG 537
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 526 TCTGGGGGACAGGCGCC--TGGGCTGTGTGTCAAGGACTACTTCCCGAACCAGGTACG 583
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 538 GTGTGCGGAACATCAGGCGCCCTGCACGAGCGGCGTGCACACTTCCCGGCTGTCTACAG 597
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 584 GTGTGCGGAACATCAGGCGCCCTGCACGAGCGGCGTGCACACTTCCCGGCTGTCTACAG 643
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OY 598 TCTTCAGAGCTCTACTCTCCCTCAGCAGCGTGTGACACCGTCCCTCCAGCAGCTTGG 652
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DB 644 TCTTCAGAGCTCTACTCTCCCTCAGCAGCGTGTGACAGTGTCCCTCCAGCAGCTTGG 698
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RESULT 10
BF663258      983 bp      mRNA      EST      21-DEC-2000
LOCUS         BF663258
DEFINITION    602144377F1 NIH-MGC_48 Homo sapiens cDNA clone IMAGE:4297818 5',
mRNA sequence.
ACCESSION     BF663258
VERSION       BF663258.1  GI:11937140
KEYWORDS
SOURCE        human.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 983)
               NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-remail.nih.gov
               Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
               CDNA Library Preparation: Ling Hong/Rubin Laboratory
               CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
               DNA Sequencing by: Incyte Genomics, Inc.
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               http://image.llnl.gov
               Plate: L1CM1152 row: 1 column: 19
               High quality sequence stop: 663.
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                 directionally cloned into EcoRI/XhoI sites using the
                 following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                 for average insert size 1.8kb. Library constructed by Ling
                 Hong in the laboratory of Gerald M. Rubin (University of
                 California, Berkeley) using ZAP-cDNA synthesis kit
                 (Stratagene) and Superscript II RT (Life Technologies).
                 Note: this is a NIH-MGC Library."
BASE COUNT   212 a      297 c      296 g      177 t      1 others
ORIGIN
Query Match      48.5%; Score 364; DB 151; Length 983;
Best Local Similarity 72.1%; Pred. No. 2.6e-92;
Matches 548; Conservative 0; Mismatches 195; Indels 17; Gaps 5;

OY 1 ATGAAGTGGAGCTGGGTTATTTCTCTCTCTGTCAGTACGCGCGGCTCCACCCAA 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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ORGANISM	Homo sapiens
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
AUTHORS	Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.
TITLE	1 (bases 1 to 489)
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cepbbs-remail.nih.gov Eco RI site shown at the beginning of the sequence. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: M.B. Soares Lab cDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/MLMW at: www-bio.11n1.gov/db/ftp/image/image.html Seq primer: M13 Forward
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BASE COUNT	116 a 159 c 126 g 88 t
ORIGIN	
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Matches 420; Conservative 0; Mismatches 65; Indels 9; Gaps 1;	
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Db 5	AGGCGGATTCACCACTCCAGACAAATACAAAGAACGCGTGATCTTCAATGAACAG 64
Qy 312	CCTGGATCGGAGGACAGCGCGCTATTATTGGCGCGTATTTTGGTTCTACGCC 371
Db 65	CCTGAGAGCCGAGGACAGCGCGCTATTATTACTGTGCGAGAGGAGCAGGAGTCCGATGC 124
Qy 372	GAATTGTATTATTGATGTTGGGATCAAGAAACCTGTGCTACATGTCGAGCGCTCCAC 431
Db 125	TTTGTATCTGTGGGCGCAAGGAGCAATGGTACCGCTCTCTACGCTCCAG 175 -----TTTGTATCTGTGGGCGCAAGGAGCAATGGTACCGCTCTCTACGCTCCAG 175
Qy 432	CAAGGCGCCATCGCTCTCCCTGGCGCCCTCTCCAGAGACACCTCTGGGGGACACG 491
Db 176	CAAGGCGCCATCGCTCTCCCTGGCGCCCTCTCCAGAGACACCTCTGGGGGACACG 235
Qy 492	GGCCCTGGGCGCTCTGTCAGAGACTACTTCCCGCAACCGGTGAGCGTGTCTGGACATC 551
Db 236	AGCCCTGGGCGCTCTGTCAGAGACTACTTCCCGCAACCGGTGAGCGTGTCTGGACATC 295
Qy 552	AGGCGCCCTGACACAGGCGGTGCACACCTTCCCGGCTGCTCAAGTCTCAGACTCTA 611
Db 296	AGGCGCCCTGACACAGGCGGTGCACACCTTCCCGGCTGCTCAAGTCTCAGACTCTA 355
Qy 612	CTCCCTCAGACAGCGTGTGACCGTCCCTCCAGACAGCTTGGGACACAGACCTACATCTG 671
Db 356	CTCCCTCAGACAGCGTGTGACCGTCCCTCCAGACAGCTTGGGACACAGACCTACATCTG 415
Qy 672	CAAGCTGAATACAGAGCCCGACACACCAAGTGGACAAAGAAAGTTGAGCCCAATCTTG 731
Db 416	CAAGCTGAATACAGAGCCCGACACACCAAGTGGACAAAGAAAGTTGAGCCCAATCTTG 475

DB	732	TGACAAACTGCACA	745	0Y
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DEFINITION	602144936p1 NIH_MGC_48	Homo sapiens	CDNA clone IMAGE:4308537 5',	
ACCESSION	Bf663033		mRNA sequence.	
VERSION	Bf663033.1	GI:11936928		
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
JOURNAL	NIH-MGC http://mhc.nci.nih.gov/ .			
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) unpublished (1999)			
	Contact: Robert Strusberg, Ph.D.			
	Email: cgabs-remail.nih.gov			
	Tissue Procurement: Louis M. Staudt, M.D., Ph.D.			
	CDNA Library Preparation: Ling Hong/Rubin Laboratory			
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)			
	DNA Sequencing by: Incyte Genomics, Inc.			
	Clone distribution: MGC clone distribution information can be			
	found through the I.M.A.G.E. Consortium/LNLN at:			
	http://image.llnl.gov			
	Plate: L16CML180 row: h column: 10			
	High quality sequence stop: 703.			
FEATURES	location/Qualifiers			
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	/db_xref="taxon:9606"			
	/clone="IMAGE:4308537"			
	/clone_1ib="NIH-MGC_48"			
	/tissue_type="primary B-cells from tonsils (cell line)"			
	/lab_host="DH10B (phage-resistant)"			
	/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;			
	Site_2: EcoRI; CDNA made by oligo-dT priming.			
	Directionally cloned into EcoRI/XhoI sites using the			
	following 5' adaptor: GGCACGAG(C). Site-constructed >500bp			
	for average insert size 1.8kb. Library constructed by Ling			
	Hong in the laboratory of Gerald M. Rubin (University of			
	California, Berkeley) using ZAP-CDNA synthesis kit			
	(Stratagene) and Superscript II RT (Life Technologies).			
	Note: this is a NIH-MGC library."			
BASE COUNT	218 a 279 c 270 g 169 t			
ORIGIN				
Query Match	48.1%; Score 360.8; DB 151; Length 936;			
Best Local Similarity	74.2%; Pred. No. 2.1e-91;			
Matches 524; Conservative	0; Mismatches 172; Indels 10; Gaps 5;			
0Y	1	ATGAAGTGAAGTGGTATTTCTCTTCCTCCCTGTAAGTACGCGCGCTCCACATGCCAA	60	
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0Y	61	GTCAACTGGTGTCAATCCGCGCGGAGTCAAGAAAGCAGGGGCTCACTCAAAGTGTCC	120	
Db	101	GTTCAGCTGTGTGCTAGTCTGGGGCTAGAGTGAGGAAGCCTGGGGCCCTCATGAAGTTTCC	160	
0Y	121	TGTAAAGCTAGCGGCTATATTTTCTTCTAATTAATTGATTCATATGGGTGCGTACGCCCC	180	
Db	161	TGCAAGGCTCTTGATACACCTTCATCAGGTACTACATCATTCATTTGGGTGCGAAGGCCCT	220	
0Y	181	GGGCAAGGCTTGAATGATTTGGTGTAGATCTTACCGGGCTCTGTGTAGCACCAGATATATNC	240	
Db	221	GGACAGAGGCTTGAATACATGTGGAAATATCAACCCCTAGTAGCGGTATGTCCAAATACGCA	280	

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 20, 2001, 02:38:19 ; Search time 181.81 Seconds
(without alignments)
2590.211 Million cell updates/sec

Title: US-08-487-283a-12

Perfect score: 750
Sequence: 1 ATGACGTGAGCTGGTTAT.....GTGACAAACTCACACATTA 750

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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22: /SIDSL/gcgdata/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the total being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	750	100.0	750	16 AAT08484	Humanised 5G1.1 VH
2	737.2	98.3	750	16 AAT08487	Humanised 5G1.1 VH
3	729.2	97.2	750	16 AAT08483	Humanised 5G1.1 VH
4	561.2	74.8	750	16 AAT08482	Chimeric heavy Cha
5	505.2	67.4	2077	21 AAA11655	Humanised anti-Fas
6	495.2	66.0	8119	20 AA90575	Plasmid p6G4V1IN35
7	495.2	66.0	8119	21 AA287975	Nucleotide sequenc
8	495.2	66.0	8120	21 AAC65515	Humanised anti-IL-
9	494	65.9	2071	19 AA90080	Anti-Fas humanised
10	494	65.9	2071	21 AAA72184	DNA encoding human
11	494	65.9	2071	21 AAA11622	Humanised HFE7A de

12	492.4	65.7	2073	21 AAA11646	Humanised anti-Fas
13	490.8	65.4	2073	21 AAA11644	Humanised anti-Fas
14	490.8	65.4	2073	21 AAA11645	Humanised anti-Fas
15	490.4	65.2	8120	19 AA94956	Anti-IL-8 humanise
16	489.2	65.2	2077	19 AA90079	Anti-Fas humanised
17	489.2	65.2	2077	21 AAA72159	DNA encoding human
18	489.2	65.2	2077	21 AAA11597	Humanised HFE7A de
19	488	65.1	799	21 AA287976	Humanised anti-IL-
20	488	65.1	800	20 AA90582	Humanised anti-IL-
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22	488	65.1	801	19 AA955073	Humanised anti-IL-
23	488	65.1	927	19 AA955072	Humanised anti-IL-
24	488	65.1	927	20 AA90578	Humanised anti-IL-
25	488	65.1	927	21 AAC65508	Anti-IL-8 6G4-2-5V
26	488	65.1	927	21 AA287969	Humanised anti-IL-
27	488	65.1	6563	19 AA94953	Anti-IL-8 humanise
28	488	65.1	6563	20 AA90579	p6G4V1IN35A.F(ab')
29	488	65.1	6563	21 AAC65509	Anti-IL-8 6G4-2-5V
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31	487.8	65.0	1449	20 AA906951	Monoclonal antibod
32	487.8	65.0	1449	20 AA906952	Monoclonal antibod
33	482.8	64.4	1418	22 AA963374	Humanised 323/A3 (
34	479.2	63.9	1413	21 AA963531	DNA encoding a dim
35	478.2	63.8	1617	14 AA035039	Antibody D heavy C
36	476	63.5	9208	15 AA065629	Vector congy. TCAR
37	476	63.5	19001	19 AA961793	Target plasmid Mol
38	472.8	62.8	6072	19 AA971266	VEGF humanised ant
39	471.2	62.8	6072	19 AA963493	Fab-display antibod
40	467.4	62.3	3282	17 AA940914	DNA encoding VH re
41	467.4	62.3	3282	21 AAA31024	Modified heavy cha
42	467.4	62.3	3282	21 AAA32164	B12 Iggl preferenc
43	467.4	62.3	13254	17 AA940915	Nucleotide sequenc
44	467.4	62.3	13254	21 AAA31025	pEel2 Combo BM 12
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ALIGNMENTS

RESULT 1	
ID AAT08484	standard; DNA; 750 BP.
XX AAT08484;	
AC	
XX	
DT 02-Apr-1996	(first entry)
XX	
DE Humanised 5G1.1 VH + IGHRLC DNA.	
XX	
KM Complement C5; haemolysis; kidney; glomerulonephritis;	
KW monoclonal antibody; anti-inflammatory; antibody engineering;	
KW humanised antibody; complementarily determining region; CDR;	
KM ds.	
XX	
XX	
OS Synthetic.	
XX	
FH Key	Location/Qualifiers
FT CDS	1..750
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PN W09529697-A1.	
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PD 09-NOV-1995.	
XX	
PF 01-MAY-1995;	95WO-US05688.
XX	
PR 02-MAY-1994;	94US-0236208.
XX	
PA (ALEX-) ALEXION PHARM INC.	

XI Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;
 XI Rother RP, Springhorn J P, Squinto SP, Thomas TC;
 PI Wang Y, Wilkins JA;
 XX
 XX WPI: 1995-392923/50.
 DR P-PSDB; AAR77611.
 XX
 XX Treating glomerulonephritis with antibody against complement C5
 PT component - to inhibit complement induced cell lysis
 XX
 XX Claim 38: Page 123-125; 181pp; English.
 XX
 CC A DNA construct (AAR084483) codes for a humanised CDR-grafted and
 CC framework sequence-altered Fd 5G1.1 VH + IGHL (AAR77610), which
 CC includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1
 CC The DNA can be subcloned together with DNA (AAR08484) coding for
 CC humanised light chain (AAR77612) into vector APEX-3p (AAR08476)
 CC expression of humanised antibody in human 293 EEN cells. Such
 CC recombinant antibodies retain the ability of Mab 5G1.1 to block
 CC human Complement C5a generation and thus to reduce glomerular
 CC inflammation and kidney dysfunction associated with
 CC glomerulonephritis.
 XX
 XX Sequence 750 BP; 163 A; 220 C; 197 G; 170 T; 0 other;

Query Match	100.0%;	Score 750;	DB 16;	Length 750;
Best Local Similarity	100.0%;	Pred. No. 2e-171;		
Matches 750; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

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Db	61	gtccaactcgtgtcaatccgcgcgcgcgaagtcaagaagcgcgcgtccatgcaagaagtcc	120
QY	121	TGTAAAGCTAGGGCTATATTTTTCATATATTTGGATTTCAATGGTGGCTCAGGCCCC	180
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RESULT 2

ID AAT08487 standard; DNA; 750 BP.

AC AAT08487;

DT 02-APR-1996 (first entry)

DE Humanised 5G1.1 VH + IGHRLD DNA.

KW Complement C5; haemolysis; kidney; glomerulonephritis;

KW humanised antibody; complementarity determining region; CDR;

KE

OS Synthetic.

FH	Key	Location/Qualifiers
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100	100	100

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FT / *tag= b

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FT      /*.tag= c
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PN W09529697-A1.

PD 09-NOV-1995.

PF 01-MAY-1995; 95WO-US05688.

PR. 02-MAY-1994; 94US-0236208.

PA (ALEX-) ALEXION PHARM INC.

PI Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;

PI Wang Y, Wilkins JA;

DR WPI; 1995-392923/50.

XX

PT component - to inhibit complement induced cell lysis

PS Claim 37; Pages 135-137; 181pp; English.

CC A DNA construct (AAT08487) codes for a humanised CDR-grafted

CC CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1. The

CC for a humanised Fd (AAK77611) into vector APEX-3P (AAT08476)

CC recombinant antibodies retain the ability of Mab 5G1.1 to blo

CC inflammation and kidney dysfunction associated with

XX

SQ Sequence 750 BP; 160 A; 223 C; 198 G; 169 T; 0 other;

Query Match 98.38; Score 737.2; DB 16; Length 750;


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RESULT 4

AAT08482 ID AAT08482 standard; DNA: 750 BP.

AC AAT08482:

DT 02-APR-1996 (first entry)

XX Chimeric heavy chain 5G1.1M1 VL HUG1 DNA.

XX Complement C5; haemolysis; kidney; glomerulonephritis;

KM monoclonal antibody; antiinflammatory; antibody engineering;

KW humanised antibody; complementarity determining region; CDR;

KM chimeric antibody; Fab; ds.

XX Synthetic.

OS Key Location/Qualifiers

FT CDS 1..750

FT sig_peptide 1..57

FT mat_peptide 58..747

FT /*tag= c

PN W09529697-A1.

XX 09-NOV-1995.

XX 01-MAY-1995; 95MO-US05688.

XX 02-MAY-1994; 94US-0236208.

XX (ALEX-) ALEXION PHARM INC.

XX Evans MJ, Matlis L, Mueller EE, Nye SH, Rollins S;

PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;

XX Wang Y, Wilkins JA;

XX WPI; 1995-392923/50.

DR P-PsDB; R776609.

XX Treating glomerulonephritis with antibody against complement C5

PT component - to inhibit complement induced cell lysis

PS Claim 26; Page 116-119; 181pp; English.

XX A DNA construct (AAT08481) codes for chimeric light chain 5G1.1M1 VL

CC Huk (AAT77608), which can form the light chain portion of an anti-C5

CC The chimeric light chain includes CDRs derived from mouse anti-C5

CC monoclonal antibody 5G1.1. The DNA can be subcloned with DNA

CC (AAT08482) coding for chimeric Fd (AAT77609) into vector APEX-3p

CC (AAT08476) for prodn. of chimeric Fab in human 293 EBNA cells. Such

CC recombinant antibodies retain the ability of Mab 5G1.1 to block human

CC complement C5a generation and thus to reduce glomerular inflammation and

CC kidney dysfunction associated with glomerulonephritis.

XX Sequence 750 BP; 174 A; 226 C; 191 G; 159 T; 0 other;

Query Match 74.8%; Score 561.2; DB 16; Length 750;

Best Local Similarity 84.3%; Pred. No. 4,9e-126;

Matches 632; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

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Db      241 gaaacttcaagagacaagggccatctcagatatactcctcacaacagcctacatg
Oy      301 GACTCTCCAGCGCTGCATGGAGAGACAGCGGCTCTATATTCGGCGCTATTTT
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Db      361 ggttagcccggaatggatgtttgtgatgttggtggtcaggaacccgtgacatgctcgc
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Db      721 cccaactcttgacaaaactcacacataa

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RESULT 5

XX MO9937779-A1.
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 XX 29-JUL-1999.
 XX
 XX 19-JAN-1999; 99WO-US01081.
 XX
 XX 24-JUL-1998; 98US-0122513.
 XX 22-JAN-1998; 98US-0012116.
 XX 20-FEB-1998; 98WO-US03337.
 XX 24-JUL-1998; 98US-0121952.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Hsai V, Koumenis I, Leong SJ, Presta LG, Shahrokhi Z;
 XX Zapata GA;
 XX
 XX WPI: 1999-469134/39.
 XX
 XX New conjugates of nonproteinaceous polymers with antibody fragments,
 XX used for treating inflammatory disorders
 XX
 XX Example; Fig 48; 360pp; English.
 XX
 XX The present invention describes a novel conjugate having one or more
 XX antibody fragments covalently attached to one or more nonproteinaceous
 XX polymer molecules, where the apparent size of the conjugate is at least
 XX about 500 kDa. Conjugates of antibody fragments which bind the human
 XX interleukin (IL) 8 with a nonproteinaceous polymer can be used for
 XX treating inflammatory disorders e.g. acute lung injury, ischemic
 XX reperfusion disorder, and autoimmune diseases. They can also be used
 XX for treating e.g. inflammatory skin diseases including psoriasis and
 XX atopic dermatitis, systemic sclerosis and scleroderma, and asthmatic
 XX diseases. The conjugates can also be used as reagents in an animal
 XX model system for in vivo study of the biological functions of the
 XX antigen recognised by the conjugate. The present sequence represents
 XX the DNA sequence of the plasmid p6G4V1N35A.chosD9 from the present
 XX invention.
 XX
 XX Sequence 8119 BP; 2024 A; 2180 C; 1959 G; 1956 T; 0 other;
 XX
 XX

Query Match 66.0%; Score 495.2; DB 20; Length 8119;
 Best Local Similarity 78.9%; Pred. No. 6e-110;
 Matches 590; Conservative 0; Mismatches 158; Indels 0; Gaps 0;
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 DB 1365 gtccagctcagtgagctcgtggtgctgctgctgctgctgctgctgctgctgctgct 1424
 QY 121 TGTAAAGCTAGCGGCTATATTTTCTTAATTTGATTCATGAGTGGTGGCTGAGGCCCC 180
 DB 1425 tgtgagagcttcgtgactccttcctcgagctactatgatcactggtcgtcgaagcccg 1484
 QY 181 GGGCAGGCGCTCGATGATGGGTAGATCTTACCGGGCTCTGGTAGCCAGCATATACC 240
 DB 1485 ggtlaaggccctggaatggtgtgatatattgactcctccaagtgtgaactactgataat 1544
 QY 241 GAAATTTTAAAGACCGTGTACTATGACGGCTGACACTTCGACTAGTACTATATCATG 300
 DB 1545 caaaagttcaaggccgttcaactatctcgcgacaactccaanaaacacacatacctg 1604
 QY 301 GAGCTCTCCAGCTTCGATCGAGAGACAGCGGCTCTATTATTTGCGCTATTATTTT 360
 DB 1605 cagttgacacagcctgctgctgagacactgctcctactactgacgaagagattat 1664
 QY 361 GGTTCTACCCGGAATGCTATTTGATGTTGGGGTCAAGAACCTGTGCTACTGCTCG 420
 DB 1665 cgtacacatgtgactggtctctcgcagctcgtggtggtcaagaacctggtcaccgctcc 1724

QY 421 AGCGCTTCACCAAGGGGCCATCGCTCTCCCTCGGCGCCCTCTCCAAAGACACCTCT 480
 DB 1725 tcggccctccacaaaggccatcggtcttccctctgacacccctctccaaagacactct 1784
 QY 481 GGGGGCACAGCGGCGCTGGGCTGCTGTCAGGACTTCTCCCGAACCGGTAGCGGTG 540
 DB 1785 gggggcacagcggccctggctgcttctgtaagaactacttcccggaacccggtgagctg 1844
 QY 541 TCGTGAACCTCAGGCGGCTGACACAGGGGGTGTGACACCTTCCGGCTGTCTACAGTCC 600
 DB 1845 tcgltgaactcagcgcccgacacagcggtgacacacttcccggtctgtctcagctcc 1904
 QY 601 TCAGAGCTTACTCCCTCAGACAGCGGTGACCGCTCCAGACGCTTGGGACCCAG 660
 DB 1905 tcagagctcactccctccagcagcggtgactgtgctcctcagacttgggacccag 1964
 QY 661 ACCTACATCTGCAACGTGAATTCACAAAGCCAGCAACCAAGGTGACAAAGATTGAG 720
 DB 1965 acctacatctgcaacggtgaatcacaagccagcaacacaaagtgagaaagattgag 2024
 QY 721 CCCAAATCTTGTGACAAACTCACACAT 748
 DB 2025 cccaatcttgtgacaaactcacacat 2052
 RESULT 7
 AAZ87975
 ID AAZ87975 standard; DNA: 8119 BP.
 AC AAZ87975;
 XX 06-JUN-2000 (first entry)
 XX
 DE Nucleotide sequence of plasmid p6G4V1N35A.chosD9.
 XX
 XX Interleukin-8; IL-8; monoclonal antibody; MAb; anti-IL-8; 6G4.2.5V1N35A;
 KM inflammatory disorder; adult respiratory distress syndrome;
 KM affinity purification; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 PN US6025158-A.
 XX 15-FEB-2000.
 PD 15-FEB-2000.
 XX
 XX 20-FEB-1998; 98US-0027449.
 XX
 XX 21-FEB-1997; 97US-0038664.
 PR 22-JAN-1998; 98US-0074330.
 PA (GETH) GENENTECH INC.
 XX
 XX Presta LG, Leong SR, Gonzalez TN;
 PI WPI: 2000-181809/16.
 DR
 XX
 XX New nucleic acid molecule encodes a polypeptide which is an
 PT anti-interleukin-8 monoclonal antibody or antibody fragment useful for
 PT the production of anti-interleukin-8 monoclonal antibodies or fragments
 PT
 PS Examples; Fig 48A-Z; 188pp; English.
 XX
 XX The invention relates to an anti-interleukin-8 (IL-8) monoclonal antibody
 CC (MAb). The anti-IL-8 MAb comprises a sequence containing the CDRs
 CC (complementarity determining regions) of the humanized anti-IL-8
 CC 6G4.2.5V1N35A light chain; and amino acids 24-253 of the humanized
 CC anti-IL-8 6G4.2.5V1N35A heavy chain. The anti-IL-8 MAb and fragments
 CC can be used in diagnosis, for affinity purification of IL-8 from
 CC recombinant cell culture or natural sources and for the treatment of
 CC inflammatory disorders e.g. adult respiratory distress syndrome. Nucleic


```

QY 421 AGCCCTCCACCAAGGCCATCGGTCTCCCTCGGCGCCCTCTCCAGAGCACCTCT 480
    |||||||
Db 1726 tcggcctccaccaggccatcggtctccctcgacacctctccagagcaacctct 1785
QY 481 GGGGGCAGCGGCGCTCGGTCTCGGTCAAGAGCTACTTCCCGAAGCGGTGACGCTG 540
    |||||||
Db 1786 gggggcagcgccctggtctgctcaagagactctcccgaaacggtgacggtg 1845
QY 541 TCGTGGAAGTACGCGCGCTGACGCGCGGTGACACCTTCCGCGTGTCTACAGTCC 600
    |||||||
Db 1846 tcggtgaactcagcgccctgacccgagcggtgtgcaacctctccgctgctcaagttcc 1905
QY 601 TCAGGACTTACTCTCCGACGCGGTGTGACCGGTCCCTCCAGAGCTTGGGCAACCCAG 660
    |||||||
Db 1906 tcagagcttactctccctcagcagcggtgtgactgtgacctcagcagcttggtgcaacccag 1965
QY 661 ACCATCATCTGCAACGTATATCACAAGCCGACAGCACCAGAGGTGACAGAAAGTTGAG 720
    |||||||
Db 1966 acctacatctgcaacgltgatacagaaccgcaaccagaagtgacagaagaagttgag 2025
QY 721 CCCAATCTTGTGACAAACTACACAT 748
    |||||||
Db 2026 cccaatctgtgacaaactcacat 2053

RESULT 9
AAV70080
ID AAV70080 standard; DNA; 2071 BP.
XX
AC AAV70080;
XX
DT 15-MAR-1999 (first entry)
XX
DE Anti-Fas humanised antibody HFE7A heavy chain DNA.
XX
KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
KW systemic lupus erythematosus; graft versus host disease;
KW Sjogren syndrome; pernicious anaemia; Addison's disease;
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
KW rheumatoid arthritis; autoimmune haemolytic anaemia;
KW myasthenia gravis; multiple sclerosis; Basedow's disease;
KW thrombopenia purpura; insulin-dependent diabetes; allergy;
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
KW transplant rejection; therapy; ds.
XX
XX Homo sapiens.
OS Synthetic.
FH
XX Key CDS
    Location/Qualifiers
    21..2039
    FT /*tag= a
    FT /note= "contains introns"
    FT 21..77
    FT /*tag= b
    FT 1..735
    FT /*tag= c
    FT /number= 1
    FT /codon_start= 21
    FT 736..1126
    FT /*tag= d
    FT /number= 1
    FT 1127..1171
    FT /*tag= e
    FT /number= 2
    FT 1172..1289
    FT /*tag= f
    FT /number= 2
    FT 1290..1619
    FT /*tag= g
    FT /number= 3
    FT 1620..1716
    FT Intron

```

```

FT FT /*tag= h
FT FT /number= 3
FT FT 1717..2071
FT FT /*tag= 1
FT FT /number= 4
XX
PN AU9859701-A.
XX
PD 08-OCT-1998.
XX
PF 30-MAR-1998; 98AU-0059701.
XX
PR 08-OCT-1997; 97JP-0276064.
PR 01-APR-1997; 97JP-0082953.
PR 25-JUN-1997; 97JP-0169088.
XX
PA (SANT ) SANKYO CO LTD.
PI Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
XX
DR MPI; 1998-543440/47.
DR P-PSDB; AAW83037.
XX
PS Claim 27; Page 223-225; 292pp; English.
XX
CC This nucleotide sequence codes for the HV type humanised heavy
CC chain (see AAW83037) of murine anti-human Fas monoclonal antibody
CC HFE7A. It was prepared from plasmid pGHS17A62 (see AAV70079) by
CC PCR amplification (see AAV70115-17), and includes humanising R44G
CC and A76T amino acid substitutions. Host cell Escherichia coli
CC pGHPDHV3 SANK 70298 harbors plasmid pGHPDHV3 carrying a fusion
CC fragment of the humanised HV type HFE7A heavy chain and DNA
CC encoding human IgG1 constant region, and is deposited as
CC FERM BP-6273 (claimed). The invention provides methods for
CC producing humanised antibodies by culturing host cells. Humanised
CC versions of HFE7A (see AAW83031-37), like native HFE7A, are capable
CC of inducing apoptosis in abnormal cells expressing Fas, and of
CC inhibiting Fas-induced apoptosis in normal cells. The humanised
CC antibodies are used to evaluate, in animal models, treatments of
CC diseases that involve Fas/Fas ligand interactions, and also to
CC treat such diseases, including autoimmune disease (e.g. systemic
CC lupus erythematosus, Hashimoto's disease, graft versus host disease,
CC Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,
CC Goodpasture syndrome, Crohn's disease, rheumatoid arthritis,
CC autoimmune haemolytic anaemia, sterility, myasthenia gravis,
CC multiple scleritis, Basedow's disease, thrombopenia purpura and
CC insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).
XX
SO Sequence 2071 BP; 460 A; 685 C; 561 G; 365 T; 0 other;

Query Match 65.9%; Score 494; DB 19; Length 2071;
Best Local Similarity 81.5%; Pred. No. 8,7e-110;
Matches 585; Conservative 0; Mismatches 130; Indels 3; Gaps 1;

```

Db 141 tgcgaagctcttcggtacacccctaccagctatgcatgagtggtgtaaacagggccct 200
 Oy 181 GGGCAGGCGCTGGAAATGATGGGTGATCTTACCGGGCTCTGTAGCACGGAATATACC 240
 Db 201 ggacaaggctcttgatggtggaagatgatgacctctctgatactataactataaat 260
 Oy 241 GAAATTTTAAAGACCGGTGTACTATGACCGGTGACACTTCCGCTACTACTATACATG 300
 Db 261 caaaagttcaaaagggcaagccatgactgtgacacatccactagcacagcctaatg 320
 Oy 301 GAGCTCTCAGGCTGGATCGGAGACAGCGCGCTATATTATGCGGGCTTTATTTT 360
 Db 321 gagctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 377
 Oy 361 GGTCTAGCCGCAATTTGATTTTGGGTGCAAGAAACCTGTGCTGCTG 420
 Db 378 gactatagtaaacacactgactcgtatgctggtggaagagcctgtcacacgtctcc 437
 Oy 421 AGCGCTCCACCAAGGCGCCATGCTTCCCTGGCGCTCTCCACAGACACTCT 480
 Db 438 tcagcctccaccaaaggccatcgtctccctctgcaacccctcccaagagcactct 497
 Oy 481 GGGGACAGCGGCGCTGGGCTGCTGCTCAAGAGACTTCCCGAAGCGGTAGCGTG 540
 Db 498 gggggacagcggccctggcctgagcagcagcagcagcagcagcagcagcagcagc 557
 Oy 541 TCGTGGAACCTCAGGCGCGCTGACAGCGGCGGTGACACTTCCCGCTGCTCAAGTCC 600
 Db 558 tcgtggaactcagcggcctgacacagcggcgtgacacactcccgctgtctcaactcc 617
 Oy 601 TCAGACTCTACTCCTCAGACAGCGGTGACCGTCCCTCCAGACCTTGGGACCCAG 660
 Db 618 tcagagctctactccctcagcagcgtgtagccgttccctcagcagcgttggcaccag 677
 Oy 661 ACCTACATCTGCAAGTGATCACAAGCCAGACACCAAGGTGAGCAAGATTG 718
 Db 678 acctacatctgacagtgatcaccaagccagacacacaaagtgagcaagagatcg 735

RESULT 10

AAA72184
ID AAA72184 standard: DNA; 2071 BP.

XX AAA72184;

XX 24-NOV-2000 (first entry)

XX DNA encoding humanised anti-Fas antibody heavy chain, SEQ ID NO:116.

XX Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;

KM murine; humanised antibody; complementarity determining region: CDR;

KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;

KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;

KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;

XX hepatitis; AIDS; graft rejection; heavy chain: ds.

OS Chimeric - Mus musculus.

XX Chimeric - Homo sapiens.

XX JP2000169393-A.

XX 20-JUN-2000.

XX 30-SEP-1999; 99JP-0278301.

XX 30-SEP-1998; 98JP-0276883.

XX (SANY) SANKYO CO LTD.

XX WPI: 2000-485645/43.

XX P-PSDB: AAB14779.

XX Preventive or treating agent for the diseases caused by an abnormality

PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 PT anti-Fas antibody
 XX
 PS Example 22; Page 106-108; 139pp; Japanese.

CC The invention relates to compositions for the prevention of treatment
 CC or diseases caused by an abnormality in the Fas/Fas ligand system
 CC containing an anti-Fas antibody as the active component. The anti-Fas
 CC antibody is either the murine-anti-human Fas monoclonal antibody HFE7A,
 CC or a humanised version of HFE7A containing identical CDRs
 CC (complementarity determining regions) to antibody HFE7A. Via its
 CC interaction with Fas, the antibody of the invention acts as a modulator
 CC of apoptosis. The compositions of the invention may therefore be used in
 CC the treatment or prevention of conditions such as autoimmune diseases,
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 CC and organ graft rejection. Sequences AAA72146, AAA72159 and AAA72184
 CC represent DNA encoding the heavy chains (or fragments thereof) of
 CC various humanised HFE7A-derived anti-Fas antibodies.

Sequence 2071 BP; 460 A; 685 C; 561 G; 365 T; 0 other;

Query Match 65.9%; Score 494; DB 21; Length 2071;
 Best Local Similarity 81.5%; Pred. No. 8.7e-110;
 Matches 585; Conservative 0; Mismatches 130; Indels 3; Gaps 1;

Oy 1 ATGAAGTGAGACTGGGTATTTCTCTCTCTGATGAATGAGCGGCGCTCAATCCAA 60
 Db 21 atggatggagctgtatctatctctctctgtgtagcaaacagctacagtgctccacttaag 80
 Oy 61 GTCCAACTGTGTCATCCGCGCGAGGTGCAAGAACCCAGGCGCTCAATGCTGC 120
 Db 81 gtccaactgtgtagctctggtggtcaggaagcctcgggctcagtgaggtgtcc 140
 Oy 121 TGTAAAGCTACGCGCTATATTTTCTTAATTGATGATCAATGGGTGCTGACGCCCC 180
 Db 141 tgcgaagctcttgctacacccctcagcagcagcagcagcagcagcagcagcagc 200
 Oy 181 GGGGAGGCGCTGGAATGATGGGTGATCTTACCGGCTCTGAGACCGCAATATACC 240
 Db 201 ggaacagggccttgatgtagatgtagatgtagatgtagatgtagatgtagatgtagat 260
 Oy 241 GAAATTTTAAAGACCGGTGTACTATGACGCGTGCACACTTGCATGATGATATACATG 300
 Db 261 caaaagttcaaaagggcaagccatgactgtagacacatccactagcagcagcactaag 320
 Oy 301 GAGCTCTCAGCCTGCGATCGGAGACAGCGCGCTCTATTATGCGCGCTTATTTT 360
 Db 321 gactcagcagcctgagatcagagcagcagcagcagcagcagcagcagcagcagc 377
 Oy 361 GGTCTACCGCGAATTTGATTTTGGGTGCAAGAACCGTCTGCTGCTGCTG 420
 Db 378 gactatagtaaacacactgactcgtatgctggtggaagaggaacccgtgtacacgtctcc 437
 Oy 421 AGCGCTCCACCAAGGCGCATCGGTCTTCCCGTGGCGCCCTCTCCAGACACTCT 480
 Db 438 tcagcctccaccaaaggccatcgtctccctcctggaacccctcccaagaagacccct 497
 Oy 481 GGGGACAGCGGCGCTGGGCTGCTGCTGCAAGACTACTTCCGAAACGGTGACGCTG 540
 Db 498 gggggacagcggccctggcctgagcagcagcagcagcagcagcagcagcagcagc 557
 Oy 541 TCGTGGAACCTCAGGCGCGCTGACAGCGGCTGACACTTCCCGCTGCTCAAGTCC 600
 Db 558 tcgtggaactcagcggcctgacacagcggcgtgacacactcccgctgtcttaagtc 617
 Oy 601 TCAGACTCTACTCCTCAGACAGCGGTGACCGGCTCCAGACAGTGGGACCCAG 660
 Db 618 tcaggaactctactccctcagcagcgtgtagccgtgctccacagagcttgggaccag 677
 Oy 661 ACCTACATCTGCAAGTGATCACAAGCCAGACACCAAGGTGAGCAAGATTG 718

Db	678	acctcactctgcaacgtgatcacaagcccaagcaacccaaggtgtgacaagagatgtg	735
		RESULT 11	
ID	AA11622	AA11622 standard; DNA; 2071 BP.	
AC	AA11622;		
XX			
DT	08-AUG-2000	(first entry)	
XX			
DE	Humanised HFE7A designed heavy chain DNA #2.		
XX			
KW	Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;		
KW	anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;		
KW	dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;		
KW	neurotropic; antinfertility; neuroprotective; antiarteriosclerotic;		
KW	hepatotropic; humanized; apoptosis; systemic lupus erythematosus;		
KW	Hashimoto disease; rheumatoid arthritis; graft versus host disease;		
KW	Strogen's syndrome; anemia; Addison's disease; scleroderma; sterility;		
KW	Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;		
KW	multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;		
KW	insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;		
KW	cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection; ss.		
XX			
OS	Synthetic.		
XX			
PN	EP990663-A2.		
XX			
PD	05-APR-2000.		
XX			
PF	29-SEP-1999; 99EP-0307711.		
XX			
PR	30-SEP-1998; 98JP-0276881.		
PR	30-SEP-1998; 98JP-0276882.		
XX			
PA	(SANY) SANKYO CO LTD.		
XX			
PI	Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;		
DR	WPI: 2000-258930/23.		
XX			
PT	P-PSDB; AAM90929.		
XX			
XX	New humanized anti-Fas antibody, useful for treating or preventing e.g.		
XX	inflammatory or autoimmune disease; induces apoptosis selectively in		
XX	cells with abnormal Fas-Fas ligand systems		
XX			
XX	Example reference 22; Page 148-150; 263pp; English.		
XX			
XX	This invention describes a novel humanized anti-Fas antibody-like		
XX	molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas		
XX	ligand system, by binding to Fas on the cell surface, and prevents		
XX	apoptosis in cells with a normal system, by inhibiting binding between		
XX	Fas and its ligand. The products of the invention have anti-inflammatory,		
XX	anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,		
XX	immunomodulatory, dermatological, immunosuppressive, thyromimetic,		
XX	antirheumatic, neurotropic, antinfertility, neuroprotective,		
XX	antiarteriosclerotic, cardiant and hepatropic activity. (I) induce		
XX	apoptosis by binding to cell surface Fas or inhibit it by competitive		
XX	inhibition of ligand binding. (I) are used to treat and/or prevent		
XX	diseases associated with the Fas/Fas ligand system, especially systemic		
XX	lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft		
XX	versus host disease, Strogen's syndrome, pernicious or hypoplastic		
XX	anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's		
XX	disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,		
XX	multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin		
XX	dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,		
XX	cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral		
XX	(B, C or D) or alcoholic), and transplant rejection. (I) selectively		
XX	inhibit apoptosis in normal cells but selectively induce it in abnormal		
XX	cells. They bind to both human and murine Fas, so can be evaluated in		
XX	murine disease models. (I) act on the active site of Fas, i.e. they mimic		
XX	the native ligand, do not induce liver disease, and have reduced risk of		

Db	83	gtccacactggtgcagctctggtggtgcgaagaagccttgggtcttcagtgaaaggtgtcc	142
Oy	121	tcgtaaagctagcggctatatttttttctaatatttgattcaatggctcgtacagccccc	180
Db	143	tgcgaagctcttgctacacaccttaccacgaactactgtagtgcagtgacagagccctc	202
Oy	181	ggcgagggcgcttgaaatngatnggttgagatctttaccgggcctctggtaccacgaattatacc	240
Db	203	ggacaaagaccttgatgtagatggagatgatgacctctgatactatactataactataac	262
Oy	241	gaaataatttttaagaccgctgttactatagacgcgcgtgacaccttcgactagtagatatacatg	300
Db	263	caaaagttcaaaagggcaagagccacattgactgtatgacacatccactgagcagaagctaatg	322
Oy	301	gagcttccagcctcgccgattcgagagacacggccgctctattatttgccggcgttatattttttt	360
Db	323	gagctcagcagcctgagatctgagacacagcggtctattactgtgcagaanaa---taag	379
Oy	361	ggtttcagccccaatttgatatttttgatgtttgggggttcanaagaaacctggtcactgctgc	420
Db	380	gactaagtaaacaaactgtagtactgtagtctggtggccaaagtaacactgtgtacacgctcc	439
Oy	421	acgcgctccaccaaagggcccatcggtcttcccccctggcgcctctccacagacacctct	480
Db	440	tcagctctccaccaaagggcccatcggtcttcccccctggcgcctctccacagacacctct	499
Oy	481	gggggcacagcggccctgggctgcctggttcacagactacttcccccgaacccggtgacggtg	540
Db	500	ggggggacagcgccctggtgctgctgctgtaagaactacttccccgaacccggtgagcggtg	559
Oy	541	tgcgtgaactcagagggccctcgacacaggggtgacacaccttccggctgtgtcnaagctgc	600
Db	560	tcgttgtaactcagcgccctgacacagcggtgacaaaccttcccggtctgtccaaagctcc	619
Oy	601	tcagacactgtacctccctcagacagcgtggtatccgctgcctccagacacttggggacaccag	660
Db	620	tcagagctctacctccctcagcagcggtgtagccggtgcctccagcaagctgtgggacaccag	679
Oy	661	acctacatctgcacagctgaattcacaagcccgacacacccaaggtggacaaagaattgtg	718
Db	680	acctacatctgcacagctgaattcacaagcccgacacacccaaggtggagacaagagtgtg	737

RESULT 13

AA11644	AA11644 standard; DNA; 2073 BP.
XX AC	AA11644;
XX	AA11644;
XX	08-AUG-2000 (first entry)
DE	Humanised anti-Fas designed heavy chain Hcu 1 DNA.
XX	Fas: antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
XX	anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant;
XX	neurotrophic; immunosuppressive; thymomelic; antirheumatic; anti-Fas;
XX	neurotrophic; antifertility; neuroprotective; antileukosclerotic;
XX	hepatotropic; humanised; apoptosis; systemic lupus erythematosus;
XX	Hashimoto disease; rheumatoid arthritis; graft versus host disease;
XX	Strogen's syndrome; anemia; Addison's disease; scleroderma; sterility;
XX	Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
XX	multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
XX	insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
XX	cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection; ss.
OS	Synthetic.
XX	EP990663-A2.
XX	05-APR-2000.
PD	
XX	29-SEP-1999; 99EP-0307711.

XX 30-SEP-1998; 98JP-0276881.
PR 30-SEP-1998; 98JP-0276882.
XX (SANY) SANKYO CO LTD.
XX Serizawa N, Hanyama H, Nakahara K, Tamaki I, Takahashi T;
PI WPI: 2000-258930/23.
DR P-PSDB; AAW90933.
XX
PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT inflammatory or autoimmune disease, induces apoptosis selectively in
PT cells with abnormal Fas-Fas ligand systems
XX
PS Claim 33; Page 166-168; 263pp; English.
XX
CC This invention describes a novel humanized anti-Fas antibody-like
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
CC antineumatic, nephrotoxic, antifertility, neuroprotective,
CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (II) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC cells. They bind to both human and murine Fas, so can be evaluated in
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC the native ligand, do not induce liver disease, and have reduced risk of
CC inducing a human anti-murine antibody response. This sequence encodes
CC a humanised anti-Fas antibody heavy chain construct designated Heu 1
CC which is described in the method of the invention.
XX
SQ Sequence 2073 BP; 462 A; 685 C; 559 G; 367 T; 0 other;

Query Match 65.4%; Score 490.8; DB 21; Length 2073;
Best Local Similarity 81.2%; Pred. No. 5.1e-109;
Matches 583; Conservative 0; Mismatches 132; Indels 3; Gaps 1;

QY 1 ATGAGTGGAGCTGGGTTATCTTCTCTGTCAGTAATGCGGCGTCACATCCCAA 60
DB 23 atggagtgagcgtatcatctctctcttgtagcaacagctacagtgctcatctcag 82
QY 61 GTCACATCTGTCAGTCCGGCGCGAGGTCAAGAACCCAGGCGCTCGTAAATGTCC 120
DB 83 gtccaactgtgcagctctgagtgagtgcaagaagcttgggtctcagtgaaagtgtcc 142
QY 121 TGTAAAGCTAGCGGCTATATTTTCTTAATTATGAGTTCAATGGGTGCGTACAGGCCCC 180
DB 143 ttcgaagctcttgctacaccttcaccagctacgtatgagtgtaaaacaggccct 202
QY 181 GGGCAGGGCTGGAATGGATGGGTGAGATCTTACCGGCTCTGGTAGCAGCAATATACC 240
DB 203 ggcacaggaacttgatgtgagagatgatcctcttcgtatgatacctaacaacat 262
QY 241 GAAATTTTAAAGACGTTTACTAGTACGGCGTGCACACTGACAGTACATATACATG 300
DB 263 caaaagtccaagggcaagccacatgtactgtagacacatccacagcagccactatg 322
QY 301 GAGCTCTCAGCCTGCGATCGAGACACGGCCGTATATATGCGCGCTTATTTT 360

DB 323 gagctcagcagcctgagatctgagacacgycgtctattactgtgcaagaa---tagg 379
QY 361 GGTTCAGCCCCAGATGTGATTTTGTATTGGGTCAGAGAACCTGTGCATGTCCTG 420
DB 380 gactatagtaaacacgtactcgatgtctggtgccaaggtatcacctgtctcc 439
QY 421 AGCGCTTCACCAAGGGCCATGCGTTCCTCCCTGGCGCCCTCTCAAGACACCTCT 480
DB 440 tcagctccaccaagggcccatctgctctcccttgacacctctcccaagacacctt 499
QY 481 GGGGACACAGCGCCCTGGGCTGCTGTCACAGACTACTTCCCGACCGGTGACGCTG 540
DB 500 gggggacagcagcgcccttggtcgtcgtgcaagactacttcccgacagcgagctg 559
QY 541 TCGTGAATCTAGCGCCCTGACACCGCGCTGACACCTTCCCGGTCTCTACAGTTC 600
DB 560 tcgtggaactcagcgccctgaccagcgctgacaccttccggtcttctacagctc 619
QY 601 TCAGGACTTACTCCCTCAGACGCTGTGACCGTCCCTCCAGAGCTTGGGACCCAG 660
DB 620 tcaggaacttactcccttcagcagcgctgtgacccgtgctcctcagcagcttgagcccg 679
QY 661 ACCTACATCTGCAACGTGAATCAACAAGCCCGACACCAAGGTGACAGAAAGTTG 718
DB 680 acctacatctgcaagctgatatcacaagccacagacacacagtgagcaagagtgtg 737

RESULT 14
AA11645
ID AA11645 standard; DNA; 2073 BP.
AC AA11645;
XX 08-AUG-2000 (first entry)
DE Humanised anti-Fas designed heavy chain Heu 2 DNA.
XX
KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
KW dermatological; immunosuppressive; thyromimetic; antineumatic; anti-Fas;
KW nephrotoxic; antifertility; neuroprotective; antiarteriosclerotic;
KW hepatropic; humanized; apoptosis; systemic lupus erythematosus;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection; ss.
OS Synthetic.
XX
PN EP990663-A2.
PD 05-APR-2000.
XX
PE 29-SEP-1999; 99EP-0307711.
XX
PR 30-SEP-1998; 98JP-0276881.
PR 30-SEP-1998; 98JP-0276882.
XX
XX (SANY) SANKYO CO LTD.
PI Serizawa N, Hanyama H, Nakahara K, Tamaki I, Takahashi T;
XX WPI: 2000-258930/23.
DR P-PSDB; AAW90934.
XX
PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT inflammatory or autoimmune disease, induces apoptosis selectively in
PT cells with abnormal Fas-Fas ligand systems
XX
PS Claim 34; Page 172-174; 263pp; English.

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 20, 2001, 02:35:04 ; Search time 86.76 Seconds
(without alignments)
1636.507 Million cell updates/sec

Title: US-08-487-283A-12

Perfect score: 750
Sequence: 1 ATGACGTGAGCTGGTTAT.....GTGACAAACTCACACATAA 750

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA.*

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6: /cgn2_6/ptodata/2/ina/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	495.2	66.0	8120	3	US-09-027-449-68 Sequence 68, Appl
2	495.2	66.0	8120	3	US-09-026-985-68 Sequence 68, Appl
3	488	65.1	800	3	US-09-027-449-69 Sequence 69, Appl
4	488	65.1	800	3	US-09-026-985-69 Sequence 69, Appl
5	488	65.1	927	3	US-09-027-449-59 Sequence 59, Appl
6	488	65.1	927	3	US-08-804-444A-59 Sequence 59, Appl
7	488	65.1	927	3	US-09-026-985-59 Sequence 59, Appl
8	488	65.1	6563	3	US-09-027-449-61 Sequence 61, Appl
9	488	65.1	6563	3	US-08-804-444A-61 Sequence 61, Appl
10	488	65.1	6563	3	US-09-026-985-61 Sequence 61, Appl
11	478.2	63.8	1617	2	US-08-378-939-9 Sequence 9, Appl
12	476	63.5	9209	1	US-08-149-099C-3 Sequence 3, Appl
13	476	63.5	9209	1	US-08-476-275-2 Sequence 2, Appl
14	476	63.5	9209	2	US-08-478-967A-3 Sequence 3, Appl
15	476	63.5	18986	2	US-08-819-866-2 Sequence 2, Appl
16	476	63.5	18986	2	US-09-023-715-2 Sequence 2, Appl
17	467.4	62.3	3282	1	US-08-276-852-154 Sequence 154, App
18	467.4	62.3	3282	1	US-08-276-852-154 Sequence 154, App
19	467.4	62.3	3282	1	US-08-899-575-154 Sequence 154, App
20	467.4	62.3	3282	1	US-08-899-575-154 Sequence 154, App
21	467.4	62.3	3282	1	US-08-899-575-154 Sequence 154, App
22	467.4	62.3	3282	1	US-08-899-575-154 Sequence 154, App
23	467.4	62.3	3282	5	PCT-US95-08743-154 Sequence 154, App
24	467.4	62.3	13254	1	US-08-276-852-156 Sequence 156, App
25	467.4	62.3	13254	1	US-08-276-852-156 Sequence 156, App
26	467.4	62.3	13254	1	US-08-276-852-170 Sequence 170, App
27	467.4	62.3	13254	1	US-08-899-575-156 Sequence 156, App

28	467.4	62.3	13254	1	US-08-899-575-170 Sequence 170, App
29	467.4	62.3	13254	1	US-08-899-575-156 Sequence 156, App
30	467.4	62.3	13254	1	US-08-899-575-170 Sequence 170, App
31	467.4	62.3	13254	5	PCT-US95-08743-156 Sequence 156, App
32	467.4	62.3	13254	5	PCT-US95-08743-170 Sequence 170, App
33	462.4	61.7	2143	4	US-09-097-309-5 Sequence 5, Appl
34	462.4	61.7	2143	4	US-09-097-171A-9 Sequence 9, Appl
35	462.4	61.7	6550	4	US-09-422-712B-1 Sequence 1, Appl
36	461.2	61.5	1655	3	US-09-049-612A-21 Sequence 21, Appl
37	459.6	61.3	762	1	US-08-398-613A-57 Sequence 57, Appl
38	459.6	61.3	762	1	US-08-398-612A-57 Sequence 57, Appl
39	459.6	61.3	762	1	US-08-398-611A-57 Sequence 57, Appl
40	459.6	61.3	762	1	US-08-396-851A-57 Sequence 57, Appl
41	459.6	61.3	762	2	US-08-491-334A-57 Sequence 57, Appl
42	459.6	61.3	762	3	US-09-027-449-43 Sequence 43, Appl
43	459.6	61.3	762	3	US-08-804-444A-43 Sequence 43, Appl
44	459.6	61.3	762	3	US-09-026-985-43 Sequence 43, Appl
45	453.8	60.5	2178	1	US-08-463-587A-24 Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-09-027-449-68
Sequence 68, Application US/09027449
Patent No. 6025158
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 8120 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-09-027-449-68
Query Match 66.0%; Score 495.2; DB 3; Length 8120;


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Db 1401 CTTCTCAGATCACTATATGACATGGGTCCGTGACAGGCCCGGGTAAGGGCTTGGATGGGT 1460
QY 201 GGGGAGATCTTACCGGGCTCTGGTAGACACCAATATACCGAAATTTTAAAGACCGGTGT 260
Db 1461 TGGATATATTGATCTCCCAATGGTGAAGAACTGCTATATATCAAAAGTTCAGGGCCGTTT 1520
QY 261 TACATATGACGGGTGACCTTGTGACTAGTACATATACATGAGAGCTCTCCAGCTGGGATC 320
Db 1521 CACTTATCTCGCAGCACTCCAAACACACACATCTGCAAGATGACACCTGCGTGC 1580
QY 321 GGAGGACACGGCCGCTTATATATGCGCGCTTATTTTGGTGTAGCCCAATGGTA 380
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QY 381 TTTTGTATTTGGGGTCAAGAAACCTTGCTGCTGAGCGCCCTCCACCAAGGGCC 440
Db 1641 CTTGAGCTCTGGGGTCAAGAAACCTTGCTGCTGAGCGCCCTCCACCAAGGGCC 1700
QY 441 ATGGGCTCTCCCGGGGGCCCTCTCCAGAGACCTCTGGGGGACAGCGGCCCTGGG 500
Db 1701 ATCGGCTCTCCCGGGGGCCCTCTCCAGAGACCTCTGGGGGACAGCGGCCCTGGG 1760
QY 501 CTGCTGTGTCAGGACTACTTCCCGGAACCGGTGACGGTGTGTTGGAATCAGCGCCCT 560
Db 1761 CTGCTGTGTCAGGACTACTTCCCGGAACCGGTGACGGTGTGTTGGAATCAGCGCCCT 1820
QY 561 GACCAAGCGGCTGACACCTTCCGGCTGTCTTACAGTCTCAGAGACTTACTCCCTAG 620
Db 1821 GACCAAGCGGCTGACACCTTCCGGCTGTCTTACAGTCTCAGAGACTTACTCCCTAG 1880
QY 621 CAGGCTGTGACCGTCCCTCCAGAGCTTGGGGACCCGAGACTTATCTGCAAGCTGAA 680
Db 1881 CAGGCTGTGACCGTCCCTCCAGAGCTTGGGGACCCGAGACTTATCTGCAAGCTGAA 1940
QY 681 TCACAAGCCGACCAACACCAAGGTGACAGAAAGTTGAGCCCAATCTTGGACAAAAC 740
Db 1941 TCACAAGCCGACCAACACCAAGGTGACAGAAAGTTGAGCCCAATCTTGGACAAAAC 2000
QY 741 TCACACAT 748
Db 2001 TCACACAT 2008

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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9681
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 6563 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
US-08-804-444a-61

Query Match          65.1%; Score 488; DB 3; Length 6563;
Best Local Similarity 79.4%; Pred. No. 1.2e-117;
Matches 578; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY 21 TCTCTTCTCTCTCTCACTAGTACTGCGGCGCTCCACTCCCAAGTCACATGGTCAATCCG 80
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QY 81 CGCCGAGTCAAGAAAGCCAGGGGCTCAGTCAAGTGTCTGTAAAGCTTAGCGCTATAT 140
Db 1341 CGGTGGCCTGTGACAGCCAGGGGCTCAGTCCGTTTGTCTGTCACACTTCTGCTACTC 1400
QY 141 TTTTCTATTTATTTGATTTAATGAGTGCCTCAGAGCCCCCGGGGAGGGCTTGAATGAT 200
Db 1401 CTTCTCAGTCACTATATATGACGTGCTCAGGCGCCGGGTAAAGGCTTGAATGGGT 1460
QY 201 GGGTGAATCTTACCGGGGCTGTGTAGTACACCGAATATACGAAATTTTAAAGACGCTG 260
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QY 261 TACTATGACCGTGCACACTTGCATAGTATACATGAGAGCTGTCACGCTGCGATC 320
Db 1521 CACTTTATCTCGGACAGACGCCAAACACAGCATCTGAGATGAAAGCGCTGCTGC 1580
QY 321 GAGAGACAGCGCGCTTATATGCGCGCTTATTTTGGTGTCTAGCCCGAATGGTA 380
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QY 441 ATCGGCTTCCCGCTGCGGCTCTCTCAAGAGACCTCTGGGGGACAGGGGCTGGG 500
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QY 501 CTGCTGTGTCAGGACTACTTCCCGGAACCGGTGACGGTGTCTGGAATCAGGGCCCT 560
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QY 621 CAGGCTGTGACCGTCCCTCCAGAGCTTGGGGACCCGAGACTTATCTGCAAGCTGAA 680
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QY 741 TCACACAT 748
Db 2001 TCACACAT 2008

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RESULT 10
US-09-026-985-61
; Sequence 61, Application US/09026985
; Patent No. 6133426

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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 18986 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-819-866-2
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Best Local Similarity 78.2%; Pred. No. 2.2e-114;
Matches 385; Conservative 0; Mismatches 160; Indels 3; Gaps 1;

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Db 9553 TGCAAGCTTCTGGCTACACATTTACCAATATGACATGAGTAAACAGACACCT 9612
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QY 241 GAAATTTTAAAGACCGTGTACTATGACGCGGTGACACTGTGACTAGTACAGTATACATG 300
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Db 9733 CAGCTCAGCACTGACATCTGAGGACCTGCGCTATTAATGCAAGATGCACTT-- 9790
QY 361 GGTCTAGCCCGAATGTGATTTGATGTTGGGGTCAAGGAACCTGGTCACTGCTCG 420
Db 9791 -ACTACGGCGGTGACTGTACTTCAATGTCTGGGGCGCAGGACCAAGCTCCTCT 9849
QY 421 AGCGCTTCACCAAGGGCCATCGGCTTCCCTGGGCGCTCTCCCAAGACACTCT 480
Db 9850 GCACGTAGCAACCAAGGGCCATCGGCTTCCCTGGGCACTCTCCCAAGACACTCT 9909
QY 481 GGGGGCACAGCGCGCTGGGCTGCTGTCAAGACTCTTCCCGAACCAGGTGAGGTG 540
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Date: Jul 19, 2001 7:55 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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-GAPEXT=4.000 -MINMATCH=0.100 -LOOPECL=0.000 -LOOPEXT=0.000
-GAPOP=4.500 -GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FCAPOP=6.000 -FCAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blsum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NOM=ext -MILEN=0 -MAXLEN=200000000
-USPR=US08487283_@CGML1_107 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPRX
-WAIT -THREADS=1

Search information block:

Query: US-08-487-283a-12_COPY_58_423
Query length: 366
Database: PIR_68: *
Database sequences: 219241
Database length: 76174552
Search time (sec): 31.370000

Sequence	Strd Orig	ZScore	Escore	Len	Documentation
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PIR2:S36265	472.00	816.55	1.5e-37	118	Ig heavy chain V region (clone
PIR2:S46393	471.50	815.02	1.6e-37	129	Ig heavy chain V region - human
PIR2:C30562	467.50	808.72	3.9e-37	119	Ig heavy chain V region (27.7.2
PIR2:E30562	464.50	803.54	7.6e-37	119	Ig heavy chain V region (27.10.
PIR2:D30562	460.50	796.63	1.9e-36	119	Ig heavy chain V region (27.4b.
PIR2:D34548	458.50	792.92	2.9e-36	123	Ig heavy chain V-1 region (W12)
PIR2:S49530	457.00	789.64	4.0e-36	135	anti-sm antibody VH chain (VH1)
PIR2:PH0954	456.00	788.08	5.0e-36	132	Ig heavy chain V region (G6+ C1
PIR2:PH0952	453.00	783.12	9.7e-36	128	Ig heavy chain V region (G6+ C1
PIR2:S26362	453.00	780.96	9.6e-36	171	Ig heavy chain V region precursor
PIR2:S31600	451.00	779.22	1.5e-35	136	Ig heavy chain V region - human
PIR2:S20783	450.50	779.23	1.7e-35	121	Ig heavy chain V region - human
PIR2:PH0959	450.00	778.68	1.9e-35	116	Ig heavy chain V region (G6+ T-
PIR2:PH0957	449.50	777.26	2.1e-35	125	Ig heavy chain V region (G6+ C1
PIR2:S36260	448.50	775.29	2.6e-35	129	Ig heavy chain V region (clone
PIR2:PH0962	448.00	774.97	3.0e-35	120	Ig heavy chain V region (G6+ T-
PIR2:S19665	445.00	769.54	5.7e-35	124	Ig heavy chain V region (alpha
PIR2:PH0955	444.50	768.50	6.4e-35	127	Ig heavy chain V region (G6+ C1
PIR2:C33548	442.50	764.70	1.0e-34	133	Ig heavy chain V region (783)
PIR2:S14683	441.50	763.09	9.4e-34	627	Ig mu chain precursor, membrane
PIR2:A33548	441.50	763.20	1.2e-34	129	Ig heavy chain V-1 region (NE1)
PIR2:S34014	440.50	761.59	1.6e-34	127	Ig heavy chain V region - human
PIR2:B33548	438.00	757.33	2.7e-34	126	Ig heavy chain V-1 region (AND)
PIR2:PH0958	436.00	754.12	4.2e-34	122	Ig heavy chain V region (G6+ C1
PIR2:S46394	436.00	753.53	4.2e-34	132	Ig heavy chain V region - human
PIR2:S29257	435.50	751.81	4.7e-34	148	Ig heavy chain V region precursor
PIR2:PH0960	434.50	749.85	6.5e-34	136	Ig heavy chain V region (G6+ T-
PIR2:PH0953	434.00	747.31	9.1e-34	135	Ig heavy chain V region (G6+ C1
PIR2:B32274	432.00	746.45	1.0e-33	135	Ig heavy chain precursor V-1 re
PIR2:MHMS18	432.00	746.23	1.0e-33	139	Ig heavy chain precursor V-1 re
PIR2:PC4402	432.00	740.80	9.9e-34	287	pelb leader/Ig heavy chain anti
PIR2:PL0089	429.50	743.08	1.8e-33	119	Ig heavy chain V region (12S18)
PIR2:S26920	429.00	743.67	2.0e-33	98	Ig heavy chain V region (DP-7)
PIR2:HVH086	429.00	742.34	2.0e-33	117	Ig heavy chain precursor V-1 re
PIR2:PL0086	428.50	741.35	2.2e-33	119	Ig heavy chain V region (E3) -
PIR2:PL0105	428.50	739.13	2.2e-33	160	anti-PR2 erythrocyte autoantib
PIR2:PH1669	428.00	741.07	2.5e-33	110	Ig heavy chain V region (clone
PIR2:1A4151	427.50	739.19	2.8e-33	126	Ig heavy chain V region (B0) -

PIR2:A30577	426.00	736.09	3.8e-33	135	Ig heavy chain precursor V r
PIR2:S36271	425.50	735.98	4.3e-33	122	Ig heavy chain V region (c1o
PIR2:S38492	425.50	735.92	4.3e-33	123	Ig heavy chain - human (frag
PIR2:B22769	425.00	735.24	4.8e-33	120	Ig heavy chain V region (B1-
PIR2:PH1667	423.00	732.17	7.5e-33	114	Ig heavy chain V region (c1o

seq_name: PIR2:A32483

seq_documentation_block:

Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996
R:Accession: A32483
R:Larick, J.W.; Danielsson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck
Biochem. Biophys. Res. Commun. 160, 1250-1256, 1989
A:Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells
A:Reference number: A32483; MUID:89273586
A:Accession: A32483
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-142 <LAR>
A:Cross-references: GB:M26463
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:25-108/Domain: Immunoglobulin homology <IMM>

alignment_scores:

Quality: 473.50 Length: 127
Ratio: 4.305 Gaps: 1
Percent similarity: 86.614 Percent identity: 75.591

alignment_block:

US-08-487-283a-12_COPY_58_423 ..

Align seg 1/1 to: A32483 from: 1 to: 142

1	CAAGTCAACGCTGTCGCAATCCGCGCGGAGTCAAGAACCCAGGCGCTC	50
11	GlnValGlnLeuValGlnSerGlyAlaGlyValGlySerProGlyAla	27
51	AGTCAAGTGCCTGTAAGCTAGCGGCTATATTTTGTAAATTTATGCA	100
27	rVallyValSerGlyAlaSerGlyTyrThrPheThrAsnTyrTyrM	44
101	TTCAATGGTGGCTGACGCGCGCGGAGCGCTGGAATGATGGTGAG	150
44	eHnIstrValArgGlnAlaProGlyGlnGlyLeuIstrPheGlyIle	60
151	ATCTTACCGGCTGCTGTAGACACCGAATATACGAAATTTAAAGCCG	200
61	IleAsnProSerGlyAsnSerThrAsnTyrAlaGlnGlyPheGlnIylar	77
201	TGTTACTATGACGCTGACACTTTCAGTACAGTACATGACATGACGCT	250
77	GAlnIstrMetThrArgAspThrSerThrSerThrValTyrMetGlnLeu	94
251	CCAGCTGCGATCGAGACAGCGCGCTATATTTGCCCGCT	294
94	eSerLeuArgSerGlnAspThrAlaValTyrTyrGlyAlaArgGlyIlys	110
295TATTTTGTCTGACCCGAAATGATATTTGATGATGTTG	335
111	LeuAlaIstrThrIlePheGlyValLeuIleIstrGlyMetAspTyrTr	127
336	GGGTCAAGAACCTGCTCCTCTGCTCGAGC	366
127	polyGlnGlyThrLeuValThrValSerSer	137

seq_name: PIR2:S36265
seq_documentation_block:
Ig heavy chain V region (clone alpha-Mucl-1) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C:Accession: S36265
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448
A:Accession: S36265
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1118 <GRI>
A:Cross-references: EMBL:218846; NID:933121; PIDN:CAAV9298.1; PID:9339900
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

alignment_scores:

Quality:	476.00	Length:	122
Ratio:	4.250	Gaps:	1
Percent Similarity:	91.803	Percent Identity:	76.230

alignment_block:

US-08-487-283a-12_COPY_58_423 x S36265 ..

Align seg 1/1 to: S36265 from: 1 to: 118

```
1 CAAGTCCAACTGCTGTCATCCGCGCCGAGTCAGCAAGCCAGGGGCTC 50
1 GlnValGlnLeuValGlnSerGlyAlaGluValLysProGlyAlaSer 17
51 AGTCAAGTCTCTGTAAGCTAGCGGCTATATTTTCTTAATTATGGA 100
17 rValLysValSerGlyLysAlaSerGlyTyrThrPheThrGlyTyr 34
101 TTCAAATGGGCTGTCAGGCCCCGCGAGGCGCTGGAATGATGGGTGAG 150
34 ethIstrpValArgGlnAlaProGlyGlnGlyLeuGlnLutPheGlyTyr 50
151 ANCTACCGGGCTGTCAGCAGCAATATACCGAAATTTAAACACCG 200
51 IleAsnProAsnSerGlyGlyThrAsnTyrAlaGlnLysPheGlnGlyTyr 67
201 TGTACTATGACGCGTGCACACTTCGACTAGTACATGATGATGACCTCT 250
67 gValThrIleThrArgAspThrSerAlaSerThrAlaTyrMetGluLeu 84
251 CCAGCTCGCATCGGAGACACGCGCGCTATATTATTCGCGGCTATTTT 300
84 erSerLeuArgSerGlnAspThrAlaValTyrTyrCysAlaArgAspPhe 100
301 TTTGCTTACCCCAATTTGATTTTGGGTCGCAAGAACCT 350
101 LeuSerGly.....TyrLeuAspTyrTyrGlyGlnGlyThr 113
351 GGTCACTGCTCTGACG 366
113 uValThrValSerSer 118
```

seq_name: p1r2:S46393

seq_documentation_block:

Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000

C:Accession: S46393

R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.

J. Mol. Biol. 239, 68-78, 1994

A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage by

A:Reference number: S46390; MUID:94254092

A:Accession: S46393

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-129 <FIG>
A:Cross-references: EMBL:231680; NID:9509786; PIDN:CAAB3485.1; PID:91335146
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

alignment_scores:

Quality:	471.50	Length:	129
Ratio:	4.210	Gaps:	2
Percent Similarity:	86.822	Percent Identity:	72.093

alignment_block:

US-08-487-283a-12_COPY_58_423 x S46393 ..

Align seg 1/1 to: S46393 from: 1 to: 129

```
1 CAAGTCCAACTGCTGTCATCCGCGCCGAGTCAGCAAGCCAGGGGCTC 50
1 GlnValGlnLeuValGlnSerGlyAlaGluValLysProGlyAlaSer 17
51 AGTCAAGTCTCTGTAAGCTAGCGGCTATATTTTCTTAATTATGGA 100
17 rValLysValSerGlyLysAlaSerGlyTyrThrPheThrGlyTyr 34
101 TTCAAATGGGCTGTCAGGCCCCGCGAGGCGCTGGAATGATGGGTGAG 150
34 ethIstrpValArgGlnAlaProGlyGlnGlyLeuGlnLutPheGlyTyr 50
151 ANCTACCGGGCTGTCAGCAGCAATATACCGAAATTTAAACACCG 200
51 IleAsnProAsnSerGlyGlyThrAsnTyrAlaGlnLysPheGlnGlyTyr 67
201 TGTACTATGACGCGTGCACACTTCGACTAGTACATGATGATGACCTCT 250
67 pValThrMetThrArgAspThrSerIleSerThrAlaTyrMetGluLeu 84
251 CCAGCTCGCATCGGAGACACGCGCGCTATATTATTCGCGGCT ..... 294
84 erArgLeuArgSerAspAspThrAlaValTyrTyrCysAlaArgAspSer 100
295 ...TATTTTGGTCT.....AGCCGAATTTGTAATTGGA 329
101 AlaTyrTyrArgSerSerGlyTyrTyrSerAlaAsnTyrTyrMetAs 117
330 TGTTTGGGTCAGGAACCTGTCACCTGTCGTCGACG 366
117 pValTyrGlyLysGlyThrThrValThrValSerSer 129
```

seq_name: p1r2:C30562

seq_documentation_block:

Ig heavy chain V region (27.7.2) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 16-Aug-1996

C:Accession: C30562

R:Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, J.

Immunol. 142, 888-893, 1989

A:Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen

A:Reference number: A30562; MUID:89110066

A:Accession: C30562

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-119 <SIK>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

alignment_scores:

Quality:	467.50	Length:	122
Ratio:	4.289	Gaps:	1
Percent Similarity:	89.344	Percent Identity:	70.492

alignment_block:
US-08-487-283a-12_copy_58_423 x C30562

Align seg 1/1 to: C30562 from: 1 to: 119

```

1 CAAGTCAACTGTGTCATCCGCGCCGAGGTCAAGAACCCAGGCGCTC 50
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
1 GlnValGlnLeuGlnInserGlyAlaGlnLeuMetLysProGlyAla 17
51 AGTCAAAAGTGTCTGTAAAGCTAGCGCTAATATTATTTTCAATTATGGA 100
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
17 rValLysIleSerCysLysAlaThrGlyTrpThrPheSerSerTyTrpI 34
101 TTCATGGGTCGTCAGAGCCCGCGGACAGGCGCTGGAATGATGGTGAG 150
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
34 leGluTrpValLysGlnArgProGlyHisGlyLeuGlnTrpIleGlyGln 50
151 ATCTTACCGGCTGTGTAGACCGAATATACGAAATTTTAAAGACCG 200
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
51 IlePheProGlySerGlySerThrAsnGlyAsnGlyLysPheLysGlyL 67
201 TGTACTATGACCGCTGACACTTCGACTAGTACAGTATACATGAGCTCT 250
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
67 salAthrPheThrAlaAspThrSerSerAsnThrAlaTrpMetGlnLeu 84
251 CCAGCTCGGATCGAGACACAGCGCGCTATTATTGCGCGCTATTATT 300
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
84 erSerLeuThrSerGlnAspSerAlaValTrpGlyCysAlaArgHisTy 100
301 TTGGTTCACGCCGAATGTATTGTTGATGTTGGGTCAGAGAACCT 350
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
101 TyrGlySerSerSer.....PheAlaTrpTrpGlyGlnGlyThrLe 114
351 GGTCACGTCTCGAGC 366
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
114 uValThrValSerAla 119

```

seq_name: p1r2:E30562

seq_documentation_block:
Ig heavy chain V region (27.10.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 16-Aug-1996
C:Accession: E30562
R:Slkder, S.K.; Borden, P.; Gruenzo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.H.
J: Immunol. 142, 888-893, 1989
A:Title: Amino acid substitutions in V-H CDR2 change the idlotype but not the antigen-bi
A:Reference number: A30562; MUID:89110066
A:Accession: E30562
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <SIK>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

alignment_scores:
Quality: 464.50 Length: 122
Ratio: 4.261 Gaps: 1
Percent Similarity: 89.344 Percent Identity: 69.672

alignment_block:
US-08-487-283a-12_copy_58_423 x E30562

Align seg 1/1 to: E30562 from: 1 to: 119

```

1 CAAGTCAACTGTGTCATCCGCGCCGAGGTCAAGAACCCAGGCGCTC 50
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
1 GlnValGlnLeuGlnInserGlyAlaGlnLeuMetLysProGlyAla 17
51 AGTCAAAAGTGTCTGTAAAGCTAGCGCTAATATTATTTTCAATTATGGA 100
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
51 AGTCAAAAGTGTCTGTAAAGCTAGCGCTAATATTATTTTCAATTATGGA 100

```

```

|||||  |||||||  |||||||  |||||||  |||||||  |||||||
17 rValLysIleSerCysLysAlaThrGlyTrpThrPheSerSerTyTrpI 34
101 TTCATGGGTCGTCAGAGCCCGCGGACAGGCGCTGGAATGATGGTGAG 150
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
34 leGluTrpValLysGlnArgProGlyHisGlyLeuGlnTrpIleGlyGln 50
151 ATCTTACCGGCTGTGTAGACCGAATATACGAAATTTTAAAGACCG 200
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
51 IlePheProGlySerGlySerThrAsnGlyAsnGlyLysPheLysGlyL 67
201 TGTACTATGACCGCTGACACTTCGACTAGTACAGTATACATGAGCTCT 250
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
67 salAthrPheThrAlaAspThrSerSerAsnThrAlaTrpMetGlnLeu 84
251 CCAGCTCGGATCGAGACACAGCGCGCTATTATTGCGCGCTATTATT 300
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
84 erSerLeuThrSerGlnAspSerAlaValTrpGlyCysAlaArgHisTy 100
301 TTGGTTCACGCCGAATGTATTGTTGATGTTGGGTCAGAGAACCT 350
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
101 TyrGlySerSerSer.....PheAlaTrpTrpGlyGlnGlyThrLe 114
351 GGTCACGTCTCGAGC 366
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
114 uValThrValSerAla 119

```

seq_name: p1r2:D30562

seq_documentation_block:
Ig heavy chain V region (27.4b.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 16-Aug-1996
C:Accession: D30562
R:Slkder, S.K.; Borden, P.; Gruenzo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison, S.H.
J: Immunol. 142, 888-893, 1989
A:Title: Amino acid substitutions in V-H CDR2 change the idlotype but not the antigen
A:Reference number: A30562; MUID:89110066
A:Accession: D30562
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-119 <SIK>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

alignment_scores:
Quality: 460.50 Length: 122
Ratio: 4.225 Gaps: 1
Percent Similarity: 89.344 Percent Identity: 68.852

alignment_block:
US-08-487-283a-12_copy_58_423 x D30562

Align seg 1/1 to: D30562 from: 1 to: 119

```

1 CAAGTCAACTGTGTCATCCGCGCCGAGGTCAAGAACCCAGGCGCTC 50
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
1 GlnValGlnLeuGlnInserGlyAlaGlnLeuMetLysProGlyAla 17
51 AGTCAAAAGTGTCTGTAAAGCTAGCGCTAATATTATTTTCAATTATGGA 100
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
17 rValLysIleSerCysLysAlaThrGlyTrpThrPheSerSerTyTrpI 34
101 TTCATGGGTCGTCAGAGCCCGCGGACAGGCGCTGGAATGATGGTGAG 150
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
34 leGluTrpValLysGlnArgProGlyHisGlyLeuGlnTrpIleGlyGln 50
151 ATCTTACCGGCTGTGTAGACCGAATATACGAAATTTTAAAGACCG 200
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
51 IlePheProGlySerGlySerThrAsnGlyAsnGlyLysPheLysGlyL 67

```

```
201 TGTACTATGACGCGTACACTGCTAGTACAGTATACATGAGACCTCT 250
      :::::||||| |||||:::|||||:::|||||:::|||||
67 salalrpherhralaasprthrserasnthralatyrmetglnleus 84
      |||||  |||||:::|||||:::|||||:::|||||
251 CCAGCCTCGATCGAGACACGCGCGCTATATTATTCGCCGCTATTTT 300
      |||||  |||||:::|||||:::|||||:::|||||
84 erSerleutrhserglnasprseralaValtyrtycysalaarghistyr 100
      |||||  |||||:::|||||:::|||||:::|||||
301 TTTGGTCTAGCCCGAATTGTATTTTGTATTTGGGTCAGAGAACCTT 350
      :::|||||  ||| |||||  |||||  |||||
101 TyrGlySerSerSer.....PhealatrYrTpGlyGlnGlyThre 114
      |||||  |||||:::|||||:::|||||
351 GGTCACTGTCTCGAGC 366
      |||||  |||||:::|||||
114 uValThrValSerala 119
      |||||  |||||:::|||||
seq_name: p1r2:D33548
seq_documentation_block:
Ig heavy chain V-1 region (WIL2) - human
C:Species: Homo sapiens (man)
C>Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C:Accession: D33548
R:Klips, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A:title: Developmentally restricted immunoglobulin heavy chain variable region gene expr
A:Reference number: A33548; MUID:89345575
A:Accession: D33548
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-123 <KIP>
C:Superfamily: immunoglobulin V region: immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>
```

```
alignment_scores:
  Quality: 458.50      Length: 123
  Ratio: 4.168        Caps: 1
  Percent Similarity: 89.431  Percent Identity: 72.358
```

alignment_block:

US-08-487-283A-12_COPY_58_423 x D33548 ..

Align seg 1/1 to: D33548 from: 1 to: 123

```
1 CAAGTCCAACTGTGTCATCGCGCGCGAGGTCAGAGCCAGGGCGCTC 50
      |||||  |||||  |||||  |||||  |||||  |||||
1 glnValGlnleuValGlnserGlyalagluVallyslsProGlyAlase 17
      |||||  |||||  |||||  |||||  |||||  |||||
51 AGTCAAAGTGTCTGTAAAGCTAGCGGCTATATTTTCTAATATATGGA 100
      |||||  |||||  |||||  |||||  |||||  |||||
17 rVallyslsValserCysgluAlaSerGlyThrPheThrGlyHisTyrM 34
      |||||  |||||  |||||  |||||  |||||  |||||
101 TTCATGGGTGCGTCAGGCCCCCGGCGAGGCGCTGGAATGGATGGTGA 150
      :::::|||||  |||||  |||||  |||||  |||||  |||||
34 ethIstrPvalArglnAlaProGlyGlnGlyleuGlnutrrmetGlyTrr 50
      |||||  |||||  |||||  |||||  |||||  |||||
151 ATCTTACCGGGCTGTGTAGACACCGAATATACGAAATTTTAAAGACCG 200
      |||||  |||||  |||||  |||||  |||||  |||||
51 lleasnProasnserGlyGlyThrAsnTyralaglnulysPheGlnGlyAr 67
      |||||  |||||  |||||  |||||  |||||  |||||
201 TGTACTATGACGCGTACACTGCTAGTACAGTATACATGAGACCTCT 250
      |||||  |||||  |||||  |||||  |||||  |||||
67 gValThrleThrArGAsprThrSerlleasnThrAlaTyrmGlnleus 84
      |||||  |||||  |||||  |||||  |||||  |||||
251 CCAGCCTCGATCGAGACACGCGCGCTATATTATTCGCCGCT...TAF 297
      |||||  |||||  |||||  |||||  |||||  |||||
84 erArgleuArGserAsprlnAlaValTyrcysAlaArGAlaser 100
      |||||  |||||  |||||  |||||  |||||  |||||
298 TTTTGTGCTTACCCCGAATTGTATTTTGTATTTGGGTCAGAGAAC 347
      :::  |||  :::  |||||  |||||  |||||
101 TyrCysGlyTyArspCysTyrrTyrrPhePheAsprTyrrPglGlnGlyTh 117
```

```
348 CCGTGTCACTGTCTCGAGC 366
      |||||  |||||  |||||  |||||  |||||  |||||
117 rleuValThrValSerSer 123
      |||||  |||||  |||||  |||||  |||||  |||||
seq_name: p1r2:S49530
```

seq_documentation_block:

anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human
C:Species: Homo sapiens (man)
C>Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
C:Accession: S49530
R:Malnoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
A:Reference number: S48797
A:Accession: S49530
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-135 <MAH>
A:Cross-references: EMBL:246348; NID:g560839; PIDN:CA86467.1; PID:g560840
C:Superfamily: immunoglobulin V region: immunoglobulin homology
F:34-117/Domain: immunoglobulin homology <IMM>

```
alignment_scores:
  Quality: 457.00      Length: 122
  Ratio: 4.311        Caps: 1
  Percent Similarity: 86.885  Percent Identity: 73.770
```

alignment_block:

US-08-487-283A-12_COPY_58_423 x S49530 ..

Align seg 1/1 to: S49530 from: 1 to: 135

```
1 CAAGTCCAACTGTGTCATCGCGCGCGAGGTCAGAGCCAGGGCGCTC 50
      |||||  |||||  |||||  |||||  |||||  |||||
20 glnValGlnleuValGlnserGlyalagluVallyslsProGlyAlase 36
      |||||  |||||  |||||  |||||  |||||  |||||
51 AGTCAAAGTGTCTGTAAAGCTAGCGGCTATATTTTCTAATATATGGA 100
      |||||  |||||  |||||  |||||  |||||  |||||
36 rVallyslsValserCysgluAlaSerGlyTyrrPheThrGlyTyrrM 53
      |||||  |||||  |||||  |||||  |||||  |||||
101 TTCATGGGTGCGTCAGGCCCCCGGCGAGGCGCTGGAATGGATGGTGA 150
      :::::|||||  |||||  |||||  |||||  |||||  |||||
53 ethIstrPvalArglnAlaProGlyGlnGlyleuGlnutrrmetGlyTrr 69
      |||||  |||||  |||||  |||||  |||||  |||||
151 ATCTTACCGGGCTGTGTAGACACCGAATATACGAAATTTTAAAGACCG 200
      |||||  |||||  |||||  |||||  |||||  |||||
70 lleasnProasnserGlyGlyThrAsnTyralaglnulysPheGlnGlyAr 86
      |||||  |||||  |||||  |||||  |||||  |||||
201 TGTACTATGACGCGTACACTGCTAGTACAGTATACATGAGACCTCT 250
      |||||  |||||  |||||  |||||  |||||  |||||
86 gValThrleThrArGAsprThrSerlleasnThrAlaTyrmGlnleus 103
      |||||  |||||  |||||  |||||  |||||  |||||
251 CCAGCCTCGATCGAGACACGCGCGCTATATTATTCGCCGCTATTTT 300
      |||||  |||||  |||||  |||||  |||||  |||||
103 erArgleuArGserAsprlnAlaValTyrcysAlaArGAlaser 119
      |||||  |||||  |||||  |||||  |||||  |||||
301 TTTGGTCTAGCCCGAATTGTATTTTGTATTTGGGTCAGAGAACCTT 350
      |||||  |||||  |||||  |||||  |||||  |||||
120 ThrGly.....TyrAsnTyrrTpGlyGlnGlyThle 130
      |||||  |||||  |||||  |||||  |||||  |||||
351 GGTCACTGTCTCGAGC 366
      |||||  |||||  |||||  |||||  |||||  |||||
130 uValThrValSerSer 135
      |||||  |||||  |||||  |||||  |||||  |||||
seq_name: p1r2:PH0954
```

seq_documentation_block:

Ig heavy chain V region (G6+ CIL-HEN) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996

C:Accession: PH0954
 R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
 J. Exp. Med. 175, 983-991, 1992
 A:Title: Evidence for somatic selection of natural autoantibodies.
 A:Reference number: PH0952; MUID:92202880
 A:Accession: PH0954
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-132 <MAR>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-30/Region: framework 1
 F:15-98/Domain: immunoglobulin homology <IMM>
 F:31-35/Region: complementarity-determining 1
 F:36-50/Region: framework 2
 F:51-67/Region: complementarity-determining 2
 F:68-98/Region: framework 3
 F:99-120/Region: complementarity-determining 3

alignment_scores:
 Quality: 456.00 Length: 132
 Ratio: 4.183 Gaps: 2
 Percent Similarity: 82.576 Percent Identity: 69.697

alignment_block:

US-08-487-283a-12_COPY_58_423 x PH0954 ..

Align seg 1/1 to: PH0954 from: 1 to: 132

```

1 CAAGTCAACTGTCGATCCGCGCCGAGGTCAGAGCCAGGCGCTC 50
|||||
1 GlnValGlnLeuValGlnSerGlyAlaGluValLysProGlySerSe 17
51 AGTCAAGTGTCTCTAAAGCTAGCGCTATATTTCTAATATATGA 100
|||||
17 rValLysValSerCysLysAlaSerGlyThrPheSerSerTyralai 34
101 TTCATGCGTGTGCTCAGGCCCGCGGAGGCGCTGAAATGATGGTGAG 150
|||||
34 leSerTrpAlaArgGlnAlaProGlyGlnGlyLeuGlnIurPmetGly 50
151 ATCTTACCGGGCTCTGTAGACACCGAATATACGAAATTTAAAGCCG 200
|||||
51 IleIleProIlePheGlyThrAlaAsnTyralGlnLysPheGlnGlyAr 67
201 TGTACTATGACGCGTACACTTCGACTAGTATGATGAGGCTCT 250
|||||
67 gValThrIleThrAlaAspLysSerThrSerThrAlaTyrmelGluLeuS 84
251 CCAGCTCGGATCGAGACGCGCGCTATATTTGCGGCGT..... 294
|||||
84 erSerLeuArgSerGlnAspThrAlaValTyrcysAlaArgProHis 100
295 .....TATTTTGTGTTCTAGCCCGAATTTGTAATTTT.. 327
|||||
101 AlaserIleAspSerPheTrpSerGlyTyrrProAsnTyrrTyrrTy 117
328 .....GATGTTGGGTCACAGAACCCGTCACCTGTCGAGC 366
|||||
117 rGlyMetAspValTrpGlyGlnGlyThrThrValThrValSerSer 132

```

seq_name: plr2:PH0952

seq_documentation_block:

Ig heavy chain V region (G6+ CIL-SMI) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
 C:Accession: PH0952
 R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
 J. Exp. Med. 175, 983-991, 1992
 A:Title: Evidence for somatic selection of natural autoantibodies.
 A:Reference number: PH0952; MUID:92202880

A:Accession: PH0952
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 1-128 <MAR>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-30/Region: framework 1
 F:15-98/Domain: immunoglobulin homology <IMM>
 F:31-35/Region: complementarity-determining 1
 F:36-50/Region: framework 2
 F:51-67/Region: complementarity-determining 2
 F:68-98/Region: framework 3
 F:99-116/Region: complementarity-determining 3

alignment_scores:
 Quality: 453.00 Length: 128
 Ratio: 4.156 Gaps: 2
 Percent Similarity: 85.156 Percent Identity: 71.875

alignment_block:

US-08-487-283a-12_COPY_58_423 x PH0952 ..

Align seg 1/1 to: PH0952 from: 1 to: 128

```

1 CAAGTCAACTGTCGATCCGCGCCGAGGTCAGAGCCAGGCGCTC 50
|||||
1 GlnValGlnLeuValGlnSerGlyAlaGluValLysProGlySerSe 17
51 AGTCAAGTGTCTCTAAAGCTAGCGCTATATTTCTAATATATGA 100
|||||
17 rValLysValSerCysLysAlaSerGlyThrPheSerSerTyralai 34
101 TTCATGCGTGTGCTCAGGCCCGCGGAGGCGCTGAAATGATGGTGAG 150
|||||
34 leSerTrpAlaArgGlnAlaProGlyGlnGlyLeuGlnIurPmetGly 50
151 ATCTTACCGGGCTCTGTAGACACCGAATATACGAAATTTAAAGCCG 200
|||||
51 IleIleProIlePheGlyThrAlaAsnTyralGlnLysPheGlnGlyAr 67
201 TGTACTATGACGCGTACACTTCGACTAGTATGATGAGGCTCT 250
|||||
67 gValThrIleThrAlaAspLysSerThrSerThrAlaTyrmelGluLeuS 84
251 CCAGCTCGGATCGAGACGCGCGCTATATTTGCGGCGT..... 294
|||||
84 erSerLeuArgSerGlnAspThrAlaValTyrcysAlaArgGlyGly 100
295 .....TATTTTGTGTTCT..ACCCGAATTTGTAATTTGATGT 332
|||||
101 AsnTyrrAspTyrrIleTrpLysSerTyrrArgSerAsnAlaPheAsp 117
333 TTGGGGTCAGAGACCCGTCGACTGTCGAGC 366
|||||
117 eTrpGlyGlnGlyThrMetValThrValSerSer 128

```

seq_name: plr2:S23623

seq_documentation_block:

Ig heavy chain V region precursor - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S23623
 R:Olée, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Defios, M.; Kozin, F.; Carson, D.A.
 J. Exp. Med. 175, 831-842, 1992
 A:Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors fro
 A:Reference number: S23623; MUID:92156804
 A:Accession: S23623
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-171 <OLE>
 A:Cross-references: EMBL:X59702; NID:g32010; PIDN:CAA4223.1; PID:g32011

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

alignment_scores:
Quality: 453.00 Length: 126
Ratio: 4.194 Gaps: 2
Percent Similarity: 85.714 Percent Identity: 71.429

alignment_block:

US-08-487-283A-12_COPY_58_423 x S23623 ..

Align seg 1/1 to: S23623 from: 1 to: 171

```

1 CAAGTCCAACTGTCGATCCGGCCGAGTCACAGACCGAGGGCCTC 50
|||||
20 GlnValGlnLeuValGlnSerGlyAlaGluValLysProGlyAlaSe 36
51 AGTCAAACTGTCCTGTAAGCTAGCGCGCTATTTTCTAATTATGGA 100
|||||
36 rValLysValSerCysGlySerGlyTyrThrPheThrAlaTyrGlnM 53
|||||
101 TTCAAATGGGTGCGTCAGGCCCCCGGAGGCGCTGGAATGATGGGTGAG 150
|||||
151 ATCTTACCGGGCTCTGTAGCAGCCAAATATACCGAAATTTTAAAGCCG 200
|||||
70 IleAsnProAsnSerGlyGlyThrGlyTyrGlnLysPheGlnGlyAr 86
|||||
201 TGTACTATGACGCGTCGACACTTCGACTAGTACGATATACGAGCTCT 250
|||||
86 gValThrLeuThrArgAspThrSerIleSerThrAlaTyrMetGluLeuS 103
|||||
251 CCAGCTCGATCGAGGAGACAGCGCGCTATATTATTCGCG...CGTAT 297
|||||
103 erArgLeuThrSerAspThrAlaValTyrTyrCysAlaIleGluTyr 119
|||||
298 TTTTGTGTTCTACG.....CCGAATTGATTTGATGTTGGGG 338
|||||
120 PheYrAspGlySerAspLeuLysProSerAspValPheAspIleTrp 136
|||||
339 TCAAGAACCCCTGCTGCTACTGTCGAGC 366
|||||
136 yGlnGlyThrMetValThrValSerSer 145

```

seq_name: p1r2:S31600

seq_documentation_block:

Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 22-Nov-1993 #sequence-revision 10-Nov-1995 #text-change 23-Jul-1999

C:Accession: S31600

R:Contributor, A.M.: Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelier, C.

submitted to the EMBL Data Library, June 1992

A:Description: Mechanisms that generate human immunoglobulin diversity operate from the

A:Reference number: S31585

A:Accession: S31600

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-136 <CUI>

A:Cross-references: EMBL:214165; NID:g30994; PIDN:CAA78534.1; PID:g30995

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

alignment_scores:

Quality: 451.00 Length: 124
Ratio: 4.295 Gaps: 2
Percent Similarity: 84.677 Percent Identity: 72.581

alignment_block:

US-08-487-283A-12_COPY_58_423 x S31600 ..

Align seg 1/1 to: S31600 from: 1 to: 136

```

1 CAAGTCCAACTGTCGATCCGGCCGAGTCACAGACCGAGGGCCTC 50
|||||
20 GlnValGlnLeuValGlnSerGlyAlaGluValLysProGlyAlaSe 36
51 AGTCAAACTGTCCTGTAAGCTAGCGCGCTATTTTCTAATTATGGA 100
|||||
36 rValLysValSerCysArgAlaSerGlyTyrThrPheThrSerTyrAsp 53
|||||
101 TTCAAATGGGTGCGTCAGGCCCCCGGAGGCGCTGGAATGATGGGTGAG 150
|||||
151 ATCTTACCGGGCTCTGTAGCAGCCAAATATACCGAAATTTTAAAGCCG 200
|||||
70 MetAsnProAsnSerGlyAsnThrGlyTyrAlaGlnLysPheGlnGlyAr 86
|||||
201 TGTACTATGACGCGTCGACACTTCGACTAGTACGATATACGAGCTCT 250
|||||
86 gValThrMetThrArgAsnThrSerIleSerThrAlaTyrMetGluLeuS 103
|||||
251 CCAGCTCGATCGAGGAGACAGCGCGCTATATTATTCGCGCGCTATTATT 300
|||||
103 erSerLeuAlaGlySerGluAspThrAlaValTyrTyrCysAlaArg..... 117
|||||
301 TTTGTTCTAGCCCGAATTGG.....TATTGATGTTTGGGGTCAGG 344
|||||
118 .....TTPArgAspAlaPheAspIleTrpGlyGlnI 128
|||||
345 AACCTGTCACGTCGTCGAGC 366
|||||
128 yThrMetValThrValSerSer 135

```

seq_name: p1r2:S20783

seq_documentation_block:

Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C>Date: 20-Feb-1995 #sequence-revision 20-Feb-1995 #text-change 21-Jan-2000

C:Accession: S20783

R:Contributor, F.: Wang, J.; Schroeder, H.W.

submitted to the EMBL Data Library, April 1992

A:Description: Analysis of human cord blood Ig heavy chain IGA and IGG repertoire.

A:Reference number: S20764

A:Accession: S20783

A:Status: preliminary

A:Molecule type: DNA

A:Cross-references: EMBL:211957; NID:g33899; PIDN:CAA78014.1; PID:g33900

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

alignment_scores:

Quality: 450.50 Length: 124
Ratio: 4.171 Gaps: 2
Percent Similarity: 87.097 Percent Identity: 73.387

alignment_block:

US-08-487-283A-12_COPY_58_423 x S20783 ..

Align seg 1/1 to: S20783 from: 1 to: 121

```

1 CAAGTCCAACTGTCGATCCGGCCGAGTCACAGACCGAGGGCCTC 50
|||||
1 GlnValGlnLeuValGlnSerGlyAlaGluValLysProGlyAlaSe 17
51 AGTCAAACTGTCCTGTAAGCTAGCGCGCTATTTTCTAATTATGGA 100

```

```

17 rValThrValSerCysAlaSerGlyTyrThrPheThrSeryrhem 34
101 TTCATGGGTGCGTCAGAGCCCGGAGGCGCTGGAATGATGGTGAG 150
34 eethrIrpValArgGlnAlaProGlyGlnGlyLeuGluTrpMetGlyMet 50
151 ATCTTACCGGGCTCTGTAGACACCGAATATACGAAATTTTAAAGCCG 200
51 lIeAspProHISglYserThrThrPheAlaGlnGlySerLeuGlnGlyAr 67
201 TGTACTATGACGCGTACACTGACACTGATACATGATGAGAGCT 250
67 gAlaThrMetThrArgAspThrSerThrSerThrValTyrMetAspLeuS 84
251 CCAGCTGGGATCGAGAGACACGCGCTATTATTCGCGCGCTATTATT 300
84 eGlyLeuArgSerGluAspThrAlaLeuTyrTrpCysAlaArg..... 98
301 TTGGTTCT.....AGCCGAATGGTATTTGATTTGGGGTCAAG 344
99 ...GlySerAspThrSerProAlaSerThrIleAspTyrTrpGlyGlnG 114
345 AACCCGTGTCATGTCGAGC 366
114 yThrLeuValThrValSerSer 121
seq_name: p1r2:PH0959

```

```

seq_documentation_block:
Ig heavy chain V region (G6+ T-126) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0959
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies.
A:Reference number: PH0952; MUID:92202880
A:Accession: PH0959
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-116 <MAR>
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-50/Region: framework 2
F:51-67/Region: complementarity-determining 2
F:68-98/Region: framework 3
F:99-104/Region: complementarity-determining 3

```

```

alignment_scores:
Quality: 450.00 Length: 122
Ratio: 4.286 Gaps: 2
Percent Similarity: 86.066 Percent Identity: 74.590

```

alignment_block:

US-08-487-283a-12_COPY_58_423 x PH0959 ..

Align seg 1/1 to: PH0959 from: 1 to: 116

```

1 CAAGTCAACTGTGCAATCCGCGCGAGGTCAAGAACCGAGGCGCTC 50
|||||
1 GlnValGlnLeuValGlnSerGlyAlaGluValLysProGlySerSe 17
51 AGTCAAGTGTCTGTAAAGCTAATTTTCTAATTAATTGA 100
|||||
17 rValLysValSerCysLysAlaSerGlyGlyThrPheSerSeryrAla 34
101 TTCATGGGTGCGTCAGAGCCCGGAGGCGCTGGAATGATGGTGAG 150
|||||

```

```

34 lSerTrpValArgGlnAlaProGlyGlnGlyLeuGluTrpMetGlyGly 50
151 ATCTTACCGGGCTCTGTAGACACCGAATATACGAAATTTTAAAGCCG 200
51 lIeIleProIlePheGlyThrAlaAsnTyrAlaGlnGlyPheGlnGly 67
201 TGTACTATGACGCGTACACTGCGCTAGTACAGTATACATGAGACTCT 250
67 gValThrIleThrAlaAspGluSerThrSerThrAlaTyrMetGluLeuS 84
251 CCAGCTGGGATCGAGAGACACGCGCTATTATTCGCGCGCTATTATT 300
84 eSerLeuArgSerGluAspThrAlaValTyrTrpCysAlaArg..... 98
301 TTGGTTCTAGCCCGAATTTGATTTGATTTGGGGTCAAGAACCT 350
99 .....GlyAspAsnTrp...PheAspProTrpGlyGlnGlyThrIe 111
351 GGTCACTGTCTGAGC 366
111 uValThrValSerSer 116
seq_name: p1r2:PH0957

```

```

seq_documentation_block:
Ig heavy chain V region (G6+ CLL-BRA) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C:Accession: PH0957
R:Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A:Title: Evidence for somatic selection of natural autoantibodies.
A:Reference number: PH0952; MUID:92202880
A:Accession: PH0957
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-125 <MAR>
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-50/Region: framework 2
F:51-67/Region: complementarity-determining 2
F:68-98/Region: framework 3
F:99-113/Region: complementarity-determining 3

```

```

alignment_scores:
Quality: 449.50 Length: 130
Ratio: 4.201 Gaps: 2
Percent Similarity: 82.308 Percent Identity: 70.000

```

alignment_block:

US-08-487-283a-12_COPY_58_423 x PH0957 ..

Align seg 1/1 to: PH0957 from: 1 to: 125

```

1 CAAGTCAACTGTGCAATCCGCGCGAGGTCAAGAACCGAGGCGCTC 50
|||||
1 GlnValGlnLeuValGlnSerGlyAlaGluValLysProGlySerSe 17
51 AGTCAAGTGTCTGTAAAGCTAATTTTCTAATTAATTGA 100
|||||
17 rValLysValSerCysLysAlaSerGlyGlyThrPheSerSeryrAla 34
101 TTCATGGGTGCGTCAGAGCCCGGAGGCGCTGGAATGATGGTGAG 150
|||||
34 lAsnTrpValArgGlnAlaProGlyGlnGlyLeuGluTrpMetGlyGly 50
151 ATCTTACCGGGCTCTGTAGACACCGAATATACGAAATTTTAAAGCCG 200
|||||
51 lIeIleProIlePheGlyThrAlaAsnTyrAlaGlnGlyPheGlnGly 67

```

```

201 TGTACTATGACGCGTGAACCTTCGACTAGTACATATACATGAGCTCT 250
|||||:||||| ||| |||||:|||||:|||||:|||||
67 gValThrIleThrIleAlaSpGluSerThrAsnThrAlaTyrMetGluLeu 84
|||||:|||||:|||||:|||||:|||||:|||||
251 CCAGCCTGCATCGAGAGACAGCGCGTCTATTATTGCGGCGT..... 294
|||||:|||||:|||||:|||||:|||||:|||||
84 erSerIleuArgSerGluAspThrAlaValTyrTyrCysAlaArgaspGly 100
|||||:|||||:|||||:|||||:|||||:|||||
295 .....TATTTTGTGTTCTAGCCCGAATTGTAATT 326
|||||:|||||:|||||:|||||:|||||
101 CysSerGlyGlySerCysTyrPheTrpGly.....TrpPh 112
|||||:|||||:|||||:|||||:|||||
327 TGATGTTGGGGTCAAGAAACCTGGTCACTGTCGAGC 366
|||||:|||||:|||||:|||||:|||||:|||||
112 eAspProTrpGlyGlnGlyThrIleuValThrValSerSer 125

```

OM of: US-08-487-283A-12_COPY_58_423 to: SwissProt_39:* out_format : pfs
Date: Jul 19, 2001 7:59 AM

About: Results were produced by the Gencore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

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-MODEL-frame+ -n2p -model -DEV-x1p  
-O/cgcn2_1/USPTO.spool/US08487283/tra.19072001.075205.246/app_query.fasta_1.444  
-DB-SwissProt_39 -OPTM-fastan -SUFFIX-tra.rsp -GAPOP=12.000  
-GABEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000 -LOOPEXT=0.000  
-GAPOP=4.500 -GABEXT=0.050 -XGAPOP=10.000 -XGABEXT=0.500  
-FGAPOP=6.000 -FGABEXT=7.000 -YGAPOP=10.000 -YGABEXT=0.500  
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX-biosum62  
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE-pct  
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL -OUTFMT=pfs  
-NORM-ext -MINLEN=0 -MAXLEN=200000000  
-USRR-US08487283_cgcn2_1.48 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPHY  
-WAIT -THREADS=1
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Search information block:

Query: US-08-487-283A-12_COPY_58_423
Query length: 366
Database: SwissProt_39:*
Database sequences: 93435
Database length: 34255486
Search time (sec): 18.580000

score_list:

Sequence	Strid Orig	ZScore	EScore	Len	Documentation
SwissProt_39:HV07_MOUSE +	432.00	860.47	2.0e-40	139	P01751 mus musculus (mouse)
SwissProt_39:HV1B_HUMAN +	429.00	855.99	4.2e-40	117	P01743 homo sapiens (human)
SwissProt_39:HV01_MOUSE +	419.50	836.61	4.9e-39	121	P01745 mus musculus (mouse)
SwissProt_39:HV1C_HUMAN +	414.00	823.81	2.1e-38	147	P01744 homo sapiens (human)
SwissProt_39:HV1G_HUMAN +	403.00	803.76	3.4e-37	117	P23083 homo sapiens (human)
SwissProt_39:HV11_MOUSE +	403.00	802.34	3.5e-37	137	P01755 mus musculus (mouse)
SwissProt_39:HV12_MOUSE +	401.50	800.75	5.0e-37	117	P01756 mus musculus (mouse)
SwissProt_39:HV50_MOUSE +	401.00	799.51	5.7e-37	120	P06529 mus musculus (mouse)
SwissProt_39:HV03_MOUSE +	388.50	794.49	1.1e-36	120	P01747 mus musculus (mouse)
SwissProt_39:HV13_MOUSE +	387.50	792.71	1.4e-36	117	P01757 mus musculus (mouse)
SwissProt_39:HV4B_MOUSE +	381.50	779.17	6.8e-36	138	P03808 mus musculus (mouse)
SwissProt_39:HV02_MOUSE +	383.50	762.97	5.3e-35	140	P01746 mus musculus (mouse)
SwissProt_39:HV51_MOUSE +	377.00	751.45	2.8e-34	118	P06530 mus musculus (mouse)
SwissProt_39:HV1A_HUMAN +	376.50	750.52	3.1e-34	117	P01742 homo sapiens (human)
SwissProt_39:HV3B_MOUSE +	370.00	737.31	1.7e-33	119	P01808 mus musculus (mouse)
SwissProt_39:HV04_MOUSE +	365.00	727.42	6.1e-33	117	P01748 mus musculus (mouse)
SwissProt_39:HV09_MOUSE +	365.00	727.42	6.1e-33	117	P01753 mus musculus (mouse)
SwissProt_39:HV1H_HUMAN +	365.00	727.19	6.1e-33	120	P80421 homo sapiens (human)
SwissProt_39:HV40_MOUSE +	363.00	725.26	7.9e-33	119	P01807 mus musculus (mouse)
SwissProt_39:HV37_MOUSE +	363.00	723.25	1.0e-32	119	P01807 mus musculus (mouse)
SwissProt_39:HV00_MOUSE +	359.00	715.60	2.8e-32	114	P01741 mus musculus (mouse)
SwissProt_39:HV05_MOUSE +	357.00	711.35	4.8e-32	117	P01749 mus musculus (mouse)
SwissProt_39:HV39_MOUSE +	353.50	704.24	1.2e-31	118	P01809 mus musculus (mouse)
SwissProt_39:HV1E_HUMAN +	351.50	699.70	2.0e-31	125	P06526 homo sapiens (human)
SwissProt_39:HV15_MOUSE +	351.00	698.94	2.0e-31	136	P01759 mus musculus (mouse)
SwissProt_39:HV49_MOUSE +	350.00	697.28	2.9e-31	117	P06528 mus musculus (mouse)
SwissProt_39:HV52_MOUSE +	350.00	697.28	2.9e-31	117	P06527 mus musculus (mouse)
SwissProt_39:HV42_MOUSE +	349.50	696.28	3.3e-31	117	P01812 mus musculus (mouse)
SwissProt_39:HV06_MOUSE +	349.00	695.27	3.8e-31	117	P01754 mus musculus (mouse)
SwissProt_39:HV01_MOUSE +	347.00	691.25	6.3e-31	117	P01750 mus musculus (mouse)
SwissProt_39:HV01_RAT +	346.50	688.51	7.4e-31	142	P01805 rat mus musculus (rat)
SwissProt_39:HV41_MOUSE +	345.50	688.24	9.3e-31	117	P01811 mus musculus (mouse)
SwissProt_39:HV3J_HUMAN +	344.50	685.93	1.2e-30	121	P01771 homo sapiens (human)
SwissProt_39:HV18_MOUSE +	342.50	681.76	2.0e-30	123	P01787 mus musculus (mouse)
SwissProt_39:HV19_MOUSE +	338.50	673.73	5.7e-30	123	P01788 mus musculus (mouse)
SwissProt_39:HV21_MOUSE +	337.00	670.79	8.3e-30	122	P01789 mus musculus (mouse)
SwissProt_39:HV21_MOUSE +	337.00	670.79	8.3e-30	122	P01790 mus musculus (mouse)
SwissProt_39:HV22_MOUSE +	336.50	669.71	9.5e-30	123	P01791 mus musculus (mouse)
SwissProt_39:HV16_MOUSE +	336.00	667.80	1.1e-29	136	P01783 mus musculus (mouse)
SwissProt_39:HV23_MOUSE +	334.50	665.69	1.6e-29	123	P01792 mus musculus (mouse)

SwissProt_39:HV1D_HUMAN + 331.00 658.59 3.9e-29 124 P01760 homo sapiens (huma
SwissProt_39:HV1E_HUMAN + 331.00 658.59 3.9e-29 124 P01761 homo sapiens (huma
SwissProt_39:HV14_MOUSE + 328.00 653.08 8.4e-29 117 P01758 mus musculus (mous
SwissProt_39:HV3D_HUMAN + 326.50 650.23 1.2e-28 115 P01765 homo sapiens (huma
SwissProt_39:HV3I_HUMAN + 324.50 645.90 2.1e-28 119 P01770 homo sapiens (huma

seq_name: SwissProt_39:HV07_MOUSE

seq_documentation_block:
ID HV07_MOUSE STANDARD; PRT; 139 AA.

AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION BI-8/186-2 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: THE BI-8 MU CHAIN MRNA WAS CLOWED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
(NPB ANTIBODIES).
CC -----

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CC -----
CC EMBL: J00529; AAA38170.1; -.
CC PIR: A02034; MMS18.
CC DR InterPro: IPR003006; -.
CC DR Pfam: PF00047; 19; 1.
CC KW Immunoglobulin V region; Signal.
CC FT SIGNAL 1 19
CC FT CHAIN 20 139 IG HEAVY CHAIN V REGION BI-8/186-2.
CC FT DOMAIN 20 49 FRAMEWORK 1.
CC FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
CC FT DOMAIN 55 68 FRAMEWORK 2.
CC FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
CC FT DOMAIN 86 117 FRAMEWORK 3.
CC FT DOMAIN 118 124 D SEGMENT.
CC FT DOMAIN 125 139 JH2 SEGMENT.
CC FT DISULFID 41 115 BY SIMILARITY.
CC FT NON_TER 139 139
CC SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

alignment_scores:
Quality: 432.00 Length: 123
Ratio: 4.037 Gaps: 2
Percent Similarity: 86.992 Percent Identity: 65.854

alignment_block:
US-08-487-283A-12_COPY_58_423 x HV07_MOUSE ..
Align seg 1/1 to: HV07_MOUSE from: 1 to: 139

1 CAAGTCAACGTGTCATCCGGCGGAGGTCACAGAGGAGGCGCTC 50
|||||
20 GlnvalGlnleuGlnGlnProGlyalactIleuVallyProGlyalase 36

```

51 ACTCAAGTGTCTGTAAGCTAGCGGCTATATTTTCTAATTATGGA 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
36 rVallysleuSerGlyAlaSerGlyThrPhenSerTyrTrpM 53
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
101 TTCATGGGTGGTCAAGCCCCGGGACAGCGCTGGAATGAGGTGAG 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
53 eHISrPvalSerGlyAlaSerGlyThrPhenSerTyrTrpM 69
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
151 ATCTTACCGGCTGTGTCAGACCGCAATATACGAAATTTTAAAGACCG 200
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
70 IleAsnProSerGlyAlaSerGlyThrPhenSerTyrTrpM 86
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
201 TGTACTATGACGCGTGCAGCTTCGACTAGTACATGATGAGGCTCT 250
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
86 gValThrMetThrAlaSerGlyAlaSerGlyThrPhenSerTyrTrpM 103
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
251 CCAGCTGCGATCGAGACGACGCGCTGATATGCGCGCTAT... 297
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
103 erSerleuThrSerGlyAlaSerGlyThrPhenSerTyrTrpM 119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
298 TTTTGTGGTTCAGCGCAATATGATTTGATTTGTTGGGCTCAAGAAC 347
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
120 TyrTyrGlySerSer.....TyrPheAspTyrTrpGlyGlnGly 133
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
348 CCTGGTCACTGTCTGAGC 366
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
133 rThrleuThrValSerSer 139
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

seq_name: SwissProt_39:HV1B_HUMAN

```

seq_documentation_block:
ID HV1B_HUMAN STANDARD; PRT; 117 AA.
AC P01743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-I REGION HG3 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83144028; PubMed=6298778;
RA Rechevi G., Ram D., Glazer L., Zakut R., Givol D.;
RT "Evolutionary aspects of immunoglobulin heavy chain variable region
RT (VH) gene subgroups";
RL Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
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CC -----
DR EMBL: J00240; AAA52988.1; -.
DR PIR: A02024; HHVHUG.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION HG3.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12946 MW; 203F92FC60CD1FE7 CRC64;

```

alignment_scores: Length: 98
Quality: 429.00 Gaps: 0
Ratio: 4.564
Percent Similarity: 95.918 Percent Identity: 83.673

alignment_block:
US-08-487-283A-12_COPY_58_423 x HV1B_HUMAN ..
Align seg 1/1 to: HV1B_HUMAN from: 1 to: 117

```

1 CAAGTCCAACTGTGTCAATCCGCGCCGAGCTCAAGAACGAGGCGCTC 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 GlnValGlnLeuValGlnSerGlyAlaGlnValLysLysProGlyAlaSe 36
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51 AGCAAGTGCCTGTAAAGCTAGCGGCTATATTTTCTAATTATGGA 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
36 rVallysValSerGlyAlaSerGlyThrPhenSerTyrTrpM 53
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
101 TTCATGGGTGGTCAAGCCCCGGGACAGCGCTGGAATGAGGTGAG 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
53 eHISrPvalArgGlnAlaProGlyGlnGlyLeuGlnTrpMetGlyIle 69
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
151 ATCTTACCGGCTGTGTCAGACCGCAATATACGAAATTTTAAAGACCG 200
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
70 IleAsnProSerGlyAlaSerGlyThrPhenSerTyrTrpM 86
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
201 TGTACTATGACGCGTGCAGCTTCGACTAGTACATGATGAGGCTCT 250
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
86 gValThrMetThrAlaSerGlyAlaSerGlyThrPhenSerTyrTrpM 103
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
251 CCAGCTGCGATCGAGACGACGCGCTGATATGCGCGCTAT... 294
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
103 erSerleuThrSerGlyAlaSerGlyThrPhenSerTyrTrpM 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

seq_name: SwissProt_39:HV01_MOUSE

```

seq_documentation_block:
ID HV01_MOUSE STANDARD; PRT; 121 AA.
AC P01745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION MPC 11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81053741; PubMed=6253904;
RA Zakut R., Cohen J., Givol D.;
RT "Cloning and sequence of the cDNA corresponding to the variable
RT region of immunoglobulin heavy chain MPC11.";
RL Nucleic Acids Res. 8:3591-3601(1980).
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: J00240; AAA52988.1; -.
DR PIR: A02027; GVSJ11.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; Ig; 1.
KW Immunoglobulin V region.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56EDBF CRC64;

```

alignment_scores: Length: 123
Quality: 419.50 Gaps: 2
Ratio: 3.921
Percent Similarity: 86.992 Percent Identity: 60.976

alignment_block:
US-08-487-283A-12_COPY_58_423 x HV01_MOUSE ..
Align seg 1/1 to: HV01_MOUSE from: 1 to: 121

```

1 CAAGTCAACTGGTGCATCCGGCCGAGGTCAAGAGAGGCGCTC 50
  : : : : : : : : : : : : : : : : : : : : : : : :
1 GIUAlaGlnLeuGlnInserGlyAlaGlnLeuValArgProGlyThrSer 17
51 AGTCAAAAGTGTCTCTAAAGCTAGCGGCTATATTTTCTAATATGGA 100
  : : : : : : : : : : : : : : : : : : : : : : : :
17 rYAllyslIleSerCysGlyAlaAlaGlyTyrThrPheThrAsnTyrTrpI 34
101 TTCATGGGTGCGTCAAGCCCGCGGAGGCGCTGGAATGATGGGTGAG 150
  : : : : : : : : : : : : : : : : : : : : : : : :
34 lEgLyThrPAllyslGlnArgProGlyHisGlyLeuGlnTyrPrlGlyAsp 50
151 AACTTACCGGGCTCTGTAGACACCGAATATACGAAATTTTAAAGCCG 200
  : : : : : : : : : : : : : : : : : : : : : : : :
51 lIeTyPProGlyGlyPheThrAsnTyrAsnAspAsnLeuLysGlyLys 67
201 TGTACTATGACGCTGACACTGACTATACATATGAGAGGCTCT 250
  : : : : : : : : : : : : : : : : : : : : : : : :
67 sAlaThrLeuThrAlaAspThrSerSerThrAlaTyrIleGlnLeuS 84
251 CCAGCTGGGATCGAGAGACGCGCTCTATTATGCGGCGT...TAT 297
  : : : : : : : : : : : : : : : : : : : : : : : :
84 eSerLeuThrSerGlnAspSerAlaIleTyrHisCysAlaArgGlyIle 100
298 TTTTGTGTTCTAGCCGAAATTTGATTTGATTTGGGCTCAAGAAC 347
  : : : : : : : : : : : : : : : : : : : : : : : :
101 TyrTyAsnSerSerPro.....TyrPheAspSerTrpGlyGlnGlyTh 115
348 CCGGTCACGTCTCGAGC 366
  : : : : : : : : : : : : : : : : : : : : : : : :
115 rThrLeuThrValSerSer 121

```

seq_name: SwissProt_39:HV1G_HUMAN

seq_documentation_block:

```

ID HV1G_HUMAN STANDARD; PRT; 147 AA.
AC P01744;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE IG HEAVY CHAIN V-I REGION ND PRECURSOR (FRAGMENTS).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83065234; PubMed=6815656;
RA Kenten J.H., Molyard H.V., Houghcon M., Derbyshire R.B., Viney J.,
RA Bell L.O., Gould H.J.;
RT "Cloning and sequence determination of the gene for the human
RT immunoglobulin epsilon chain expressed in a myeloma cell line.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN [2]
RP SEQUENCE OF 20-147.
RA Benich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL (in) Bach M.K. (eds.);
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL Marcel Dekker, New York (1978).
CC -I- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN.
DR PIR: A02026; EIHUND.
DR Pfam: PF00047; Ig_1.
KW Immunoglobulin V region. Signal.
FT SIGNAL 1 19
FT CHAIN 20 147 IG HEAVY CHAIN V-I REGION ND.
FT MOD_RES 20 20 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 41 115
FT CONFLICT 21 21 T -> V (IN REF. 2).
FT CONFLICT 53 54 IH -> HI (IN REF. 2).
FT CONFLICT 67 68 VG -> GV (IN REF. 2).
FT CONFLICT 125 125 MISSING (IN REF. 2).
FT NON_TER 147 147

```

SO SEQUENCE 147 AA; 16491 MW; 948F9F72A5366C20 CRC64;

alignment_scores:
 Quality: 414.00 Length: 132
 Ratio: 3.869 Gaps: 3
 Percent Similarity: 81.061 Percent Identity: 62.879

alignment_block:
 us-08-487-283a-12_copy_58_423 x HV1G_HUMAN ..
 Align seg 1/1 to: HV1G_HUMAN from: 1 to: 147

```

1 CAAGTCAACTGGTGCATCCGGCCGAGGTCAAGAGAGGCGCTC 50
  : : : : : : : : : : : : : : : : : : : : : : : :
20 GlnThrGlnLeuValGlnInserGlyAlaGlnLeuValArgLysProGlyAlaSer 36
51 AGTCAAAAGTGTCTCTAAAGCTAGCGGCTATATTTTCTAATATGGA 100
  : : : : : : : : : : : : : : : : : : : : : : : :
36 rValArgValSerCysLysAlaSerGlyTyrThrPheIleAspSerTyrI 53
101 TTCATGGGTGCGTCAAGCCCGCGGAGGCGCTGGAATGATGGGTGAG 150
  : : : : : : : : : : : : : : : : : : : : : : : :
53 lEhstrPrlEArgGlnAlaProGlyHisGlyLeuGlnTyrPAlGlyTrp 69
151 AACTTACCGGGCTCTGTAGACACCGAATATACGAAATTTTAAAGCCG 200
  : : : : : : : : : : : : : : : : : : : : : : : :
70 lIeAsnProAsnSerGlyGlyThrAsnTyrAlaProArgPheGlnGlyLys 86
201 TGTACTATGACGCTGACACTTGCATAGTACATATGATGAGGCTCT 250
  : : : : : : : : : : : : : : : : : : : : : : : :
86 gValThrMetThrArgAspAlaSerPheSerThrAlaTyrMetAspLeuA 103
251 CCAGCTGGGATCGAGAGACGCGCTCTATTATGCGGCTTATTTT 300
  : : : : : : : : : : : : : : : : : : : : : : : :
103 rGSerLeuThrSerAspAspSerAlaValPheTyrCysAlaLys..... 117
301 TTTGTTCTAGCCGCAATTGC.....TATTTT..... 327
  : : : : : : : : : : : : : : : : : : : : : : : :
118 .....SerAspProPheThrSerAspTyrTyrAsnPheAspTyrSerTyr 132
328 .....GATGTTGGGCTCAAGAACCTGCTGCTCTCGAGC 366
  : : : : : : : : : : : : : : : : : : : : : : : :
132 rThrLeuAspValTrpGlyGlnGlyThrThrValThrValSerSer 147

```

seq_name: SwissProt_39:HV1G_HUMAN

seq_documentation_block:

```

ID HV1G_HUMAN STANDARD; PRT; 117 AA.
AC P23083;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUN-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-I REGION V35 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88296408; PubMed=2841108;
RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA Ohno H., Fukushima S., Honjo T.;
RT "Dispersed localization of D segments in the human immunoglobulin
RT heavy-chain locus."
RL EMBO J. 7:1047-1051(1988).
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CC -----
DR EMBL; X07448; NOT_ANNOTATED_CDS.
DR PIR; S00476; HVH035.
DR InterPro; IPR003006; -
DR Pfam; PF00047; Ig; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL
FT CHAIN 1 19
FT NON_TER 20 117 IG HEAVY CHAIN V-I REGION V35.
FT SEQUENCE 117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;
SQ

alignment_scores:
Quality: 403.00 Length: 98
Ratio: 4.380 Gaps: 0
Percent Similarity: 93.878 Percent Identity: 77.551

alignment_block:
US-08-487-283A-12_COPY_58_423 x HV1G_HUMAN ..

Align seg 1/1 to: HV1G_HUMAN from: 1. to: 117

1 CAAGTCCAACTGTCATCCGCGCCGAGTCACAGACCGAGGCGCTC 50
|||||
20 GlnValGlnLeuValGlnSerGlyAlaGluValLysProGlyAlaSe 36
51 AGTCAAAAGTCTCTGTAAGCTAGCGGCGATATTCTTAATTATGGA 100
|||||
36 rValLysValSerCysLysAlaSerGlyTyrThrPheThrGlyTyrTrm 53
101 TTCATGGGTCGTCAGCGCCCGGCGAGGCGCTGATGATGGGTAG 150
|||||
53 ethStrpValAlaGlnAlaProGlyGlnGlyLeuGluTrpMetGlyArg 69
151 ATCTTACCGGCTCTGTAGACACCGAATATACGAAATTTAAAGACCG 200
|||||
70 IleAspProAsnSerGlyGlyThrAsnTyrAlaGlnLysPheGlnGlyArg 86
201 TGTTCATGACGCGCTGACACTTGCATAGTACAGTATACATGAGACTCT 250
|||||
86 rValThrSerThrArgAspThrSerIleSerThrAlaTyrMetGluLeu 103
251 CCAGCGCTCGATCGAGGACGCGCGCTATATTGCGCGCGT 294
|||||
103 eArgLeuArgSerAspThrValTyrTyrCysAlaArg 117

seq_name: SwissProt_39:HV11_MOUSE
seq_documentation_block:
ID HV11_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION S43 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
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CC -----
DR EMBL; J00539; AAA38172.1; -
DR PIR; A02038; G2MS43.
DR InterPro; IPR003006; -
DR Pfam; PF00047; Ig; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL
FT CHAIN 1 19
FT NON_TER 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARTY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARTY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 137 137
FT SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;
SQ

alignment_scores:
Quality: 403.00 Length: 122
Ratio: 3.990 Gaps: 1
Percent Similarity: 82.787 Percent Identity: 63.115

alignment_block:
US-08-487-283A-12_COPY_58_423 x HV11_MOUSE ..

Align seg 1/1 to: HV11_MOUSE from: 1 to: 137

1 CAAGTCCAACTGTCATCCGCGCCGAGTCACAGACCGAGGCGCTC 50
|||||
20 GlnValGlnLeuGlnGlnProGlyAlaGluPheValLysProGlyAlaSe 36
51 AGTCAAAAGTCTCTGTAAGCTAGCGGCGATATTCTTAATTATGGA 100
|||||
36 rValLysLeuSerCysLysAlaSerGlyTyrThrPheThrSerTyrLeu 53
101 TTCATGGGTCGTCAGCGCCCGGCGAGGCGCTGATGATGGGTAG 150
|||||
53 ethStrpValAlaGlnAlaProGlyGlnGlyLeuGluTrpMetGlyArg 69
151 ATCTTACCGGCTCTGTAGACACCGAATATACGAAATTTAAAGACCG 200
|||||
70 IleAspProAsnSerGlyGlyThrThrTyrAsnGlnLysPheArgSerIle 86
201 TGTTCATGACGCGCTGACACTTGCATAGTACAGTATACATGAGACTCT 250
|||||
86 sAlaThrLeuThrIleAspLysProSerSerThrAlaTyrMetGlnLeu 103
251 CCAGCGCTCGATCGAGGACGCGCGCTATATTGCGCGCGTATTTT 300
|||||
103 eArgLeuThrSerGlnAspSerAlaValTyrTyrCysAlaArgTyrArg 119
301 TTTGGTCTTAGCCCGAATGATTTGATGTTGGGTGCAAGAACCTT 350
|||||
120 LeuGlyArg.....TyrPheAspTyrTrpGlyGlnGlyThr 132
351 GGTCACTGTCGAGC 366
132 rLeuThrValSerSer 137

seq_name: SwissProt_39:HV12_MOUSE
seq_documentation_block:
ID HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;

21-JUL-1986 (Rel. 01, Last Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION MOPC 104E.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_Taxid=10090;
[1]
SEQUENCE.
MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
Hood L.E.;
"Complete amino acid sequence of a mouse mu chain: homology among
heavy chain constant region domains."
Biochemistry 21:5415-5424(1982).
-1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
PROTEIN HAS ALSO BEEN DETERMINED.
-1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
PIR: A02039; MHMS4E.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; 19; 1.
KW Immunoglobulin V region; Glycoprotein.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12963 MW; 3CF8ACE4BE47E41 CRC64;

alignment_scores:

Quality: 401.50 Length: 122
Ratio: 3.861 Gaps: 1
Percent Similarity: 85.246 Percent Identity: 59.836

alignment_block:

US-08-487-283a-12_COPY_58_423 x HV12_MOUSE ..

Align seg 1/1 to: HV12_MOUSE from: 1 to: 117

```
1 CAAGTCCAACTGGTGCATCCGCGCCGAGTCAAGACCGAGGCGCTC 50
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
1 GlnValGlnLeuGlnGlnSerGlyProGlnLeuValLysProGlnAlaSer 17
51 AGTCAAGTGTCTCTGTAAGCTAGCGGCTATATTTTCTAATTATTTGA 100
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
17 rValLysMetSerCysLysAlaSerGlyTyrThrPheThrAspTyrTrpM 34
101 TTCAATGGGCGCTCAGAGCCCGGCGAGGCGCTGGAATGATGGGTGAG 150
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
34 eTyrStrValLysGlnSerHisGlyLysSerLeuGlnTyrPheLeGlyAsp 50
151 ATCTTACCGGCGCTCGTGCATCCGCGCCGAGTCAAGACCGAGGCGCTC 200
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
51 IleAsnProAsnAsnGlnGlyThrSerTyrAsnGlnLysPheLysGlyLys 67
201 TGTACTATGACCGCTGCACACTTGCAGTACAGTATACATGAGAGCTCT 250
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
67 salAthrLeuThrValAspLysSerSerThrAlaTyrMetGlnLeuA 84
251 CCAGCGCTGCATCGAGAGACAGCGCGCTATATTTTCCGCGCTTATTTT 300
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
84 snSerLeuThrSerGlnAspSerAlaValTyrTyrCysAlaArgAspTyr 100
301 TTTGGTTCTAGCCCGAATGTTATTTGATTTGGGTCACAGAACCGCT 350
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
101 .....AspTyrTyrPheAspValTyrPheGlnAlaGlyThrTh 112
351 GGTCACTGTCTCGAGC 366
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
112 rValThrValSerSer 117
```

seq_name: SwissProt_39:HV50_MOUSE

seq_documentation_block:
ID HV50_MOUSE STANDARD; PRT: 120 AA.
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
IG HEAVY CHAIN V REGION AC38 15.3.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_Taxid=10090;
[1]
SEQUENCE.
MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Boyens J., Silevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
lymphocytes is encoded by a large set of antibody structural genes";
EMBO J. 3:517-523(1984).
PIR: A02037; MHMS15.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; 19; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 105 D SEGMENT.
FT DOMAIN 106 120 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13311 MW; 914453FA26F09834 CRC64;

alignment_scores:

Quality: 401.00 Length: 122
Ratio: 3.819 Gaps: 1
Percent Similarity: 86.066 Percent Identity: 60.656

alignment_block:

US-08-487-283a-12_COPY_58_423 x HV50_MOUSE ..

Align seg 1/1 to: HV50_MOUSE from: 1 to: 120

```
1 CAAGTCCAACTGGTGCATCCGCGCCGAGTCAAGACCGAGGCGCTC 50
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
1 GlnValGlnLeuGlnGlnSerGlyProGlnLeuValLysProGlnAlaSer 17
51 AGTCAAGTGTCTCTGTAAGCTAGCGGCTATATTTTCTAATTATTTGA 100
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
17 rValAsnLeuSerCysLysAlaSerGlyTyrThrPheThrSerTyrTrpM 34
101 TTCAATGGGCGCTCAGAGCCCGGCGAGGCGCTGGAATGATGGGTGAG 150
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
34 eHisTyrPheArgGlnArgProGlnGlnGlyLeuGlnTyrPheLeGlyLys 50
151 ATCTTACCGGCGCTCGTGCATCCGCGCCGAGTCAAGACCGAGGCGCTC 200
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
51 IleAsnProSerAsnGlnGlyThrSerTyrAsnGlnLysPheLysSerLys 67
201 TGTACTATGACCGCTGCACACTTGCAGTACAGTATACATGAGAGCTCT 250
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
67 salAthrLeuThrValAspLysSerSerSerThrAlaTyrMetGlnLeuA 84
251 CCAGCGCTGCATCGAGAGACAGCGCGCTATATTTTCCGCGCTTATTTT 300
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
84 eThrThrProThrSerGlnAspSerAlaValTyrTyrCysAlaArgTyrPasp 100
301 TTTGGTTCTAGCCCGAATGTTATTTGATTTGGGTCACAGAACCGCT 350
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
101 Tyr.....GlnGlyAspArgTyrPheAspValTyrPheGlnAlaGlyThrTh 115
351 GGTCACTGTCTCGAGC 366
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
115 rValThrValSerSer 120
```

seq_name: SwissProt_39:HV03_MOUSE

seq_documentation_block:
 ID HV03_MOUSE STANDARD; PRT; 120 AA.
 AC P01747;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION 36-65.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8313846; PubMed=6186498;
 RA Stekevitz M., Geffer M.L., Brodeur P., Riblet R.,
 RA Marshak-Rothstein A.;
 RT "The genetic basis of antibody production: the dominant anti-arsonate
 RT idiotype response of the strain A mouse."
 RL Eur. J. Immunol. 12:1023-1032(1982).
 CC -I- MISCELLANEOUS: THE SIZES OF SEVERAL OTHER
 CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
 CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
 CC SEGMENT, JH2.
 CC PIR: A02028; HWSG7.
 DR Interpro: IPR003006; -.
 DR Pfam: PF00047; Ig; 1.
 KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
 FT NON_TER 120 120
 FT SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

alignment_scores:
 Quality: 398.50 Length: 123
 Ratio: 3.946 Gaps: 2
 Percent Similarity: 82.114 Percent Identity: 62.602

alignment_block:

US-08-487-283A-12_COPY_58_423 x HV03_MOUSE ..

Align seg 1/1 to: HV03_MOUSE from: 1 to: 120

```

4 GTCCAACTGTCGCAATCCGCGCCGAGTCAAGAAGCCAGGGCCCTCAGT 53
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 ValGlnLeuGlnGlnSerGlyAlaGluLeuValArgAlaGlySerSerVa 17
54 CAAGTGTCTGCTAAAGCTAGCGGCTATATTTTCTAATTAATTGATTC 103
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
17 llyMetSerCysLysAlaSerGlyTyrThrPheThrSerTyrGlyIleA 34
104 AATGGCTGCTCAGGCCCCCGGCGAGGCTCGAATGATGGGTGAGATC 153
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
34 snTPValLysGlnArgProGlyGlnGlyLeuGluTrpIleGlyTyrIle 50
154 TTACGGGCTCTGTAGACACGAAATATACGAAATTTTAAGACGCTGT 203
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
51 AsnProGlyAsnGlyTyrThrLysTyrAsnGlyLysPheLysGlyLysTh 67
204 TACTATGACGGCTGACACTTCGACTAGTACAGTATACATGAGCTCTCA 253
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
67 rThrLeuThrValAspLysSerSerSerThrAlaTyrMetGlnLeuArgS 84
254 GCCTCGATTCGAGAGACAGCGCCGCTATATATGCGCGCT.....TAT 297
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
84 erLeuThrSerGlnAspSerAlaValTyrPheCysAlaArgSerValTyr 100
298 TTTTGGTCTTAGCCCAATGATTTTGAAGTTTGGGCTCAAGACAC 347
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
101 TyrGlyGlySer.....TyrTyrPheAspTyrTrpGlyGlnGlyTh 114
348 CCGTCACATGCTCTGAGC 366
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
114 rThrLeuThrValSerSer 120

```

seq_name: SwissProt_39:HV13_MOUSE
 seq_documentation_block:
 ID HV13_MOUSE STANDARD; PRT; 117 AA.
 AC P0157;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION J558.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=80078170; PubMed=6765983;
 RA Schilling J., Clevinger B., Davie J.M., Hood L.;
 RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
 RT rearrangements in heavy chain V-region gene segments."
 RL Nature 283:35-40(1980).
 CC -I- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
 CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
 CC WHICH OCCUR IN THE D AND J SEGMENTS.
 CC PIR: A26242; MHMSJ5.
 DR Interpro: IPR003006; -.
 DR Pfam: PF00047; Ig; 1.
 KW Immunoglobulin V region.
 FT DISULFID 22 96
 FT NON_TER 117 117
 FT SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

alignment_scores:
 Quality: 397.50 Length: 122
 Ratio: 3.859 Gaps: 1
 Percent Similarity: 84.426 Percent Identity: 59.836

alignment_block:

US-08-487-283A-12_COPY_58_423 x HV13_MOUSE ..

Align seg 1/1 to: HV13_MOUSE from: 1 to: 117

```

1 CAAGTCCCACTGTCGCAATCCGCGCCGAGTCAAGAAGCCAGGGCCCTC 50
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 GluValGlnLeuGlnGlnSerGlyProGluLeuValLysProGlyAlaSe 17
51 AGTCAAGTGTCTGCTAAAGCTAGCGGCTATATTTTCTAATTAATTGGA 100
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
17 rValLysMetSerCysLysAlaSerGlyTyrThrPheThrAspTyrTrm 34
101 TTCAAATGGTGCCTCAGGCCCCCGGCGAGGCGCTGAAATGAGTGTGAG 150
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
34 etLysTrpValLysGlnSerHisGlyLysSerLeuGluTrpIleGlyAsp 50
151 ATCTTACCGGCTCTGTAGACACGAAATATACGAAATTTTAAGACCG 200
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
51 lIleAsnProAsnGlnGlyThrSerTyrAsnGlnLysPheLysGlyLys 67
201 TGTACTATACGCGCTGACACTTCGACTAGTACAGTATACATGAGGCTCT 250
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
67 sAlaThrLeuThrValAspLysSerSerSerThrAlaTyrMetGlnLeuA 84
251 CCAAGCTCGCATCGAGAGACAGCGCCGCTATATATGCGCGCTATATTT 300
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
84 snSerLeuThrSerGlnAspSerAlaValTyrTyrCysAlaArgAspArg 100
301 TTTGGTCTTAGCCCAATGATTTTGAAGTTTGGGCTCAAGACACCT 350
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
101 Tyr.....TyrTyrPheAspValTrpGlyAlaGlyThrTh 112
351 GGTACATGCTCTGAGC 366

```

|||||
112 rValthrValSerSer 117

seq_name: SwissProt_39:HV48_MOUSE

seq_documentation_block:

ID HV48_MOUSE STANDARD; PRT; 138 AA.
AC P03980;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION TEPC 1017 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
RT delta in an Igd-secreting plasmacytoma."
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR PIR: A02033; HVMST7.
DR InterPro; IPR003006; .
DR Pfam; PF00047; 1g; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 1 138 IG HEAVY CHAIN V REGION TEPC 1017.
FT DOMAIN 21 49 FRAMEWORK 1
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 128 138 FRAMEWORK 4.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 138 138
SO SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;

alignment_scores:
Quality: 392.50 Length: 124
Ratio: 3.886 Gaps: 2
Percent Similarity: 81.452 Percent Identity: 61.290

alignment_block:

US-08-487-283a-12_COPY_58_423 x HV48_MOUSE ..

Align seg 1/1 to: HV48_MOUSE from: 1 to: 138

1 CAAGTCCAACTGCTGCAATCCGGCGCGAGTCAGACAGACGGGCGCTC 50
|||||
20 GlnValGlnLeuGlnGlnProGlyAlaGlnLeuValLysProGlyAlaSe 36
51 AGTCAAGTGTCTCTAAAGCTAGCGGCTATATTTTCTAATATATGGA 100
|||||
36 rValGlnLeuSerCysAlaSerGlyHisThrPheThrAsnTyrTrpI 53
101 TTCATGGGTGCTCAGAGCCCGCGGCGAGGCGCTGAATGATGGGTGAG 150
|||||
53 LeHisrTrpValLysGlnArgProGlyGlnGlyLeuTrpIleGlyGlu 69
151 ATCTTACCGGGCTCTGGTAGCACCAGATATACGAAATTTTAAAGACG 200
|||||
70 IleAsnProAsnAspGlyArgSerAsnTyrAsnGluLysPheLysAsnLy 86
201 TGTACTATGACCGCGTACACTTCGACTACTAGATATACATGAGCTCT 250
|||||
86 sAlaThrLeuThrValAspLysSerSerSerTrpAlaTyrMetGlnLeu 103
251 CCAGCTGCGATCGAGACACGCGCTATATATTGCGCGCTTATTTT 300

|||||
103 erSerLeuThrProGlnGlnPheAlaValTyrTyrCysAlaArg..... 117
301 TTGGTTCAGCCCGAATGTAT.....TTGATGTTTGGGTCACAG 344
|||||
118SerAspGlyTyrTyrAsnTrpPheValTyrTrpGlyGlnG 131
345 AACCTGTCAGTCTCGAGC 366
|||||
131 ThrLeuValThrPheSerAla 138

seq_name: SwissProt_39:HV02_MOUSE

seq_documentation_block:

ID HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 9367 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A/J;
RX MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT Immunoglobulin heavy chain."
RL Science 216:309-311(1982).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00493; AAA38128.1; .
DR PIR: A02028; HVMST7.
DR InterPro; IPR003006; .
DR Pfam; PF00047; 1g; 1.
KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 9367.
FT NON_TER 140 140
SO SEQUENCE 140 AA; 15514 MW; 25ACBBE31DA5CE8 CRC64;

alignment_scores:
Quality: 383.50 Length: 123
Ratio: 3.760 Gaps: 2
Percent Similarity: 82.927 Percent Identity: 60.163

alignment_block:

US-08-487-283a-12_COPY_58_423 x HV02_MOUSE ..

Align seg 1/1 to: HV02_MOUSE from: 1 to: 140

1 CAAGTCCAACTGCTGCAATCCGGCGCGAGTCAGACAGACGGGCGCTC 50
|||||
20 GlnValGlnLeuGlnGlnSerGlyAlaGlnLeuValAlaGlySerSe 36
51 ACTCAAGTGTCTCTAAAGCTAGCGGCTATATTTTCTAATATATGGA 100
|||||
36 rAllyLysMetSerCysLysAlaSerGlyTyrThrPheThrSerTyrGly 53
101 TTCATGGGTGCTCAGAGCCCGCGGCGAGGCGCTGAATGATGGGTGAG 150
|||||


```

1 CAAGTCCAACTGGTGCATCCGGCCGAGGTCAAGAAGCCAGGGCCCTC 50
  |||||||
1 GluValGlnLeuValGlnSerGlyAlaGlnValLysLysProGlySerSe 17
  |||||||
51 ACTCAAGTCTCCTGTAAAGCTAGCGGCTATATTTTCTAATTATTGGA 100
  |||||||
17 ValLysValSerCysLysAlaSerGlyGlyThrPheSerArgSerAlaI 34
  |||||||
101 TTCAAATGGGTGCGTCAGGCCCCCGGCGCAGGCGCTGGAATGATGGGTAG 150
  |||||||
34 LeuLeuPValArgGlnAlaProGlyGlnGlyLeuGlnTrpMetClyGly 50
  |||||||
151 AACTTACCGGGCTCTGTAGCACCGCAATATACCAAAATTTTAAAGCCG 200
  |||||||
51 IleValProMetPheGlyProProAsnTrpAlaGlnLysPheGlnGlyAr 67
  |||||||
201 TGTACTATGACCGCTGTGACACTTCGACTAGTACATGATGAGCGCT 250
  |||||||
67 GValThrIleThrAlaAspGlnSerThrAsnThrAlaTyrMetGlnLeuS 84
  |||||||
251 CCAGCCTGCATCGGAGACACGGCCGCTCTATTTATGCGCGCTTATTTT 300
  |||||||
84 eSerLeuArgSerGlnAspThrAlaPheTyrPheCysAlaGlyGlyTyr 100
  |||||||
301 TTTCGTTCTAGCCCGAATGCTATTGATGTTGGGTCAGAGAACCT 350
  |||||||
101 GlyIleTyrSerProGlnGlnTyr.....AsnGlyGlyLe 112
  |||||||
351 GGTACGTCTCGAGC 366
  |||||||
112 uValThrValSerSer 117

```

seq_name: SwissProt_39:HV38_MOUSE

```

seq_documentation_block:
ID HV38_MOUSE STANDARD: PRT: 119 AA.
AC P01808:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION T601.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE-79223895; PubMed-111245;
RA Rao D.N., Rudikoff S., Kruttsch H., Potter M.;
RT "Structural evidence for independent joining region gene in
RT immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT its potential role in generating diversity in
RT complementarity-determining regions."
RL Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
CC THAT BINDS GALACTAN.
DR PIR: A02078; AVMS76.
DR HSSP: P01810; 2FBI.
DR InterPro: IPR003006; -.
DR Pfam: PF00047; 1g; 1.
KW Immunoglobulin V region.
FT NON TER 119 119
SQ SEQUENCE 119 AA: 13169 MW: BC38CC84E6EA00E8 CRC64:

```

alignment_scores:

```

Quality: 374.00 Length: 123
Ratio: 3.631 Gaps: 2
Percent Similarity: 83.740 Percent Identity: 54.472

```

alignment_block:

US-08-487-283a-12_COPY_58_423 x HV38_MOUSE

Align seg 1/1 to: HV38_MOUSE from: 1 to: 119

```

1 CAAGTCCAACTGGTGCATCCGGCCGAGGTCAAGAAGCCAGGGCCCTC 50
  |||||||
1 GluValLysLeuLeuGlnSerGlyGlyGlyLeuValGlnProGlyLys 17
  |||||||
51 ACTCAAGTCTCCTGTAAAGCTAGCGGCTATATTTTCTAATTATTGGA 100
  |||||||
17 LeuLysLeuSerCysAlaAlaSerGlyPheAspPheSerArgTyrTrp 34
  |||||||
101 TTCAAATGGGTGCGTCAGGCCCCCGGCGCAGGCGCTGGAATGATGGGTAG 150
  |||||||
34 eSerTrpValArgGlnAlaProGlyLysGlyLeuGlnTrpIleGlyGln 50
  |||||||
151 AACTTACCGGGCTCTGTAGCACCGCAATATATACCAAAATTTTAAAGCCG 200
  |||||||
51 IleAsnProAspSerSerThrIleAsnTyrThrProSerLeuLysAsp 67
  |||||||
201 TGTACTATGACCGCTGTGACACTTCGACTAGTACATGATGAGCGCTCT 250
  |||||||
67 sPheIleIleSerArgAspAsnAlaLysAsnThrLeuTyrLeuGlnMetS 84
  |||||||
251 CCAGCCTGCATCGGAGACACGGCCGCTCTATTTATGCGCGCTTATTTT 297
  |||||||
84 eLysValArgSerGlnAspThrAlaLeuTyrTyrCysAlaArgLeuGly 100
  |||||||
298 TTTCGTTCTAGCCCGAATGCTATTGATGTTGGGTCAGAGAAC 347
  |||||||
101 TyrTyrGly.....TyrPheAspValTrpGlyAlaGly 112
  |||||||
348 CCTGTACTGTCTCGAGC 366
  |||||||
112 rThrValThrValSerSer 118

```


OM of: US-08-487-283A-12_COPY_58_423 to: SPTRMBL_16.* out_format : pfs
Date: Jul 19, 2001 8:00 AM

About: Results were produced by the Gencore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

-MODEL=frame+12p_model -DEV=xlp
-O/cgn2.1/USPRO_spool/US08487283/runat_19072001_075205_227/app-query.fasta.1.444
-DB=SPTRMBL_16 -OPT=fastan -SUFFIX=tra.rspt -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPTOL=0.000 -LOOPTXT=0.000
-OGAPOP=4.000 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELPO=6.000 -DELEXT=7.000 -START=1 -MATRIX=blissum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NOR=ext -MINLEN=0 -MAXLEN=200000000
-USER=US08487283_ecgn1_1186 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPPX
-WAIT -THREADS=1

Search information block:

Query: US-08-487-283A-12_COPY_58_423
Query length: 366
Database: SPTRMBL_16.*
Database sequences: 425026
Database length: 132305027
Search time (sec): 51.820000

score_list:

Sequence	Strd Orig	ZScore	EScore	Len	Documentation
SP_human:09UL92	+	482.00	947.65	1.2e-44	124
SP_human:09UL94	+	451.50	887.66	2.7e-41	119
SP_human:09UL95	+	446.50	877.36	9.8e-41	125
SP_human:09UL89	+	445.00	875.02	1.4e-40	116
SP_invertebrate:09GY22	+	430.50	846.12	5.7e-39	119
SP_human:09UL92	+	419.00	823.44	1.0e-37	118
SP_human:09UL94	+	411.50	806.20	7.2e-37	157
SP_human:09UL95	+	394.50	772.95	5.3e-35	150
SP_human:09UL89	+	389.50	765.15	1.9e-34	117
SP_human:09UL92	+	373.50	733.50	1.1e-32	117
SP_human:09UL89	+	369.00	724.82	3.4e-32	114
SP_human:09UL77	+	367.00	721.16	5.6e-32	110
SP_human:09UL83	+	359.00	705.34	4.2e-31	110
SP_human:09UL75	+	359.00	696.95	4.6e-31	298
SP_human:09UL75	+	356.00	699.48	9.1e-31	109
SP_human:09UL86	+	341.50	670.20	3.6e-29	117
SP_human:09UL88	+	341.50	669.25	3.6e-29	131
SP_human:09UL71	+	339.50	665.96	6.0e-29	121
SP_human:09UL95	+	334.00	653.44	2.5e-28	147
SP_human:09UL81	+	328.00	643.86	1.1e-27	112
SP_human:09UL84	+	328.00	643.14	1.1e-27	122
SP_human:09UL90	+	327.50	642.80	1.3e-27	113
SP_human:09UL91	+	327.00	641.44	1.4e-27	118
SP_human:09UL72	+	322.00	631.55	1.2e-26	118
SP_human:09UL85	+	318.50	625.29	5.1e-27	109
SP_human:09UL93	+	315.50	618.84	2.6e-26	116
SP_mammal:09U0M4	+	312.00	611.35	6.5e-26	124
SP_mammal:09U0M6	+	309.00	605.42	1.4e-25	124
SP_human:09UL73	+	299.50	584.99	2.0e-24	119
SP_human:09UL87	+	289.50	568.32	1.9e-23	104
SP_human:09UL79	+	281.50	552.62	1.5e-22	102
SP_human:09UL83	+	281.50	551.87	1.5e-22	112
SP_human:09UL84	+	281.00	539.43	1.9e-22	437
SP_human:09UL86	+	280.00	550.29	2.1e-22	95
SP_human:09UL86	+	273.00	532.60	1.3e-21	150
SP_human:09UL75	+	242.00	473.01	3.2e-18	122
SP_human:09UL96	+	234.50	458.24	2.2e-17	121
SP_human:09UL86	+	222.00	423.12	5.9e-16	416
SP_human:075732	+	217.00	426.90	1.8e-15	82
SP_human:075741	+	215.50	424.46	2.7e-15	77

SP_human:075729	+	215.50	423.93	2.7e-15	80	075729	homo sapiens (human)
SP_human:075727	+	215.00	423.15	3.0e-15	82	075727	homo sapiens (human)
SP_human:075719	+	210.00	413.15	1.1e-14	81	075719	homo sapiens (human)
SP_human:075740	+	209.50	411.66	1.2e-14	86	075740	homo sapiens (human)
SP_human:09UL74	+	209.50	409.00	1.3e-14	118	09UL74	homo sapiens (human)

seq_name: SP_human:09UL92

seq_documentation_block:

ID	Q9UL92	PRELIMINARY	PRT	124 AA
AC	Q9UL92			
DT	01-MAY-2000	(TREMBLrel. 13, Created)		
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)		
DT	01-MAY-2000	(TREMBLrel. 16, Last annotation update)		
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT)			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBT:taxid:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE:98277139; PubMed:9614934;			
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,			
RA	Young D.C.;			
RT	Myosin-reactive autoantibodies in rheumatic carditis and normal			
RT	fetus."			
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).			
CC	-I SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX			
CC	DOMAIN			
DR	EMBL: AF035022; AAD56258.1; -			
DR	InterPro: IPR003006; -			
DR	InterPro: IPR003596; -			
DR	Pfam: PF00047; 1g; 1.			
DR	SMART: SM00406; IGV; 1.			
FT	NON_TER	1		
FT	NON_TER	124		
FT	SEQUENCE	124 AA; 13580 MW; 1BAAACBD96ACD2A2 CRC64;		

alignment_scores:

Quality	482.00	Length	124
Ratio	4.342	Gaps	1
Percent Similarity	89.516	Percent Identity	76.613

align seg 1/1 to: Q9UL92 from: 1 to: 124

US-08-487-283A-12_COPY_58_423 x Q9UL92

1	CAAGTCCAACTGGTGCATCCGCGCGGCAAGGAGGCGGCTC	50
1	GLVAlGlnIeuValGluSerGlyAlaGluValLysProGlyAla	17
51	AGTCAAGTCTCTGTAACCTAGCGGCTATTTTCTTAATTATGGA	100
17	ValLysValSerCysLysAlaSerGlyTyrThrPheSerSerTyr	34
101	TTCAATGGGAGGTCAGGCGCGGCGGAGGCGGATGATGATGAG	150
34	EthIstrPValArgGlnAlaProGlyInGlyLeuGlnTyrMetGly	50
151	ATCTTACCGGCGCTGGTACACCAATATACGAAATTTTAAAGCG	200
51	IleAsnProSerGlySerThrSerTyrAlaGlnLysPheGlnGly	67
201	TGTTACTATGACCGGTGACCTTGACTAGTACATGATGAGCTCT	250
67	GValThrMetThrArgAspThrSerThrSerThrValTyrMetGly	84
251	CGAGCGTGGATGGAGGAGGAGCGGCTATATTCGGCGGATATTT	300
84	EterLeuArgSerGluAspThrAlaValTyrTyrCysAlaArgGly	100

```
301 TTGGTCTACCCGGAATGCTAT.....TTTGATTTGGGCTCAAG 344
    ::::: ||||| ||||| |||||
101 TTTValValValProAlaAlaPheSerArgPheAspTyrTrpGlyGlnG 117
345 AACCGTGTCTACTGCTCGAGC 366
||||| ||||| ||||| |||||
117 yThrLeuValThrValSerSer 124
```

seq_name: sp_human:Q9UL94

seq_documentation_block:

```
ID Q9UL94 PRELIMINARY; PRT; 119 AA.
AC Q9UL94;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
EMBL: AF035020; AAD56256.1; -
DR InterPro: IPR003006; -
DR InterPro: IPR003596; -
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
DR NON_TER 1
FT NON_TER 119
FT SEQUENCE 119 AA; 13205 MW; 13E64F53454FA16E CRC64;
```

alignment_scores:

```
Quality: 451.50 Length: 122
Ratio: 4.142 Gaps: 1
Percent Similarity: 89.344 Percent Identity: 71.311
```

alignment_block:

US-08-487-283a-12_COPY_58_423 x Q9UL94 ..

Align seg 1/1 to: Q9UL94 from: 1 to: 119

```
1 CAAGTCCAACTGCTGCAATCCGGCCGCGAGGTCAAGACGAGGCGCTC 50
    ::::: ||||| ||||| ||||| |||||
1 GluValGlnLeuValGlnSerGlyAlaGluValLysProGlyAlaSer 17
51 AGTCAAGTGTCTGTAAGCTGAGCGGTATATTTTCTAATTATTTGA 100
||||| ||||| ||||| ||||| |||||
17 rValLysValSerCysLysAlaSerGlyTyrThrPheThrGlyTyrM 34
101 TTCATGGGTGCGTCAGCCCGCGGCGAGGCGCTGGAATGATGAGGTGAG 150
::::: ||||| ||||| ||||| |||||
34 eHisTrpValArgGlnAlaProGlyGlnGlyLeuGluTrpMetGlyTyr 50
151 ATCTTACCGGCGCTGCTGAGCACCGCAATATACCGAAATTTTAAAGCCG 200
||| ||||| ||||| ||||| |||||
51 IleAsnProAsnSerTrpThrThrAsnTyrAlaGlnLysPheGlnGly 67
201 TGTACTATGACGCGTGACACTTGACTAGATACATGATGAGAGCTCT 250
.:||| ||||| ||||| ||||| ||||| |||||
67 sValThrMetThrLysAspThrSerIleSerThrAlaTyrMetGlnLeuS 84
251 CCAGCGTGCATGAGGACAGGACGCGCTATATTTGCGGCGCTTATTTT 300
|| 4||||| ||||| ||||| ||||| ||||| |||||
```

```
84 eArgLeuArgSerAspThrAlaValTyrTyrCysAlaArg..... 98
301 TTGGTCTACCCGGAATGATTTGATTTGGGGCTCAAGAACCT 350
||||| ::::: ||||| ||||| |||||
99 ..GlyGlyGlyArgGlyLeuThrPheAspProTyrGlyGlnGlyThrLe 114
351 GGTCACTGTCTCGAGC 366
||||| ||||| ||||| |||||
114 uValThrValSerSer 119
```

seq_name: sp_human:Q9UL95

seq_documentation_block:

```
ID Q9UL95 PRELIMINARY; PRT; 125 AA.
AC Q9UL95;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
EMBL: AF035019; AAD56255.1; -
DR InterPro: IPR003006; -
DR InterPro: IPR003596; -
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
DR NON_TER 1
FT NON_TER 125
FT SEQUENCE 125 AA; 13516 MW; 0D3CD5C232488EAC CRC64;
```

alignment_scores:

```
Quality: 446.50 Length: 125
Ratio: 4.096 Gaps: 1
Percent Similarity: 87.200 Percent Identity: 69.600
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alignment_block:

US-08-487-283a-12_COPY_58_423 x Q9UL95 ..

Align seg 1/1 to: Q9UL95 from: 1 to: 125

```
1 CAAGTCCAACTGCTGCAATCCGGCCGCGAGGTCAAGACGAGGCGCTC 50
    ::::: ||||| ||||| ||||| |||||
1 GluValGlnLeuValGlnSerGlyAlaGluValLysProGlyAlaSer 17
51 AGTCAAGTGTCTGTAAGCTGAGCGGTATATTTTCTAATTATTTGA 100
||||| ||||| ||||| ||||| |||||
17 rValLysValSerCysLysAlaSerGlyTyrThrPheThrGlyTyrM 34
101 TTCATGGGTGCGTCAGCCCGCGGCGAGGCGCTGGAATGATGAGGTGAG 150
::::: ||||| ||||| ||||| |||||
34 eHisTrpValArgGlnAlaProGlyGlnGlyLeuGluTrpMetGlyTyr 50
151 ATCTTACCGGCGCTGCTGAGCACCGCAATATACCGAAATTTTAAAGCCG 200
||| ||||| ||||| ||||| |||||
51 IleAsnProAsnSerGlyGlyThrAsnTyrAlaGlnLysValGlnGlyAr 67
201 TGTACTATGACGCGTGACACTTGACTAGATACATGATGAGAGCTCT 250
||||| ||||| ||||| ||||| ||||| |||||
67 gValThrMetThrArgAspThrThrIleSerThrAlaTyrMetGlnLeuS 84
```

251 CCAGCCGTCGAGACACGCGCTATATATGCGCCGTTATTT 300
 11. |||||.....
 84 eraIrgleuAargSerAspAspThrAlaValTyrTyrCysAlaArgSerGln 100
 301 TTTGGT.....TCTAGCCCAATGGATTTGATGTTGGGCTCA 341
 |||
 101 GYGLYGLYArgIleAlaAlaIleGlyAspAlaIleAspIleTyrGly 117
 342 AGGAACCCGTCACGTCGTCGAC 366
 |||||.....
 117 nGlyThrMetValThrValSerSer 125

seq_name: sp_human:Q9UL89

seq_documentation_block:
 ID Q9UL89 PRELIMINARY; PRT; 116 AA.
 AC Q9UL89;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 16, Last sequence update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 OX [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalls N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 CC -1 SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN
 DR EMBL: AF035025; AAD56261.1; -.
 DR InterPro: IPR003006; -.
 DR InterPro: IPR003596; -.
 DR Pfam: PF00047; 1g; 1.
 DR SMART: SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 116
 SO SEQUENCE 116 AA; 12605 MW; C8F9131DE13EA898 CRC64;

alignment_scores:
 Quality: 445.00 Length: 118
 Ratio: 4.320 Gaps: 1
 Percent Similarity: 87.288 Percent Identity: 73.729

alignment_block:
 US-08-487-283A-12_COPY_58_423 x Q9UL89 ..

Align seg 1/1 to: Q9UL89 from: 1 to: 116

13 GTGCAATCCGCGCCGAGTCACAGACCGAGCGCTCATGCAAGTCTC 62
 |||||.....
 1 ValGlnSerIleValIleValIleValIleValIleValIleValIle 17
 63 CTGTAAAGTAGCGGCTATATTTTCTAATATGATTCATCAATGGTGC 112
 |||||.....
 17 rcysLysAlaSerGlyGlyThrPheSerSerTyrAlaIleSerTyrVal 34
 113 GTAGAGCCCCGGGCGAGCGCTGGAATGATGGGTGAGATCTTACCGGC 162
 |||||.....
 34 rrgInIaPrgIyngInGlyLeuGluTrrPmetGlyArgIleIleProlle 50
 163 TCTGTAGTAGCGCAATATACGAAATTTTAAAGACCGTGTACTATGAC 212
 |||
 51 LeuGlyIleIleAlaSnTyrAlaGlnLysPheGlnIleYalrValTrrIleTh 67
 213 GCCTGACACTTCGACTAGTACATATACATGAGACTCTCCAGCTGCAT 262
 ||| |||||.....

67 rAlaAspLysSerThrSerThrAlaTyrMetGluLeuSerSerLeuArgS 84
 263 CGAGAGACACGCGCGCTATATATGCGCGCTATTTTGGTCTAC 312
 |||||.....
 84 ecLunSpThrAlaValTyrTyrCysAlaSerSerAsnTyrGly..... 98
 313 CGGAATGGTATTTTATGTTGGGTCAGAGAACCTGTCTACTGCTC 362
 |||
 99 ProTyrTrrPtyrPheAspLeuTrrPglyArgGlyThrLeuValThrValSe 115
 363 GAGC 366
 ||||
 115 rSer 116

seq_name: sp_invertebrate:Q9GYZ2

seq_documentation_block:
 ID Q9GYZ2 PRELIMINARY; PRT; 119 AA.
 AC Q9GYZ2;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DE MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 HEAVY CHAIN VARIABLE REGION
 DE (FRAGMENT).
 OS Schistosoma japonicum (Blood fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
 OC Trematoda; Digenea; Strigoidida; Schistosomatidae; Schistosomatidae;
 OC Schistosoma.
 OX NCBI_TaxID=6182;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA Song X.T., Feng Z.Q., Guan X.H.;
 RT "Amplification, cloning and sequence analysis of the heavy chain
 RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
 RT Schistosoma japonicum";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF282622; AAC01452.1; -.
 FT NON_TER 1
 FT NON_TER 119
 SO SEQUENCE 119 AA; 13567 MW; BA893873FD5FA6AB CRC64;

alignment_scores:
 Quality: 430.50 Length: 122
 Ratio: 4.100 Gaps: 1
 Percent Similarity: 86.066 Percent Identity: 67.213

alignment_block:
 US-08-487-283A-12_COPY_58_423 x Q9GYZ2 ..

Align seg 1/1 to: Q9GYZ2 from: 1 to: 119

1 CAAGTCAACTGTGTCGAATCCGCGCCGAGGTCACAGACCGAGGCGCTC 50
 |||||.....
 1 GlnValGlnLeuValGlnSerGlyAlaGlnValAlaGlySerProGlyAlaSe 17
 51 AGTCAAGTCTCTGCTGAAGCTAGCGGCTATATTTTCTAATATGGA 100
 |||||.....
 17 rValArgValSerCysLysAlaSerGlyTyrThrPheThrGlyTyrTyrM 34
 101 TTCAAATGGTGGTGCAGCGCCGCGGCGAGCGCTGGAATGAGATGGGTGAG 150

 34 eLAsnTrrPValArgGlnAlaPrgIyngInGlyLeuGluTrrPleGlyTyr 50
 151 ATCTTACCGGCTCTGTGTAGACACCGAATATACGAAATTTTAAAGACG 200
 |||
 51 IleAsnProSerArgGlyTyrThrAsnTyrAsnGlnLysPheLysAspAr 67
 201 TGTACTATGACGCGGTGACACTTCGACTAGTACATATACATGAGACTCT 250
 |||||.....
 67 gValThrMetTrrThrAspLysSerPheSerThrAlaTyrMetAspLeuA 84
 251 CCAGCTGCGATCGGAGACGCGCGCTATATATGCGCGCTTATTTT 300


```
|||||
84 rgsSerLeuArgSerAlaaspSerAlaValTyrTyrIcysAlaArgTyr 100
301 TTGTGTTCAAGCCGCAATGTTGATTTGATTTGGGTCACGAGCCCT 350
101 .....AspAspHisTyrIcysLeuAspTyrTrpGlyGlnGlyThr 114
351 GGTCACTGTCGAGC 366
|||||
114 rAlthrValSerSer 119

seq_name: sp_rudent:0921C4

seq_documentation_block:
ID 0921C4 PRELIMINARY; PRT; 118 AA.
AC 0921C4;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DE 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Mattis L.M., Evans M.J.;
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT 1962/64 constant regions block human leukocyte binding to porcine
RT endothelial cells.";
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -! SIMILARITY: TO IMMNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; U78801; AAD00293.1; -.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 13036 MW; 90ECC559D31EC4FC CRC64;

alignment_scores:
Quality: 423.00 Length: 122
Ratio: 4.147 Gaps: 1
Percent Similarity: 83.607 Percent Identity: 63.934

alignment_block:
US-08-487-283A-12_COPY_58_423 x 0921C4 ..
Align seg 1/1 to: 0921C4 from: 1 to: 118

1 CAACTCCAACGTGTCGAATCCGGCCGAGTCGAAGACCGAGGCGCTC 50
|||||
1 GlnValGlnValGlnGlnSerGlyAlaGlnLeuAlaArgProTrpAla 17
51 AGTCAAAGTGTCTGTAAGCTAGCGGCTATATTTTCTTAATATTGA 100
|||||
17 rValIysLeuSerGlyAlaSerGlyTyrAsnPhaSerSerTrpM 34
101 TTCAATGGGTGCTCAGGCCCGGCGAGGCGCTGGAATGATGGGTGAG 150
|||||
34 eGlnTrpValIysGlnArgProGlyGlnGlyLeuGlnTrpIleGlyAla 50
51 AATCAACGGGCTGTGTAGCACCGAATATACGAATAATTTTAAACCG 200
|||||
51 IleTyrProGlyAspGlyAspThrSerTyrTrpGlnLysPheArgGly 67
201 TGTACTATGACGCGTACACTTCAGACTAGTACAGTATACATGACCTCT 250
|||||
```

```
67 sAlaThrLeuThrAlaAspLysSerSerThrAlaTyrIcysLeu 84
251 CCAAGTCGATCGAGACACAGCGCGCTCTATTTATTTGGCGCGTTATTT 300
|||||
84 erSerLeuAlaSerGlnAspSerAlaValTyrTyrIcysAlaArgThr 100
301 TTGTGTTCAAGCCGCAATGTTGATTTGATTTGGGTCACGAGCCCT 350
|||||
101 ValGlyGly.....TyrPheAspTyrTrpGlyGlnGlyThr 113
351 GGTCACTGTCGAGC 366
|||||
113 rLeuThrValSerSer 118

seq_name: sp_human:095978

seq_documentation_block:
ID 095978 PRELIMINARY; PRT; 157 AA.
AC 095978;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE VH1 PROTEIN PRECURSOR (FRAGMENT).
DE VH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PERIPHERAL BLOOD;
RA Jox A., Zander T., Kuipers R., Irach J., Kanzler H., Kornacker M.,
RA Bohlen H., Diehl V., Wolf J.;
RT "Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a
RT patient with mixed cellularly Hodgkin's disease is associated with
RT somatic mutations within the untranslated regions of rearranged and
RT class switch recombinated Ig genes.";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
CC -! SIMILARITY: TO IMMNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AJ005570; CAA06599.1; -.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
FT SIGNAL 1
FT SIGNAL 21
FT NON_TER 157
FT NON_TER 157
SQ SEQUENCE 157 AA; 17304 MW; 86986EDDA84D8B5 CRC64;

alignment_scores:
Quality: 411.50 Length: 122
Ratio: 4.115 Gaps: 1
Percent Similarity: 81.967 Percent Identity: 68.852

alignment_block:
US-08-487-283A-12_COPY_58_423 x 095978 ..
Align seg 1/1 to: 095978 from: 1 to: 157

1 CAACTCCAACGTGTCGAATCCGGCCGAGTCGAAGACCGAGGCGCTC 50
|||||
20 GlnValGlnLeuValGlnSerGlyAlaGlnLeuLysArgProGlyAla 36
51 AGTCAAAGTGTCTGTAAGCTAGCGGCTATATTTTCTTAATATTGA 100
|||||
36 rValIysValHisCysLysThrSerGlyTyrValPheThrSerTyrTr 53
101 TTCAATGGGTGCTCAGGCCCGGCGAGGCGCTGGAATGATGGGTGAG 150
|||||
53 LeuThrValArgGlnProArgGlyGlnGlyLeuGlnTrpMetGlyGly 69
|||||
```

151 ATCTACCGGGCTGTGGTACGACCGAATATACGAAATTTTAAAGCCG 200
|||||
70 ILGLYPRGILVALIGLYSERTHMETCYSLAGLULYSPHEGLYLAR 86
201 TGTACTATACCGCTGACACTTCGACTAGTACAGTATACGAGCCT 250
|||||
86 GLEUTHMETHTHRAIGSNTHRSERTHRTHRVALTLYRMTGLULEUS 103
251 CCAGCTCGGATCGAGACGCGCGCTATATATTCGCGCGTTATTTT 300
|||||
103 ERARGLEUARGPHEGLUASPTHRALVALTYRPHCYSGLYARGLYGLY 119
301 TTGGGTTCTAGCCCGAATGTGATTTGATGTTGGGTCAGAACCCCT 350
|||||
120 ARGTRPARGSERGLYASN...TYRANGLYHISRPGLYGLINGLYTHPR 135
351 GGTCACTGTCTCGAGC 366
|||||
135 OVALTHRVALSER 140

seq_name: sp_human:09Y298

seq_documentation_block:

PRELIMINARY; PRT; 150 AA.

ID 09Y298
AC 09Y298:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE ICG VH PROTEIN PRECURSOR (FRAGMENT).
GN ICG VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96322155; PubMed=9657749;
RA "Mechanism M.G., Vander Elst L.P.L.;
RT IgG monoclonal antibody derived from a hemophilia A patient with
RT inhibitor."
RL Blood 92:496-506(1998).
CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
CC EMBL; AJ224083; CAAL1829.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam: PF00047; 1g; 1.
DR SMART; SM00406; Igv; 1.
DR SIGNAL.
KW SIGNAL.
FT NON_TER 1 19
FT SEQUENCE 150 AA; 16031 MW; 563D164AB2280ZD5 CRC64;

alignment_scores:

Quality: 394.50 Length: 122
Ratio: 3.830 Gaps: 2
Percent Similarity: 84.426 Percent Identity: 65.574

alignment_block:

US-08-487-283A-12_COPY_58_423 x 09Y298 ..

Align seg 1/1 to: 09Y298 from: 1 to: 150

1 CAAGTCCAACTGGTGCATCCGGCGCGAGGTCAAGACGAGCGGCCTC 50
|||||
20 GLNVALGINLEUVALGINSERGLYALAGLULYLSYSPROGLYALASE 36
51 AGTCAAAGTGTCTGTAAAGTACGCGCTATATTTTCTAATTAATGGA 100
|||||
36 VALYSVALISERCYSLYSVALSERGLYTYRTHLEUTHRCGLUENUPROV 53

101 TTCATGGGTGGCTGACGCCCCCGGCGAGGCGCTGGAATGAGGGGTGAG 150
|||||
53 ALHISRPVALIGLYGINALAPROGLYLSGLYLEUENLUTRPVALIGLYSE 69
151 ATCTACCGGGCTGTGGTACGACCGAATATACGAAATTTTAAAGCCG 200
|||||
70 PHEASPRPROGLUSERGLYGLUSERLLETYRVALAARGLUPHEGLINLYSE 86
201 TGTACTATACGCGCTGACACTTCGACTAGTACAGTATACGAGCCTCT 250
|||||
86 RVALTHMETHTHRAIASPTHRSERTHRASPILEALATYRMTGLULEUS 103
251 CCAGCTCGGATCGAGACGCGCGCTATATATTCGCGCGCTTATTTT 300
|||||
103 ERSERLEUARGSERASPSPHRLALVALTYRTRCYSLA..... 116
301 TTGGGTTCTAGCCCGAATGTGATTTGATGTTGGGTCAGAACCCCT 350
|||||
117 ...VALPROASPRPROASP...ALAPHEASPILETTRPGLYGLINGLYTHRME 131
351 GGTCACTGTCTCGAGC 366
|||||
131 TVALTTHRVALSER 136

seq_name: sp_rodent:09QXF0

seq_documentation_block:

PRELIMINARY; PRT; 117 AA.

ID 09QXF0
AC 09QXF0:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademakers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ225171; CAB65236.1; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003596; -.
DR Pfam; PF00047; 1g; 1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1 117
FT SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;

alignment_scores:

Quality: 389.50 Length: 122
Ratio: 3.745 Gaps: 1
Percent Similarity: 85.246 Percent Identity: 58.197

alignment_block:

US-08-487-283A-12_COPY_58_423 x 09QXF0 ..

Align seg 1/1 to: 09QXF0 from: 1 to: 117

1 CAAGTCCAACTGGTGCATCCGGCGCGAGGTCAAGACGAGCGGCCTC 50
|||||
1 GLNVALGINLEUVALGINSERGLYPROGLULLEUVALYSPROGLYALASE 17
51 AGTCAAAGTGTCTGTAAAGTACGCGCTATATTTTCTAATTAATGGA 100
|||||
17 VALYSMETSERCYSLYSVALSERGLYTYRTHRPHETNHSPTLYTRGM 34
101 TTCATGGGTGGCTGACGCCCCCGGCGAGGCGCTGGAATGAGGGGTGAG 150
|||||
34 ELYSTRVALYLSGINSERHISGLYLSERLEUENLUTRPILIEGLYASP 50

```

151 ATCTTACGGGGCTCGGTGAGACCGCAATATACCGAAATTTTAAACACG 200
152 ||| |||||:::|||||:::|||||:::|||||:::|||||::: 201
51 ILEAsnPRoMaSnAsnglyGlyrHisSerIyrAsnGlnGlyPheNysGly 67
201 TGTACTAGTATGACGGCGTGACACTTGCAGCTAGTACAGATATACATGAGCCTT 250
:::|||||:::||||| ||| |||||:::|||||:::|||||:::||||| 251
67 sAlAtThrLeuHisValAlaPlySerSerSerThrAlaIyrMetGlnLeu 84
:::|||||:::|||||:::|||||:::|||||:::|||||:::||||| 300
251 CCAGCTGCGCATGGAGAGAACCGGCGCTATATTATGGCCGGCTATTTT 350
84 snSerLeuThrSerGlnAspSerAlaValAlaIyrTyrGlySalaArg..... 98
301 TTTTGTTCTTACGCCCGCAATTTGATTTTGTATGTTGGGGGTCAAGAACCTT 350
::: |||:::|||||:::|||||:::|||||:::|||||:::||||| 351
99 .....AspLysAspTyrTyrPheAspIyrTrpGlyGlnGlyThrTrh 112
351 GGTGCATGCTCTTCGAGC 366
112 rLeuThrValSerSer 117

```

seq_name	sp_rodent:Q9QX99
seq_documentation_block:	
ID_Q9QX99	PRELIMINARY; PRT; 117 AA.
AC_Q9QX99	
DT 01-MAY-2000 (TREMBlrel. 13, Created)	
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)	
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)	
DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).	
OS Mus musculus (Mouse).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus	
OX NCBI_TaxID=10099;	
[11]	
RN SEQUENCE FROM N.A.	
RA Clemens A., Rademaekers A., Specht C., Koelsch E.;	
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.	
DR EMBL: AJ225174; CAB65237.1; -.	
DR InterPro: IPR003006; -.	
DR InterPro: IPR003596; -.	
DR Pfam: PF00047; 1g; 1.	
DR SMART: SM00406; 1g; 1.	
FT NON_TER 1	
FT NON_TER 117	
SQ SEQUENCE 117 AA; 13000 MW; CDDE2AF64D49734 CRC64;	

alignment_scores:		
Quality:	373.50	Length: 1227
Ratio:	3.662	Gaps: 1
Percent Similarity:	83.607	Percent Identity: 57.3777

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alignment_block:
  no 00 407 10 0000 20 4000 30 0000 40 0000 50 0000 60 0000 70 0000 80 0000 90 0000 100 0000 110 0000 120 0000 130 0000 140 0000 150 0000 160 0000 170 0000 180 0000 190 0000 200 0000 210 0000 220 0000 230 0000 240 0000 250 0000 260 0000 270 0000 280 0000 290 0000 300 0000 310 0000 320 0000 330 0000 340 0000 350 0000 360 0000 370 0000 380 0000 390 0000 400 0000 410 0000 420 0000 430 0000 440 0000 450 0000 460 0000 470 0000 480 0000 490 0000 500 0000 510 0000 520 0000 530 0000 540 0000 550 0000 560 0000 570 0000 580 0000 590 0000 600 0000 610 0000 620 0000 630 0000 640 0000 650 0000 660 0000 670 0000 680 0000 690 0000 700 0000 710 0000 720 0000 730 0000 740 0000 750 0000 760 0000 770 0000 780 0000 790 0000 800 0000 810 0000 820 0000 830 0000 840 0000 850 0000 860 0000 870 0000 880 0000 890 0000 900 0000 910 0000 920 0000 930 0000 940 0000 950 0000 960 0000 970 0000 980 0000 990 0000 1000 0000 1010 0000 1020 0000 1030 0000 1040 0000 1050 0000 1060 0000 1070 0000 1080 0000 1090 0000 1100 0000 1110 0000 1120 0000 1130 0000 1140 0000 1150 0000 1160 0000 1170 0000 1180 0000 1190 0000 1200 0000 1210 0000 1220 0000 1230 0000 1240 0000 1250 0000 1260 0000 1270 0000 1280 0000 1290 0000 1300 0000 1310 0000 1320 0000 1330 0000 1340 0000 1350 0000 1360 0000 1370 0000 1380 0000 1390 0000 1400 0000 1410 0000 1420 0000 1430 0000 1440 0000 1450 0000 1460 0000 1470 0000 1480 0000 1490 0000 1500 0000 1510 0000 1520 0000 1530 0000 1540 0000 1550 0000 1560 0000 1570 0000 1580 0000 1590 0000 1600 0000 1610 0000 1620 0000 1630 0000 1640 0000 1650 0000 1660 0000 1670 0000 1680 0000 1690 0000 1700 0000 1710 0000 1720 0000 1730 0000 1740 0000 1750 0000 1760 0000 1770 0000 1780 0000 1790 0000 1800 0000 1810 0000 1820 0000 1830 0000 1840 0000 1850 0000 1860 0000 1870 0000 1880 0000 1890 0000 1900 0000 1910 0000 1920 0000 1930 0000 1940 0000 1950 0000 1960 0000 1970 0000 1980 0000 1990 0000 2000 0000 2010 0000 2020 0000 2030 0000 2040 0000 2050 0000 2060 0000 2070 0000 2080 0000 2090 0000 2100 0000 2110 0000 2120 0000 2130 0000 2140 0000 2150 0000 2160 0000 2170 0000 2180 0000 2190 0000 2200 0000 2210 0000 2220 0000 2230 0000 2240 0000 2250 0000 2260 0000 2270 0000 2280 0000 2290 0000 2300 0000 2310 0000 2320 0000 2330 0000 2340 0000 2350 0000 2360 0000 2370 0000 2380 0000 2390 0000 2400 0000 2410 0000 2420 0000 2430 0000 2440 0000 2450 0000 2460 0000 2470 0000 2480 0000 2490 0000 2500 0000 2510 0000 2520 0000 2530 0000 2540 0000 2550 0000 2560 0000 2570 0000 2580 0000 2590 0000 2600 0000 2610 0000 2620 0000 2630 0000 2640 0000 2650 0000 2660 0000 2670 0000 2680 0000 2690 0000 2700 0000 2710 0000 2720 0000 2730 0000 2740 0000 2750 0000 2760 0000 2770 0000 2780 0000 2790 0000 2800 0000 2810 0000 2820 0000 2830 0000 2840 0000 2850 0000 2860 0000 2870 0000 2880 0000 2890 0000 2900 0000 2910 0000 2920 0000 2930 0000 2940 0000 2950 0000 2960 0000 2970 0000 2980 0000 2990 0000 3000 0000 3010 0000 3020 0000 3030 0000 3040 0000 3050 0000 3060 0000 3070 0000 3080 0000 3090 0000 3100 0000 3110 0000 3120 0000 3130 0000 3140 0000 3150 0000 3160 0000 3170 0000 3180 0000 3190 0000 3200 0000 3210 0000 3220 0000 3230 0000 3240 0000 3250 0000 3260 0000 3270 0000 3280 0000 3290 0000 3300 0000 3310 0000 3320 0000 3330 0000 3340 0000 3350 0000 3360 0000 3370 0000 3380 0000 3390 0000 3400 0000 3410 0000 3420 0000 3430 0000 3440 0000 3450 0000 3460 0000 3470 0000 3480 0000 3490 0000 3500 0000 3510 0000 3520 0000 3530 0000 3540 0000 3550 0000 3560 0000 3570 0000 3580 0000 3590 0000 3600 0000 3610 0000 3620 0000 3630 0000 3640 0000 3650 0000 3660 0000 3670 0000 3680 0000 3690 0000 3700 0000 3710 0000 3720 0000 3730 0000 3740 0000 3750 0000 3760 0000 3770 0000 3780 0000 3790 0000 3800 0000 3810 0000 3820 0000 3830 0000 3840 0000 3850 0000 3860 0000 3870 0000 3880 0000 3890 0000 3900 0000 3910 0000 3920 0000 3930 0000 3940 0000 3950 0000 3960 0000 3970 0000 3980 0000 3990 0000 4000 0000 4010 0000 4020 0000 4030 0000 4040 0000 4050 0000 4060 0000 4070 0000 4080 0000 4090 0000 4100 0000 4110 0000 4120 0000 4130 0000 4140 0000 4150 0000 4160 0000 4170 0000 4180 0000 4190 000
```

US-08-48/-283A-12_COPY_58_423 x Q9QXE9 . .

Align seg 1/1 to: Q9QXE9 from: 1 to: 117

```

51  CAGGTCCCACTGGTGTGCAATTCGGGCGCCGAGCAAGAACCCAGGGGCGCTC 50
1   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1   GUAValGlnLeuGlnInsInserGlyProGlnLeuValYsProGlnAlaIse 17
51  AGTCAAGAGTGCTCCGTAAAGCAAGCGGCTATATTTTCTTAATTAATGGA 100
17  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
17  YAllysMetSerCysLysAlaSerGlyThrPheThrAspTyrTyrIm 34
101 TTCAATGGGTGCGCTCAGGCCCGCCGGGACAGGCCCTGGAATGATGGGTAG 150
34 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
34 eTrysTrpAllysGlnSerHisGlyLysSerLeuGlnVtrPleileGlyasp 50
151 AATCTACGGGGCTCGCTGAGCAACCGAATTACCAGAAATTTTAAAGACCG 200
151 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
151 IlaAsnProGlnAsnMetLysLysThrSerTyrAsnGlnLysPheLysGlyL 67

```

[illegible]

seq_documentation_block:		PTI:	114 AA.
ID	09J181		
AC	09J181;		
DT	01-OCT-2000 (TREMblrel. 15, Created)		
DT	01-Oct-2000 (TREMblrel. 15, Last sequence update)		
DT	01-MAR-2001 (TREMblrel. 16, Last annotation update)		
DE	ANTI-MYOSIN IMMUNOLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxId=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-BALB/C;		
RA	Malikl S., Liao L., Cunningham M.W., Diamond B.;		
RT	"Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis."		
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF206025; AAF69323.1; -.		
DR	InterPro; IPR003006;		
DR	InterPro; IPR003596; -.		
DR	Pfam; PF00047; 1g; 1.		
DR	SMART; SM00406; 1Gv; 1.		
FT	NON_TER 1		
FT	NON_TER 114		
SO	SEQUENCE 114 AA; 12829 MW; 404885FDE6BA56F8 CRC64;		

```
alignment_scores:
  Quality: 373.00      Length: 113
  Ratio: 3.885         Gaps: 0
Percent Similarity: 84.956      Percent Identity: 59.292
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```
alignment_block:
```

US-08-48/-283A-12_COPY_58_423 X Q9JL81 ..

Align seg 1/1 to: Q9JL81 from: 1 to: 114

228 TAGTACAGTATACATGAGAGCTCTCCAGGCTGGATCGGAGGACAGGCGC 2777

```

|||||.....|
68 rserThrAlaTyrMetGlnLeuSerSerProThnSerGlnuSperLay 85
278 TCTATTATTCGCCCGCTTATTTTGGTCTAGCCCGAATGGTATT 327
85 altyrTyrCysAlaArgSerAsnTyrGlySerSerLeuTyrTyrPhe 101
328 GATGTTGGGTCAGGAACCCGTGACGTCTCGAGC 366
|||.....|
102 AspTyrTrpGlyGlnGlyThrLeuThrValSerSer 114
seq_name: sp_rodent:Q9JL77

```

```

seq_documentation_block:
ID Q9JL77 PRELIMINARY; PRT; 110 AA.
AC Q9JL77;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BA/2;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF206029; AAF69327.1; -.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
FT NON_TER 1
FT NON_TER 110
SQ SEQUENCE 110 AA; 12138 MM; 2EDE81F85862C9AF CRC64;

```

```

alignment_scores:
Quality: 371.00 Length: 110
Ratio: 3.989 Gaps: 1
Percent Similarity: 84.545 Percent Identity: 62.727

```

alignment_block:
US-08-487-283a-12_COPY_58_423 x Q9JL77 ..

Align seg 1/1 to: Q9JL77 from: 1 to: 110

```

37 AAGCCAGGAGCCCTCAGTCAAGTGTCTGTAAGCTAGCGGTATATTT 86
.....|
5 ArgProGlyAlaSerValLysLeuSerCysLysAlaSerGlyTyrThrPh 21
87 TCTAATATTTGGATTCATAGGTGGCTCAGGCCCGCGGAGGGCCCTGG 136
.....|
21 eThrSerSerTrpMetHisTrpAlaLysGlnArgProGlyGlnGlyLeuG 38
137 AATGATGGGTGAGATCTTACCGGGCTGTGAGACACCGAATATACGAA 186
|||.....|
38 lntTrpLeuGlyGlnLysLeuSerProAsnSerGlyHisThrAsnTyrAsnGln 54
187 AATTTAAAGACCGGTGTACTATAGCGCGTGCACCTCGACCTAGTAGT 236
|||.....|
55 LysPheLysGlyLysAlaThrLeuThrValAspThrSerSerSerThrAl 71
237 ATACATGAGACTCTCCAGCTCGATCGAGGACACAGCGCGTCTATTATT 286
|||.....|
71 altyrValaLysPheLeuSerSerLeuThrSerGlnuSperAlaValTyrTyrC 88
287 GCGCGCGTTATTTTGGTCTAGCCCGAATGGTATTTGATGTTTGG 336
|||||.....|

```

```

88 yAlaArg.....GlnArgAsnTyrAlaMetAspTyrTrp 100
337 GGTCAAGAACCCGTGTCACGTCTCGAGC 366
|||||.....|
101 GlyGlnGlyThrSerValThrValSerSer 110
seq_name: sp_rodent:Q9JL83

```

```

seq_documentation_block:
ID Q9JL83 PRELIMINARY; PRT; 110 AA.
AC Q9JL83;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF206023; AAF69321.1; -.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
FT NON_TER 1
FT NON_TER 110
SQ SEQUENCE 110 AA; 12052 MM; 84E6F2AD219AF95E CRC64;

```

```

alignment_scores:
Quality: 360.00 Length: 115
Ratio: 4.000 Gaps: 2
Percent Similarity: 78.261 Percent Identity: 60.000

```

alignment_block:
US-08-487-283a-12_COPY_58_423 x Q9JL83 ..

Align seg 1/1 to: Q9JL83 from: 1 to: 110

```

28 GAGGTCAAGAACCCAGGCGCTCAGTCAAGTGTCTGTAAGCTAGCGG 77
|||||.....|
2 GluLeuValLysProGlyAlaSerValLysLeuSerCysLysAlaSerG 18
78 CTATATTTTCTAATTTATTTGATTCATAGGTGGCTGCTAGCGCCGGCC 127
|||.....|
18 yTyrThrPheSerAsnSerTrpMetAsnTrpValLysLeuArgProGlyG 35
128 AGGCGCTGGAATGATGTGGTGAATCTTACCGGGCTGTGAGACACCGAA 177
|||||.....|
35 lngLysLeuGlnTrpLeuGlyArgGlyTyrProGlyLysPheLysAlaTyr 51
178 TATACCGAAATTTTAAAGCCGTGTACTATAGACCGCGTGCACCTGCAG 227
|||.....|
52 TyrAsnGlyLysPheLysGlyLysAlaThrLeuThrAlaAspLysSerSe 68
228 TAGTACAGTATACATGAGCTCTCCAGCTCGGAGTGGAGACACAGCGCG 277
|||.....|
68 rSerThrAlaTyrMetGlnLeuSerSerLeuThrSerValAspSerAla 85
278 TCTATTATTCGCCCGCTTATTTTGGTCTAGCCCGAATGG..... 321
|||||.....|
85 altyrPheLysAlaArg.....SerAsnTrpAspVal 95
322 TATTTTGGATGTTGGGTCAGGAACCCGTGTCACGTCTCGAGC 366
|||.....|
96 ArgPheAlaTyrTrpGlyGlnGlyThrLeuValThrValSerAla 110
|||||.....|

```

```

seq_name: sp_rudent:Q9QXF0
seq_documentation block:
ID Q9QXF0 PRELIMINARY; PRT: 298 AA.
AC Q9QXF0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE CN 8 SCFV.
CN 8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE=SPLEEN;
RA Shiohara N., Demura T., Fukuda H.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE=SPLEEN;
RA Shiohara N., Demura T., Fukuda H.;
RT "Isolation of a novel type of vascular cell wall-specific monoclonal
RT antibody recognizing a cell polarity using a phage display subtraction
RT method."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB036341; BAF8633.1; -
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; -
DR InterPro: IPR003596; -
DR Pfam: PF00047; Ig: 2.
DR SMART: SM00406; IGV: 1.
DR SMART: SM00406; IGV: 1.
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

```

```

alignment_scores:
Quality: 359.00 Length: 123
Ratio: 3.626 Gaps: 2
Percent Similarity: 80.488 Percent Identity: 55.285

```

```

alignment_block:
US-08-487-283A-12_COPY_58_423 x Q9QXF0 ..

```

```

Align seg 1/1 to: Q9QXF0 from: 1 to: 298

```

```

1 CAAGTCAAGTGTGCAATCCGCGCCGAGGTCAAGACCCAGGCGCTC 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
40 GlnValLysLeuGlnInserGlyGlyLeuValLysProGlyGlyLys 56
51 AGTCAAAGTGTCTGTAAGCTAGCGGCTATATTTTCTATATTTGCA 100
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
56 rleuLysLeuSerGlyAlaAlaInserGlySerAspPheSerArgTyrPM 73
101 TTCAATGGGTGCTGACGGCCCGCGGAGGCTGGAATGGGTGAG 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
73 eSerTyrPalaIrgGlnAlaProGlyLysGlyLeuGlnTyrPileGlyGln 89
151 ATCTTACCGGGCTGTGTAGACACCAATATACGAAATTTTAAAGCCG 200
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
90 IleAsnProAspSerSerThrIleAsnTyrThrProSerLeuLysAspLys 106
201 TGTACTGTATGACGCGTACACTTGTGACTAGTACATGATGAGAGCTCT 250
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
106 sPheIleIleSerArgAspAsnAlaLysAsnThrLeuTyrLeuGlnMetS 123
251 CCAGCGCTGATGAGAGACGAGCGCGCTATATTTATGCGCGCT...TAT 297
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
123 eLysValArgSerGlnAspThrAlaLeuTyrTyrCysAlaArgAlaSer 139
298 TTTTGGTGTTCAGCCGCAATGATATTGATGTTGGGTCACAGAAC 347
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

140 TyrTyrGlyHisSerAla.....TyrTrpGlyGlnGlyTh 151
348 CCTGGTCACTGTCTCGAGC 366
| |||||:|||||:|||||:|||||:|||||:|||||:|||||:
151 rThrValThrValSerSer 157

```

```

seq_name: sp_rudent:Q9JL75
seq_documentation block:
ID Q9JL75 PRELIMINARY; PRT: 109 AA.
AC Q9JL75;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA Malxiet S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF206031; AAF69329.1; -
DR InterPro: IPR003006; -
DR InterPro: IPR003596; -
DR Pfam: PF00047; Ig: 1.
DR SMART: SM00406; IGV: 1.
DR NON_TER 1
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 12118 MW; FF65E441BBF936A6 CRC64;

```

```

alignment_scores:
Quality: 356.00 Length: 114
Ratio: 3.870 Gaps: 2
Percent Similarity: 80.702 Percent Identity: 61.404

```

```

alignment_block:
US-08-487-283A-12_COPY_58_423 x Q9JL75 ..

```

```

Align seg 1/1 to: Q9JL75 from: 1 to: 109

```

```

28 GAGGTCAAGAACCCAGGCGCTGACGTCAAGTGTCTGTAAGCTAGCGG 77
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 GlnLeuValLysProGlyAlaSerValLysMetSerCysLysAlaSerG1 17
78 CTATATTTTCTAATATTTGATTCATGAGTGGTGGCGAGCCCGGGGC 127
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17 yTyrThrPheThrSerTyrValMetHisTyrValLysGlnLysProGlyG 34
128 AGGCGCTGGAATGATGGGTGAGATCTTACCGGCGCTGCTGAGACCGAA 177
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34 lngLysLeuGlnTyrPileGlyTyrIleAsnProTyrAsnAspGlyThrLys 50
178 TATACGAAATTTTAAAGACCGTGTACTATGACGGGTGACTGTGAC 227
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51 TyrAsnGlnLysPheLysGlyLysAlaThrLeuThrSerAspLysSerSe 67
228 TAGTACAGTATACATGAGCTCTCCAGCGCTGATCGAGAGACAGCGCG 277
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
67 rSerThrAlaTyrMetGlnLeuSerSerLeuThrSerGlnAspSerAlaV 84
278 TCTATTTGCGCGCGTATTTTGTGCTGACTAGCCGCAATGGAT... 324
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
84 aLysTyrCysAlaArg.....AspGlyAsnTyrTargly 95
325 TTTGATGTTGGGGTCAAGAACCTGTGCTACTGTCTGAGC 366
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
96 PheAspTyrTrpGlyGlnGlyThrThrLeuThrValSerSer 109

```

alignment_scores:

Quality: 652.00 Length: 122
Ratio: 5.344 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-487-283A-12_COPY_58_423 x AAR77607 ..

Align seg 1/1 to: AAR77607 from: 1 to: 248

```
1 CAAGTCCAACTGCTGCAATCCGGCCCGCAAGGCAAGAACCCAGGGGCTCT 50
|||||
127 GlnValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyAlaSe 143
51 AGTCAAGTCTGCTGCTTAAGCGAGCGGCTATATTTTCTAATTTTGA 100
|||||
143 rValLysValSerCysLysAlaSerGlyTyrIlePheSerAsnTyrTrpI 160
101 TTCAATGGGTGCGTCAGACCCCGGCGAGGCGCTGAATGATGGGTGAG 150
|||||
160 legIntPrValArgGlnAlaProGlyGlnGlyLeuGluTrpMetGlyGlu 176
151 ATCTTACCGGGCTCTGTTAGCACCGAATATACCGAAATTTTAAAGACG 200
|||||
177 IleuProGlySerGlySerThrGluTyrThrGluAspPheLysAspAr 193
201 TGTACTATGACGGCTGACACTGCTAGCTAGTACATATACATGAGGCTCT 250
|||||
193 gValThrMetThrAlaGAspThrSerThrValTyrMetGluLeuS 210
251 CCAGCTTCGATCGAGAGACAGCGCGCTATATTATTCGCGCGTATTTT 300
|||||
210 erSerLeuArgSerGlnAspThrAlaValTyrTyrCysAlaArgTyrPhe 226
301 TTGGTTCCTAGCCCGCAATGATGATTTTGGTGGGCTCAAGAACCTCT 350
|||||
227 PheGlySerSerProAsnTyrPyrPheAspValTrpGlyGlnGlyThrLe 243
351 GGTCACTGCTCGAGC 366
|||||
243 uValThrValSerSer 248
```

seq_name: /SID8/gcgdata/geneseq/geneseqp/AA1995.DAT:AAR77611

seq_documentation_block:

ID AAR77611 standard; Protein: 249 AA.

XX AAR77611:

DT 02-APR-1996 (first entry)

XX Humanised 561.1 VH + IGHRLC.

XX Complement C5; haemolysis; kidney; glomerulonephritis;

XX monoclonal antibody; antiinflammatory; antibody engineering;

XX humanised antibody; complementarity determining region; CDR.

XX Synthetic.

XX Key Location/Qualifiers

XX Peptide 1..19 /label= sig-peptide

XX Peptide 20..249 /label= mat-peptide

XX W09529697-A1.

XX 09-NOV-1995.

XX 01-MAY-1995; 95WO-US05688.

XX 02-MAY-1994; 94US-0236208.

XX (ALEX-) ALEXION PHARM INC.

XX Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;

XX Rother RP, Springhorn J P, Squinto SP, Thomas TC;

XX Wang Y, Wilkins JA;

XX WPI: 1995-392923/50.

XX DR N-PSDB: AAT08484.

XX Treating glomerulonephritis with antibody against complement C5

XX component - to inhibit complement induced cell lysis

XX Claim 38; Page 123-125; 181pp; English.

XX A DNA construct (AAT08483) codes for a humanised CDR-grafted and

XX framework sequence-altered Fd 561.1 VH + IGHRL (AAR77610), which

XX includes CDRs derived from mouse anti-C5 monoclonal antibody 561.1.

XX The DNA can be subcloned together with DNA (AAT08484) coding for a

XX humanised light chain (AAR77612) into vector APEX-3P (AAT08476) for

XX expression of humanised antibody in human 293 EBNA cells. Such

XX recombinant antibodies retain the ability of Mab 561.1 to block

XX human complement C5a generation and thus to reduce glomerular

XX inflammation and kidney dysfunction associated with

XX glomerulonephritis.

XX Sequence 249 AA:

alignment_scores:

Quality: 652.00 Length: 122
Ratio: 5.344 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-487-283A-12_COPY_58_423 x AAR77611 ..

Align seg 1/1 to: AAR77611 from: 1 to: 249

```
1 CAAGTCCAACTGCTGCAATCCGGCCCGAGGTCAAGAACCCAGGGGCTCT 50
|||||
20 GlnValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyAlaSe 36
51 AGTCAAGTCTGCTGCTTAAGCGAGCGGCTATATTTTCTAATTTTGA 100
|||||
36 rValLysValSerCysLysAlaSerGlyTyrIlePheSerAsnTyrTrpI 53
101 TTCAATGGGTGCGTCAGACCCCGGCGAGGCGCTGAATGATGGGTGAG 150
|||||
53 legIntPrValArgGlnAlaProGlyGlnGlyLeuGluTrpMetGlyGlu 69
151 ATCTTACCGGGCTCTGTTAGCACCGAATATACCGAAATTTTAAAGACG 200
|||||
70 IleuProGlySerGlySerThrGluTyrThrGluAspPheLysAspAr 86
201 TGTACTATGACGGCTGACACTTCTAGCTAGTACATATGAGGCTCT 250
|||||
86 gValThrMetThrAlaGAspThrSerThrValTyrMetGluLeuS 103
251 CCAGCTTCGATCGAGAGACAGCGCGCTATATTATTCGCGCGTATTTT 300
|||||
103 erSerLeuArgSerGlnAspThrAlaValTyrTyrCysAlaArgTyrPhe 119
301 TTGGTTCCTAGCCCGCAATGATGATTTTGGTGGGCTCAAGAACCTCT 350
|||||
120 PheGlySerSerProAsnTyrPyrPheAspValTrpGlyGlnGlyThrLe 136
351 GGTCACTGCTCGAGC 366
|||||
136 uValThrValSerSer 141
```

seq_name: /SID8/gcgdata/geneseq/geneseqp/AA1995.DAT:AAR77615


```

seq_documentation_block:
ID AAR7615 standard; Protein: 249 AA.
XX
AC AAR7615:
XX
DT 02-APR-1996 (first entry)
XX
DE Humanised 5G1.1 VH + IGHRLD.
XX
KW Complement C5; haemolysis; kidney; glomerulonephritis;
RM monoclonal antibody; anti-inflammatory; antibody engineering;
KV humanised antibody; complementarity determining region; CDR.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= sig_peptide
FT /label= mat-peptide
FT /label= mat-peptide
XX
MN W09529697-AI.
XX
PD 09-NOV-1995.
XX
PF 01-MAY-1995; 95MO-USO5688.
XX
PR 02-MAY-1994; 94US-0236208.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Evans MJ, Matlis L, Mueller EE, Nye SH, Rollins S;
PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;
PI Wang Y, Wilkins JA;
XX
WP: 1995-392923/50.
DR N-PSDB; AAT08487.
XX
PT Treating glomerulonephritis with antibody against complement C5
PT component - to inhibit complement induced cell lysis
XX
PS Claim 37; Pages 135-137; 181pp; English.
XX
CC A DNA construct (AAT08487) codes for a humanised CDR-grafted
CC light chain, designated 5G1.1 VL + IGHRLD (AAR7615), which includes
CC CDS derived from mouse anti-C5 monoclonal antibody 5G1.1. The
CC DNA can be subcloned together with DNA (AAT08484) coding
CC for a humanised Fd (AAR7611) into vector APEX-3P (AAT08476) for
CC repression of humanised antibody in human 293 EBNA cells. Such
CC recombinant antibodies retain the ability of Mab 5G1.1 to block
CC human complement C5a generation and thus to reduce glomerular
CC inflammation and kidney dysfunction associated with
CC glomerulonephritis.
XX
Sequence 249 AA:

alignment_scores:
    Quality: 627.00      Length: 122
    Ratio: 5.182        Gaps: 0
Percent Similarity: 99.180 Percent Identity: 95.902

alignment_block:
US-08-487-283A-12_COPY_58_423 x AAR7615 ..
Align seg 1/1 to: AAR7615 from: 1 to: 249

1 CAAGTCAACAGTGTCGAATCCGGCGCCGAGGTCAAGACCAGCGGCCTC 50
|||||
20 GlnValGlnLeuValGlnSerGlyAlaGluValLysProGlyAla 36
|||||
51 AATCAAAGTCTCCTGTAAGACTAGCGGCATATATTTCATATTATGGA 100
|||||

```

36	rallysValSerCysLysAlaSerIlyrIlePheSerAsnTyTrrI	53
101	TTCAATGGGTGGCTCAGGCCCCCGGCGAGCCCTGGAAATGATGGGTAG	150
53	leclIntrpValarGlnAlaProGlyGlnGlyLeuGlnTrpMetGlyGln	69
151	ANCTTACCGGGCCGTCGTAGCAACCGAATATPACCGAAATTTAAACACCG	200
70	IleLeuProGlySerIlySerThrGlyTrpAlaGlnLysPheGlnGlyAr	86
201	TGTACTATGACGCGTGACACTTCGACTGTACAGTATCATGAGAGCTT	250
86	gValThrMetThrArgAspThrSerThrSerThrValTrpMetGlnLeuS	103
103	erSerLeuArgSerGlnAspThrAlaValTrpTyrCysAlaArgTyrPhe	119
251	CCAGCCTGCGATCGAGACAGACGGCCGTATTATTGCGCGTTATTTT	300
301	TTTGTTCTACGCCCAATGTGATTTTGTATGTTGGGCAAGAAACCT	350
120	PheGlySerSerProAsnTrpTyrPheAspValTrpGlyGlnGlyThrIe	136
351	GGTCACTGTCTCGAGC 366	
136	uValThrValSerSer 141	
seq_name: /SID58/gcdata/geneseq/geneseqp/AA195.DAT:AA77616		
seq_documentation_block:		
ID	AA77616 standard; Protein; 248 AA.	
AC	AA77616;	
DT	15-MAR-1996 (first entry)	
XX	Humanised CDR-grafted 5G1.1 scFv D012.	
DE		
XX	Complement C5; haemolysis; kidney; glomerulonephritis;	
KW	monoclonal antibody; antiinflammatory; antibody engineering;	
KW	humanised antibody; complementarity determining region; CDR;	
XX	single chain antibody; scFv.	
OS	Synthetic.	
XX		
XX	Key	Location/Qualifiers
FT	Region	26..36
FT	Region	/label- CDR-L1
FT	Region	52..58
FT	Region	/label- CDR-L2
FT	Region	91..99
FT	Region	/label- CDR-L3
FT	Region	152..161
FT	Region	/label- CDR-H1
FT	Region	176..186
FT	Region	/label- CDR-H2
FT	Region	225..237
FT	Region	/label- CDR-H3
XX		
XX	W0529697-A1.	
XX		
PD	09-NOV-1995.	
XX		
XX	01-MAY-1995;	95WO-USO5688.
XX		
PR	02-MAY-1994;	94US-0236208.
XX		
PA	(ALEX-) ALEXION PHARM INC.	
XX		
PI	Evens MJ, Matlis L, Mueller EE, Nye SH, Rollins S;	
PI	Rother RP, Springhorn J P, Squinto SP, Thomas TC;	
PI	Wang Y, Wilkins JA;	
XX		
DR	WPI; 1995-392923/50.	

DR N-PSDB; AAT08488.
 XX Treating glomerulonephritis with antibody against complement C5
 PT component - to inhibit complement induced cell lysis
 XX
 PS Example 11; Page 138-140; 181pp; English.
 XX
 CC A humanised CDR-grafted scFv, designated 5G1.1 scFV D012 (AAR77616),
 CC includes CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1.
 CC The scFv can be expressed in Escherichia coli ME1 cells by subcloning
 CC of encoding DNA (AAT08488) into vector pET T16/S05/N1. This 5G1.1 to
 CC humanised, recombinant antibody retained the ability of Mab 5G1.1 to
 CC block human complement C5a generation and thus to reduce glomerular
 CC inflammation and kidney dysfunction associated with
 CC glomerulonephritis.
 CC
 SQ Sequence 248 AA:

alignment_scores:
 Quality: 623.00 Length: 122
 Ratio: 5.149 Gaps: 0
 Percent Similarity: 99.180 Percent Identity: 95.082

alignment_block:
 US-08-487-283A-12_COPY_58_423 x AAR77616 ..

Align seg 1/1 to: AAR77616 from: 1 to: 248

```

1 CAAGTCCAACTGGTGCAATCCGGCCGAGGTCAAGAACCGAGGCGCTC 50
  |||
127 GlnValGlnLeuValGlnSerGlyAlaGlnValGlnLysProGlyAla 143
  |||
51 AGTCAAAAGTCTCCTTAAGCTAAGCGGCTATTTTCTATATATGGA 100
  |||
143 rValLysValSerCysLysAlaSerGlyTyrIlePheSerAsnTyrTrpI 160
  |||
101 TTCATGGGTGCGTCAGAGCCCCCGGCGAGGCGCTGAATGATGGGTGAG 150
  |||
160 LegIntPrValArgGlnAlaProGlyGlnGlyLeuGlnTyrPheMetGlyGlu 176
  |||
151 ATCTTACCGGGCTCTGTAGACACCGAATATACCGAAATTTTAAAGACCG 200
  |||
177 IleuPProGlySerGlySerThrGlnTyrAlaGlnLysPheGlnGlyLys 193
  |||
201 TGTACTATGACGGGTGACACTTGACAGTACAGTATATCATGAGAGCTCT 250
  |||
193 gValThrMetThrArgAspPheSerThrSerThrValTyrMetGlnLeuS 210
  |||
251 CCAGCCTCGATCGAGGAGACAGCGCGCTATATTGCGCGGCTATTTT 300
  |||
210 erSerLeuArgSerGlnAspThrAlaValTyrTyrCysAlaArgTyrPhe 226
  |||
301 TTTGGTCTACCCGGAATGTGATTATTGATGTTGGGCTCAAGAACCTC 350
  |||
227 PheGlySerSerProAsnTyrPyrPheAspValTyrGlyGlnGlyThr 243
  |||
351 GGTCACTGCTCTCGAGC 366
  |||
243 uValThrValSerSer 248
  |||
seq_name: /SIDS98/geneseq/geneseq/AA1995.DAT: AAR77610
seq_documentation_block:
ID AAR77610 standard; Protein: 249 AA.
XX
AC AAR77610;
XX
XX
DT 15-MAR-1996 (first entry)
XX
DE Humanised 5G1.1 VH + IGHR.L.
XX
KW Complement c5; haemolysis; kidney; glomerulonephritis;
```

KW monoclonal antibody; antiinflammatory; antibody engineering;
 KW humanised antibody; complementarity determining region; CDR.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= sig_peptide
 FT Peptide 20..249
 FT /label= mat_peptide
 FT Region 45..54
 FT /label= CDR-H1
 FT Region 69..79
 FT /label= CDR-H2
 FT Region 118..130
 FT /label= CDR-H3
 XX
 PN W09529697-A1.
 XX
 PD 09-NOV-1995.
 XX
 PF 01-MAY-1995; 95MO-US05688.
 XX
 PR 02-MAY-1994; 94US-0236208.
 XX
 PA (ALEX-) ALEXION PHARM INC.
 XX
 PI Evans MJ, Matlis L, Mueller EF, Nye SH, Rollins S;
 PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;
 PI Wang Y, Wilkins JA;
 XX
 DR WPI: 1995-392923/50.
 DR N-PSDB; AAT08483.
 XX
 PT Treating glomerulonephritis with antibody against complement C5
 PT component - to inhibit complement induced cell lysis
 XX
 PS Example 11; Page 119-122; 181pp; English.
 XX

alignment_scores:
 Quality: 617.00 Length: 122
 Ratio: 5.142 Gaps: 0
 Percent Similarity: 98.361 Percent Identity: 94.262

alignment_block:
 US-08-487-283A-12_COPY_58_423 x AAR77610 ..

Align seg 1/1 to: AAR77610 from: 1 to: 249

```

1 CAAGTCCAACTGGTGCAATCCGGCCGAGGTCAAGAACCGAGGCGCTC 50
  |||
20 GlnValGlnLeuValGlnSerGlyAlaGlnValLysProGlyAla 36
  |||
51 AGTCAAAAGTCTCCTTAAGCTAAGCGGCTATTTTCTATATATGGA 100
  |||
36 rValLysValSerCysLysAlaSerGlyTyrIlePheSerAsnTyrTrpI 53
  |||
101 TTCATGGGTGCGTCAGAGCCCCCGGCGAGGCGCTGAATGATGGGTGAG 150
  |||
53 LegIntPrValArgGlnAlaProGlyGlnGlyLeuGlnTyrPheMetGlyGlu 69
  |||
```

```
151 ATCTACCGGCTCTGTAGCAGCAATATACGAAATTTTAAGACCG 200
|||||
70 IleleuproglysergylserthrghlufyrAlaGlnLysPheGlnGlyAr 86
201 TGTACTATGACCGCTGACACTTCGACTACTACAGTATACATGAGCTCT 250
|||||
86 gValThrMetThrAlaAspThrSerThrSerThrAlaTyrMetClnLus 103
251 CCAGCTGCGATCGAGACACGCGCTGATATATGCGCGCTTATTTT 300
|||||
103 erSerLeuArSerGluAspThrAlaValTyrCysAlaArgTyrPhe 119
301 TTTGGTTCTAGCCGCAATGTTGATTTTGATTTGGGCTCAAGAACCT 350
|||||
120 PheGlySerSerProAsnTrpTyrPheAspValTrpGlyGlnGlyThrLe 136
351 GGTCACTGTCTCGAGC 366
|||||
136 vValThrValSerSer 141
seq.name: /SIDS8/gcdata/geneseq/geneseqp/AA1995.DAT.AAR77606
seq_documentation_block:
ID AAR77606 standard; Protein: 248 AA.
AC AAR77606;
XX
XX 15-MAR-1996 (first entry)
DT
XX
XX Murine 5G1.1M1 scfv.
XX
XX Complement C5; haemolysis; kidney; glomerulonephritis;
KW monoclonal antibody; antiinflammatory; antibody engineering;
KW humanised antibody; complementarity determining region; CDR
XX single chain antibody; scfv.
XX
XX Mus sp.
OS
XX
XX Key Location/Qualifiers
FH 28..34
FT Region /Label- CDR-L1
FT 52..54
FT Region /Label- CDR-L2
FT 93..98
FT Region /Label- CDR-L3
FT 156..159
FT Region /Label- CDR-H1
FT 179..183
FT Region /Label- CDR-H2
FT 226..236
FT Region /Label- CDR-H3
FT
XX
XX W09529697-A1.
XX
XX 09-NOV-1995.
XX
XX 01-MAY-1995; 95WO-US05688.
XX
XX 02-MAY-1994; 94US-0236208.
XX
XX (ALEX-) ALEXION PHARM INC.
XX
XX Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;
XX Rother RP, Springhorn J P, Squinto SP, Thomas TC;
XX Wang Y, Wilkins JA;
XX
XX WPI; 1995-392923/50.
XX
XX N-PSDB; AAT08479.
XX
XX
XX Treating glomerulonephritis with antibody against complement C5
XX component - to inhibit complement induced cell lysis
XX
XX Example 11: Page 107-110; 181pp; English.
```

```
XX
XX Murine scfv 5G1.1M1 (AAR77606) is the product of a DNA construct
CC (AAR08479) obtd. from DNA of hybridoma ATCC HB 11625, which produces
CC anti-C5 monoclonal antibody (Mab) 5G1.1. Recombinant scfv 5G1.1M1 is
CC obtd. by expression of this DNA in Escherichia coli using vector PET
CC Trc S05/NI. The light and/or heavy chain CDRs of scfv 5G1.1M1 can
CC be combined with CDRs from other 5G1.1-derived antibodies, fds and
CC light chains (AAR77607-16) in the prodn. of recombinant, including
CC humanised, antibodies that retain the ability of Mab 5G1.1 to block
CC human complement C5a generation and thus to reduce glomerular
CC inflammation and kidney dysfunction associated with
CC glomerulonephritis.
XX
XX Sequence 248 AA;
SQ
alignment_scores:
Quality: 555.00 Length: 122
Ratio: 4.826 Gaps: 0
Percent Similarity: 94.262 Percent Identity: 81.148
alignment_block:
US-08-487-283A-12_COPY_58_423 x AAR77606
Align seg 1/1 to: AAR77606 from: 1 to: 248
1 CAAGTCCAACTGTGTCATCGGCGCGCGAGTCAAGACGAGCGGCTC 50
|||||
127 GlnValGlnLeuGlnGlnInseryGlyAlaGlnLeuMetLysProGlyAlaLe 143
51 AGTCAAGTGTCTCTGTAAGCTAGCGGCTATATTTTCTATATATGGA 100
|||||
143 rValLysMetSerCysLysAlaThrClyrLlePheSerAsnTyrTrpI 160
101 TTCATGAGGTGCGTCAGCGCCCGGCGAGGCTGGAATGATGGCTGAG 150
|||||
160 legInTrpLleLysGlnArGProGlyHisGlyLeuGlnTrpLleGlyGln 176
151 ATCTTACCGGCTCTGTAGCAGCAATATACGAAATTTTAAGACCG 200
|||||
177 IleleuproglysergylserthrghlufyrThnGlnAsnPhelyAspLys 193
201 TGTACTATGACCGCTGACACTTCGACTAGTACATGATACATGAGCTCT 250
|||||
193 sAlaAlaPheThrAlaAspThrSerSerAsnThrAlaTyrMeGlnLus 210
251 CCAGCTGCGATCGAGACACGCGCTGATATATGCGCGCTTATTTT 300
|||||
210 erSerLeuThrSerGluAspSerAlaValTyrTyrCysAlaArgTyrPhe 226
301 TTTGGTTCTAGCCGCAATGTTGATTTTGATTTGGGCTCAAGAACCT 350
|||||
227 PheGlySerSerProAsnTrpTyrPheAspValTrpGlyAlaGlyThrH 243
351 GGTCACTGTCTCGAGC 366
|||||
243 rValThrValSerSer 248
seq.name: /SIDS8/gcdata/geneseq/geneseqp/AA1995.DAT.AAR77609
seq_documentation_block:
ID AAR77609 standard; Protein: 249 AA.
XX
XX AAR77609;
XX
XX 02-APR-1996 (first entry)
DT
XX
XX Chimeric heavy chain 5G1.1M1 VL HuG1.
XX
XX Complement C5; haemolysis; kidney; glomerulonephritis;
KW monoclonal antibody; antiinflammatory; antibody engineering;
KW humanised antibody; complementarity determining region; CDR;
KW chimeric antibody; Fab.
```

```

XX Synthetic.
OS
XX Key location/Qualifiers
FH Peptide 1..19
FT /label= sig_peptide
FT 20..249
FT /label= mat_peptide
XX
XX MO9529697-A1.
XX
XX 09-NOV-1995.
XX
XX 01-MAY-1995; 95MO-US05668.
XX
XX 02-MAY-1994; 94US-0236208.
XX
XX (ALEX-) ALEXION PHARM INC.
XX
XX Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;
XX Rother RP, Springhorn J P, Squinto SP, Thomas TC;
XX Wang Y, Wilkins JA;
XX WPI; 1995-392923/50.
XX N-PSDB; AAT08482.
XX
XX Treating glomerulonephritis with antibody against complement C5
XX component - to inhibit complement induced cell lysis
XX
XX Claim 26; Page 116-119; 181pp; English.
XX
XX A DNA construct (AAT08481) codes for chimeric light chain 5G1.IM1 VL
XX HUK (AAR77608), which can form the light chain portion of an Fab.
XX The chimeric light chain includes CDRs derived from mouse anti-C5
XX monoclonal antibody 5G1.1. The DNA can be subcloned with DNA
XX (AAT08482) coding for chimeric Fd (AAR77609) into vector Apex-3p
XX (AAT08476) for prodn. of chimeric Fab in human 293 EBNA cells. Such
XX recombinant antibodies retain the ability of Mab 5G1.1 to block human
XX complement C5a generation and thus to reduce glomerular inflammation and
XX kidney dysfunction associated with glomerulonephritis.
XX
XX Sequence 249 AA:
SQ

```

```

alignment_scores:
Quality: 555 00 Length: 122
Ratio: 4.826 Gaps: 0
Percent Similarity: 94.262 Percent Identity: 81.148

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alignment_block:

US-08-487-283A-12_COPY_58_423 x AAR77609 ..

Align seg 1/1 to: AAR77609 from: 1 to: 249

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1 CAACTCAACTGGTGGCAATCCGCGCCGAGTCAAGACCGAGGGCCCTC 50
|||||  |||||||  |||||||  |||||||  |||||||  |||||||
20 GlnvalGlnleuGlnGlnSerGlnGlnleuMetLysProGlnYAlaase 36
51 AGTCAAGTGTCTGTAAAGCTAGCGGCTATATTTTCTAATATATGGA 100
|||||  |||||||  |||||||  |||||||  |||||||  |||||||
36 rValIysMetSerCysLysAlaThrGlyTyrIlePheSerAsnTyrTrpI 53
101 TTCATGGTGGTGGTCAAGCGCCGCGGAGGCTGGAATGATGGTGGAG 150
|||||  |||||||  |||||||  |||||||  |||||||  |||||||
53 legItrIleLysGlnArgProGlnHisGlyLeuGlnTrpIleGlyGlu 69
70 IleLeuProGlnSerGlySerThrGlnTyrThrGlnAsnPhelYAspIy 86
151 ATCTACCGGGCTGTGTAGACACCGAATATACGAAATTTTAAAGACCG 200
|||||  |||||||  |||||||  |||||||  |||||||  |||||||
70 IleLeuProGlnSerGlySerThrGlnTyrThrGlnAsnPhelYAspIy 86
201 TGTACTATGACGCGTACACTTGCACCTAGTACAGTATACATGAGACTCT 250
|||||  |||||||  |||||||  |||||||  |||||||  |||||||
86 salaIaIaPheThrAlaAspThrSerSerAsnThrAlaTyrMetGlnLeu 103

```

```

251 CCAGCCGTCGATCGAGACACGCGCCGCTATATATGCGCGCTATATTT 300
|||||  |||||||  |||||||  |||||||  |||||||  |||||||
103 erSerLeuThrSerGlnAspSerAlaValTyrTyrCysAlaArgTyrPhe 119
301 TTTGGTTCAGCCCGAATGTTGATGTTGGGTCACGACCGCT 350
|||||  |||||||  |||||||  |||||||  |||||||  |||||||
120 PheGlySerSerProAsnTrpTyrPheAspAlaTrpIleGlyThrTh 136
351 GGTCACTGTCTCCAGC 366
|||||  |||||||  |||||||  |||||||  |||||||  |||||||
136 rAlThrValSerSer 141
seq_name: /SID8/gcgdata/geneseq/geneseq/AA2000.DAT:AAW90936
seq_documentation_block:
ID AAW90936 standard; Protein; 470 AA.
XX
XX AAW90936;
XX
XX 08-AUG-2000 (first entry)
XX
XX Humanised HFE7A designed heavy chain HHH type protein.
XX
XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
XX anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant;
XX dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
XX nephrotropic; antifertility; neuroprotective; antianteriosclerotic;
XX hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
XX Hashimoto disease; rheumatoid arthritis; graft versus host disease;
XX Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
XX Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
XX multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
XX insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
XX cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX
XX Synthetic.
XX
XX EP990663-A2.
XX
XX 05-APR-2000.
XX
XX 29-SEP-1999; 99EP-0307711.
XX
XX 30-SEP-1998; 98RP-0276881.
XX
XX 30-SEP-1998; 98RP-0276882.
XX
XX (SANY ) SANKYO CO LTD.
XX
XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
XX WPI: 2000-258930/23.
XX N-PSDB: AAl1655.
XX
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
XX inflammatory or autoimmune disease, induces apoptosis selectively in
XX cells with abnormal Fas-Fas ligand systems -
XX
XX Claim 2; Page 188-189; 263pp; English.
XX
XX This invention describes a novel humanized anti-Fas antibody-like
XX molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
XX ligand system, by binding to Fas on the cell surface, and prevents
XX apoptosis in cells with a normal system, by inhibiting binding between
XX Fas and its ligand. The products of the invention have anti-inflammatory,
XX anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
XX immunomodulatory, dermatological, immunosuppressive, thyromimetic,
XX antirheumatic, nephrotropic, antifertility, neuroprotective,
XX antianteriosclerotic, cardiant and hepatropic activity. (I) induce
XX apoptosis by binding to cell surface Fas or inhibit it by competitive
XX inhibition of ligand binding. (I) are used to treat and/or prevent
XX diseases associated with the Fas/Fas ligand system, especially systemic
XX lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft

```

CC. versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A heavy chain construct HHH type
 CC which is described in the method of the invention.

XX Sequence 470 AA:

alignment_scores: Length: 125
 Quality: 514.50 Gaps: 2
 Ratio: 4.553
 Percent Similarity: 90.400 Percent Identity: 80.000

alignment_block:

US-08-487-283a-12_COPY_58_423 x AAW90936 ..

Align seg 1/1 to: AAW90936 from: 1 to: 470

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1  CAAGTCAACTGGTGCATCCGGCGGAGGTCAAGAACGAGGGGCTC 50
   |||||
20 GlnValGlnLeuValGlnSerGlyAlaGlnValLysProGlyAla 36
   |||||
51 AGTCAAGTGTCTCTTAAGCTAGCGGCTATATTTTCTAATATTGA 100
   |||||
36 rValLysValSerCysLysAlaSerGlyThrPheThrSerTyrTrp 53
   |||||
101 TTCATGGGCGCTCAGAGCCCGGCGAGGGCTCGAATGATGGTGAG 150
   |||||
53 etcIntrpValArgGlnAlaProGlyGlnGlyLeuGlnTrpMetGlyGlu 69
   |||||
151 ANCTTACCGGGCTCTGTAGCAGCAATNACGAAATTTTAAAGACG 200
   |||||
70 IleAspProSerAspSerTyrThrAsnTyrAsnGlnLysPheLysGly 86
   |||||
201 TGTATATGACGCGTACACTTCAGACTAGTACATGATGAGGCTCT 250
   |||||
86 gValThrIleThrArgAspThrSerThrAlaTyrMetClnLeu 103
   |||||
251 CCAGCGTGGATCGAGACACGCGCTATATTGCGCGCT. .... 294
   |||||
103 etSerLeuArgSerGlnAspThrAlaValTyrTyrCysAlaArgAsnArg 119
   |||||
295 ...TATTTTTCGTCTAGCCCGAATGTGATTTTGATTTGGGCTCA 341
   |||||
120 AspTyr. ....SerAsnAsnTrpTyrPheAspValTrpGly 132
   |||||
342 AGGAACCTGTGTCATGCTCTCGAGC 366
   |||||
132 uGlyThrLeuValThrValSerSer 140

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seq_name: /SIDS8/gcdata/geneseq/geneseqp/AA2000.DAT:AAW90935

seq_documentation_block:

ID AAW90935 standard; Protein: 470 AA.

XX AAW90935:

DT 08-AUG-2000 (first entry)

XX Humanised anti-Fas designed heavy chain Heu 3 protein.

KW Fas: antibody; human: anti-inflammatory; anti-anemic; antidiabetic;
 anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiac;

KW dermatological; immunosuppressive; thyromimetic; anti-rheumatic; anti-Fas;
 KW nephrotropic; antifertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

OS Synthetic.

PN EP990663-A2.

PD 05-APR-2000.

PF 29-SEP-1999; 99EP-0307711.

PR 30-SEP-1998; 98JP-0276881.

PR 30-SEP-1998; 98JP-0276882.

PA (SANY) SANKYO CO LTD.

PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;

DR WPI; 2000-258930/23.

DR N-PSDB; AAA11646.

PT New humanized anti-Fas antibody, useful for treating or preventing e.g.

PT inflammatory or autoimmune disease, induces apoptosis selectively in

PT cells with abnormal Fas-Fas ligand systems

XX Claim 2: Page 180-182; 263pp; English.

XX This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antifertility, neuroprotective,
 CC antiarteriosclerotic, cardiac and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody heavy chain construct designated Heu 3
 CC which is described in the method of the invention.

SO Sequence 470 AA:

alignment_scores: Length: 125
 Quality: 503.50 Gaps: 2
 Ratio: 4.496
 Percent Similarity: 89.600 Percent Identity: 78.400

alignment_block:

US-08-487-283a-12_COPY_58_423 x AAW90935 ..

Align seg 1/1 to: AAM62209 from: 1 to: 470

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1 CAAGTCCAACTGTCGAATCCGGCCCGAGTCAAGAACCCAGGGCCCTC 50
  |||||
20 GlnValGlnLeuValGlnSerGlyAlaGlnValLysProGlyAlaIse 36
  |||||
51 AGTCAAGTGTCTCTAAAGCTAGCGGCTATATTTCTAATTAATGGA 100
  |||||
36 rValLysValSerCysLysAlaSerGlyTyrThrPheThrSerTyrTrpM 53
  |||||
101 TTCATGGGTGGTCAGGCCCCGGGCGGCTGGAATGATGGGTGAG 150
  |||||
53 eGlnTyrValArgGlnAlaProGlyGlnGlyLeuGlnTyrPheMetGlyGlu 69
  |||||
151 ATCTTACCGGGCTGTGTAGACCGCAATATACGAAATTTTAAAGACCG 200
  |||||
70 IleAspProSerAspSerTyrThrAsnTyrAsnGlnLysPheLysGlyIly 86
  |||||
201 TGTATCATGACGCGTGTACACTTGTGACTAGTACAGTATACATGAGACTCT 250
  |||||
86 sAlaThrLeuThrValAspThrSerThrSerThrAlaTyrMetGluLeuS 103
  |||||
251 CCAGCTGCGATCGAGGACAGCGCCGCTATATTCGCCGCGT..... 294
  |||||
103 erSerLeuArgSerGlnAspThrAlaValTyrTyrCysAlaArgAsnArg 119
  |||||
295 ...TATTTTGTGTTCTAGCCCAATTGGTATTTTGAATGGGTGCA 341
  |||||
120 AspTyr.....SerAsnAsnTrpTyrPheAspValTrpIleGly 132
  |||||
342 AGGAACCTGTGCTACTGTCTGAGC 366
  |||||
132 nGlyThrLeuValThrValSerSer 140
  |||||

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seq_name: /SID58/gcgdata/geneseq/geneseq/AA1998.DAT: AAM62209

seq_documentation_block:

ID AAM62209 standard; protein; 139 AA.

AC AAM62209;

DT 21-SEP-1998 (first entry)

DE Humanised anti-HM1.24 antibody H chain V region HEF-RVNA-AHM g-gamma-1.

XX Mouse; human: humanised: anti-HM1.24 antibody; myeloma: FR; CDR:

KM framework region; complementarity determining region; antigenicity.

XX Synthetic.

OS Mus sp.

OS Homo sapiens.

XX MO9814580-A1.

XX 09-APR-1998.

XX 03-OCT-1997; 97WO-JP03553.

XX 04-OCT-1996; 96JP-0264756.

XX (CHUGAI SEIYAKU KK.

PA Koshihara Y, Kosaka M, Ohtomo T, Ono K, Tsuchiya M;

PI Yoshimura Y;

XX WPI; 1998-286421/25.

DR N-PSDB; AAV39396.

XX Humanised anti-HM1.24 antibody - for treatment of myeloma

PT Example. 9; Page 106-107; 210pp; Japanese.

PS A humanised anti-HM1.24 antibody has been developed which comprises

CC human L and H chain C regions, and L and/or H chain V regions
 CC containing material originating in mouse anti-HM1.24 antibody. The V
 CC regions contain framework (FR) regions of human origin and
 CC complementarity determining regions (CDR) of mouse origin, leading to
 CC a reshaped humanised antibody. The C regions are human Ck (L-chain) and
 CC human C gamma (especially C gamma 1) (H-chain). The FR regions of the
 CC L chain V region are derived from human subtype H5G1 (e.g. from human
 CC antibody RE1) and the FR regions of the H chain V region are derived
 CC from human subtype H5G1 (e.g. FR1-3 from human antibody H53 and FR4
 CC from human antibody JH6). The present sequence represents an H chain
 CC V region from the present invention. The antibodies are used for
 CC the treatment of myeloma, especially by injection, intravenously,
 CC intramuscularly or subcutaneously. The antibodies are used at 0.01-1000
 CC (especially 5-100) mg/kg body weight. The humanised antibody has low
 CC antigenicity and is therefore effective therapeutically in humans.
 XX
 SQ Sequence 139 AA.

alignment_scores:

Quality: 502.00 Length: 122

Ratio: 4.564 Gaps: 1

Percent Similarity: 90.164 Percent Identity: 79.508

alignment_block:

US-08-487-283A-12_COPY_58_423 x AAM62209 ..

Align seg 1/1 to: AAM62209 from: 1 to: 139

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1 CAAGTCCAACTGTCGAATCCGGCCCGAGTCAAGAACCCAGGGCCCTC 50
  |||||
20 GlnValGlnLeuValGlnSerGlyAlaGlnValLysProGlyAlaIse 36
  |||||
51 AGTCAAGTGTCTCTAAAGCTAGCGGCTATATTTCTAATTAATGGA 100
  |||||
36 rValLysValSerCysLysAlaSerGlyTyrThrPheThrProTyrTrpM 53
  |||||
101 TTCATGGGTGGTCAGGCCCCGGGCGGCTGGAATGATGGGTGAG 150
  |||||
53 eGlnTyrValArgGlnAlaProGlyGlnGlyLeuGlnTyrPheMetGlySer 69
  |||||
151 ATCTTACCGGGCTGTGTAGACCGCAATATACGAAATTTTAAAGACCG 200
  |||||
70 IlePheProGlyAspGlyAspThrArgTyrSerGlnLysPheLysGlyArg 86
  |||||
201 TGTATCATGACGCGTGTACACTTGTGACTAGTACAGTATACATGAGACTCT 250
  |||||
86 gValThrMetThrAlaAspThrSerThrSerThrValTyrMetGluLeuS 103
  |||||
251 CCAGCTGCGATCGAGGACAGCGCCGCTATATTCGCCGCGTATATTTT 300
  |||||
103 erSerLeuArgSerGlnAspThrAlaValTyrTyrCysAlaArgGlyLeu 119
  |||||
301 TTTGGTCTAGCCCAATTGGTATTTGATGTTGGGGTCAAGAACCTT 350
  |||||
120 .....ArgArgGlyGlyTyrTyrPheAspTyrTrpGlyGlnGlyThrTh 134
  |||||
351 GGTACTGTCTCGAGC 366
  |||||
134 rValThrValSerSer 139
  |||||

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seq_name: /SID58/gcgdata/geneseq/geneseq/AA1999.DAT: AAV02555

seq_documentation_block:

ID AAV02555 standard; protein; 139 AA.

AC AAV02555;

DT 16-JUL-1999 (first entry)

DE Humanised H chain V region of antiHM1.24 antibody.

XX Reconstituted human antibody; peptide antigen HM1.24; framework region;

KM complementary determining region; CDR: anti-HM1.24 antibody; myeloma;
 KW humanised antibody.
 XX
 OS Synthetic.
 OS Mus sp.
 XX
 PN W09918212-A1.
 XX
 PD 15-APR-1999.
 XX
 PF 02-OCT-1998; 98WO-JP04469.
 XX
 PR 03-OCT-1997; 97JP-0271726.
 XX
 PA (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Tsuchiya M;
 XX
 DR WPI: 1999-277273/23.
 XX N-PSDB; AAX36290.
 XX
 PT Reconstituted human antibody useful in the treatment of myeloma
 XX
 PS Disclosure; Page 86-87; 256pp; Japanese.
 XX
 CC The specification describes a reconstituted human antibody recognizing
 CC the peptide antigen HM1.24. This human antibody contains natural human
 CC framework regions modified by amino acid substitutions to provide
 CC homogeneity with a previously designed framework region (which may
 CC arise from a human or non-human source); and complementary determining
 CC regions (CDR) derived from a non-human anti-HM1.24 antibody. The
 CC reconstituted antibody is useful in the treatment of diseases in which
 CC the surface antigen HM1.24 is implicated such as myeloma. The present
 CC sequence is used in the creation of the antibodies of the invention.
 XX
 XX Sequence 139 AA:

alignment_scores: Length: 122
 Quality: 502.00 Gaps: 1
 Ratio: 4.564
 Percent Similarity: 90.164 Percent Identity: 79.508

alignment_block:
 US-08-487-283a-12_COPY_58_423 x AAY02555 ..

Align seg 1/1 to: AAY02555 from: 1 to: 139

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1 CAAGTCCAACTGTCGATCCGCGCCGAGGTCAAGACCGAGGCGCTC 50
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20 GlnValGlnLeuValGlnSerGlyAlaGluValLysProGlyAla 36
  |||||||
51 AGTCAAGTCTCTGTAAGCTAAGCTATATTTTCTAATTATGGA 100
  |||||||
36 TallysValSerCysLysAlaSerGlyTrpPheThrProTyrTrpM 53
  |||||||
101 TTCATGGGTCGTCAGGCCCGCGGAGGCTGGAATGATGGAGG 150
  ::|||
53 eGlnTrpValArgGlnAlaProGlyGlnGlyLeuGlnTrpMetGlySer 69
  |||
151 ANCTTACCGGGCTGTGTAGACACCAATATACGAAATTTTAAAGCCG 200
  |||
70 IlePheProGlyAspGlyAspTrpArgTrpSerGlnLysPheLysGlyAr 86
  |||
201 TGTTCATATGACCGCTGACACTTCGACTAGTACGATACATGAGCTCT 250
  |||
86 GValThrMetTrpAlaAspTrpSerThrSerThrValTyrMetGlnLeuS 103
  |||
251 CCAGCTGGATCGGACGACGCGCTCTATATATGCGCGCTTATTTT 300
  |||
103 eSerLeuArgSerGlnAspTrpAlaValTyrTrpCysAlaArgGlyLeu 119
  |||
301 TTTGGTTTACGCCGAAATGATTTTGAATGTTTGGGGTCAAGAACCC 350
  |||

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seq_name: /SID58/gcgdata/geneseq/geneseq/AA2000.DAT:AAW90933
 seq_documentation_block:
 ID AAW90933 standard; Protein: 470 AA.
 XX
 AC AAW90933;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Humanised anti-Fas designed heavy chain Neu 1 protein.
 XX
 KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX
 OS Synthetic.
 XX
 PN EP990663-A2.
 XX
 PD 05-APR-2000.
 XX
 PE 29-SEP-1999; 99EP-0307711.
 XX
 PR 30-SEP-1998; 98JP-0276881.
 XX
 PR 30-SEP-1998; 98JP-0276882.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 DR WPI: 2000-258930/23.
 XX N-PSDB; AAA11644.
 XX
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems -
 XX
 PS Claim 2; Page 169-170; 263pp; English.
 XX
 CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral

(B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanized anti-Fas antibody heavy chain construct designated Heu 1 which is described in the method of the invention.

SO Sequence 470 AA;

alignment_scores:

Quality: 500.50 Length: 125
Ratio: 4.469 Gaps: 2
Percent Similarity: 89.600 Percent Identity: 77.600

alignment_block:

US-08-487-283A-12_COPY_58_423 x AAW90933 ..

Align seg 1/1 to: AAW90933 from: 1 to: 470

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1 CAATGCCAAGTGTGCAATCCGGCCCGAGGTCAAGACCGAGGCGCTC 50
|||||
20 GlnValGlnLeuValGlnSerGlyAlaGluValLysProGlyAlaSer 36
51 AGTCAAGTGTCTGCTAAGCTAGCGGCTATTTTCTAATTAATGGA 100
|||||
36 ValLysValSerCysLysAlaSerGlyTyrThrPheThrSerTyrTrpM 53
101 TTCATGGGTCGTCAGCCCGCCGAGGCGCTGGAATGATGGTGAG 150
|||||
53 etGlnTrpValLysGlnAlaProGlyGlnGlyLeuGlnTrpMetGlyGlu 69
151 ATCTACCGGCGCTGTGACACGCAATATACCGAAATTTTAAAGCCG 200
|||||
70 IleAspProSerAspSerTyrThrAsnTyrAsnGlnLysPheLysGly 86
201 TGTACTATGACGCGTGCACACTGCTAGTACATGATACATGAGCGCTC 250
|||||
86 SalAlaThrLeuThrValAlaSerThrSerThrAlaTyrMetGlnLeuS 103
251 CCAGCGTCGATCGAGGACACGCGCGCTATATTATGCGCGCT..... 294
103 etSerLeuArgSerGlnAspThrAlaValTyrTyrCysAlaArgAsnArg 119
295 ...TATTTTGTGTTCTAGCCCGAATTGGTATTTGGATGTTGGGCTCA 341
120 AspTyr.....SerAsnAsnTrpTyrPheAspValTrpGlyGlu 132
342 AGGAACCTGTCACACTGTCGAGC 366
|||||
132 nGlyThrLeuValTrpValSerSer 140
seq_name: /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:AAW90934
seq_documentation_block:
ID AAW90934 standard; Protein: 470 AA.
AC AAW90934;
XX
XX
DT 08-AUG-2000 (first entry)
XX
XX
DE Humanised anti-Fas designed heavy chain Heu 2 protein.
XX
XX
Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiac;
dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
nephrotropic; antifertility; neuroprotective; antiseriosclerotic;
hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
Hashimoto disease; rheumatoid arthritis; graft versus host disease;
Storzen's syndrome; anemia; Addison's disease; scleroderma; sterility;
Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;

```

KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KM insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

OS Synthetic.

PN EP990663-A2.

PD 05-APR-2000.

PE 29-SEP-1999; 99EP-0307711.

PR 30-SEP-1998; 98QP-0276881.

PR 30-SEP-1998; 98QP-0276882.

PA (SANY) SANKYO CO LTD.

PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;

PI WPI; 2000-258930/23.

DR N-PSDB; AAA11645.

PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT inflammatory or autoimmune disease, induces apoptosis selectively in
PT cells with abnormal Fas-Fas ligand systems

PS Claim 2 ; Page 174-176; 263pp; English.

This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ligand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, antirheumatic, nephrotropic, antifertility, neuroprotective, antiseriosclerotic, cardiac and hepatotropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft versus host disease, Sjorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis fulminant, chronic, viral (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a humanized anti-Fas antibody heavy chain construct designated Heu 2 which is described in the method of the invention.

SO Sequence 470 AA;

alignment_scores:

Quality: 499.50 Length: 125
Ratio: 4.460 Gaps: 2
Percent Similarity: 89.600 Percent Identity: 77.600

alignment_block:

US-08-487-283A-12_COPY_58_423 x AAW90934 ..

Align seg 1/1 to: AAW90934 from: 1 to: 470

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1 CAATGCCAAGTGTGCAATCCGGCCCGAGGTCAAGACCGAGGCGCTC 50
|||||
20 GlnValGlnLeuValGlnSerGlyAlaGluValLysProGlyAlaSer 36

```



```

51 AGCAAGTCTCTCTTAAGCTAGCGCTATATTTTCTAATTATGGA 100
   |||||
36 rVallyValSerCysAlaSerIleValThrPheThrSerTrpM 53
   |||||
101 TTCAATGGGTGCGTCAGCCCCGGGAGGCGCTGAATGATGGTGAG 150
   |||||
53 eGlnTrpAllySGlnAlaProGlyGlnIleuGlnTrpMetGlyGln 69
   |||||
151 AACTACCGGGCTCTGTAGACCGAATATACGAAATTTTAAAGCCG 200
   |||||
70 IleAspProSerAspSerTrpThrAsnTrpAsnGlnLysPheLysGly 86
   |||||
201 TGTTCATAGACCGCTGACACTGACATGATATACATGAGCTCT 250
   |||||
86 sAlaThrIleThrValAlaSerThrSerThrAlaValMetGlnLeu 103
   |||||
251 CCAGCTCGGATCGAGACAGCGCGCTATATGCGCGCT 294
   |||||
103 erSerLeuArgSerGlnAspThrAlaValIleValTrpCysAlaArgAsnArg 119
   |||||
295 ...TATTTTGGTTCTAGCCGAAATGGTATTTGATGTTGGGCTCA 341
   |||||
120 AspTyr.....SerAsnAsnTrpTyrPheAspValTrpGly 132
   |||||
342 AGAACCCTGGTCACTGTCGAGC 366
   |||||
132 nGlyThrLeuValThrValSerSer 140

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seq_name: /SID58/gcgdata/geneseq/geneseq/AA1998.DAT:AAW62210

seq_documentation_block:

ID AAW62210 standard; Protein: 139 AA.

AC AAW62210;

DT 21-SEP-1998 (first entry)

DE Humanised anti-HM1.24 antibody H chain V region HEF-RVHb-AHM g-gamma-1.

KW Mouse; human; humanised; anti-HM1.24 antibody; myeloma; FR: CDR; framework region; complementarity determining region; antigenicity.

XX Synthetic.

OS Mus sp.

OS Homo sapiens.

PN W09814580-A1.

XX 09-APR-1998.

PF 03-OCT-1997; 97WO-JP03553.

PR 04-OCT-1996; 96JP-0264756.

PA (CHUS) CHUGAI SEIYAKU KK.

PI Koishihara Y, Kosaka M, Ohtomo T, Ono K, Tsuchiya M;

PI Yoshimura Y;

DR WPI; 1998-286421/25.

DR N-PSDB; AAV39399.

PT Humanised anti-HM1.24 antibody - for treatment of myeloma

PS Example 9; Page 108-109; 210pp: Japanese.

CC A humanised anti-HM1.24 antibody has been developed which comprises

CC human L and H chain C regions, and L and/or H chain V regions

CC containing material originating in mouse anti-HM1.24 antibody. The V

CC regions contain framework (FR) regions of human origin and

CC complementarity determining regions (CDR) of mouse origin, leading to

CC a reshaped humanised antibody. The C regions are human Ck (L-chain) and

CC human C gamma (especially C gamma 1) (H-chain). The FR regions of the

CC L chain V region are derived from human subtype HSG1 (e.g. from human
CC antibody RE1) and the FR regions of the H chain V region are derived
CC from human subtype HSG1 (e.g. FR1-3 from human antibody Hg3 and FR4
CC from human antibody J6). The present sequence represents an H chain
CC V region from the present invention. The antibodies are used for
CC the treatment of myeloma, especially by injection, intravenously,
CC intramuscularly or subcutaneously. The antibodies are used at 0.01-1000
CC (especially 5-100) mg/kg body weight. The humanised antibody has low
CC antigenicity and is therefore effective therapeutically in humans.

SO Sequence 139 AA;

alignment_scores:

Quality	Ratio	Length	Gaps
499.00	4.536	122	1
Percent Similarity: 90.164	Percent Identity: 78.689		

alignment_block:

US-08-487-283a-12_COPY_58_423 x AAW62210 ..

Align seg 1/1 to: AAW62210 from: 1 to: 139

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1 CAAGTCCAACTGTCGATCCGGCGCCGAGTCAGAAAGCCAGGCGCTC 50
   |||||
20 GlnValGlnLeuValGlnSerIleValGlnValLysProGlyAla 36
   |||||
51 AGTCAAACTGTCCTGTAAGCTAGCGGCTATATTTTCTAATTATGGA 100
   |||||
36 rVallyValSerCysLysAlaSerGlyTrpThrPheThrProTyrTrpM 53
   |||||
101 TTCAATGGGTGCGTCAGCCCCGGGAGGCGCTGAATGATGGGCTGAG 150
   |||||
53 eGlnTrpValArgGlnAlaProGlyGlnIleuGlnTrpMetGlySer 69
   |||||
151 ATCTTACCGGGCTCTGTAGACCGAATATACGAAATTTTAAAGCCG 200
   |||||
70 IlePheProGlyAspGlyAspThrArgTrpSerGlnLysPheLysGly 86
   |||||
201 TGTTCATAGACCGCTGACACTGACATGATATACATGAGCTCT 250
   |||||
86 sValThrMetThrAlaAspThrSerThrSerThrValIleMetGlnLeu 103
   |||||
251 CCAGCTCGGATCGAGACAGCGCGCTATATGCGCGCTATATTTT 300
   |||||
103 erSerLeuArgSerGlnAspThrAlaValIleValTrpCysAlaArgGlyLeu 119
   |||||
301 TTGCTTCTAGCCGAAATGGTATTTGATGTTGGGTCAGAAACCT 350
   |||||
120 .....ArgArgGlyGlyTyrTrpPheAspTyrTrpGlyGlnGlyThrH 134
   |||||
351 GGTCACTGTCGAGC 366
   |||||
134 rValThrValSerSer 139

```

seq_name: /SID58/gcgdata/geneseq/geneseq/AA1999.DAT:AAV02556

seq_documentation_block:

ID AAV02556 standard; Protein: 139 AA.

AC AAV02556;

DT 16-JUL-1999 (first entry)

DE Humanised H chain V region of antiHM1.24 antibody.

KW Reconstituted human antibody; peptide antigen HM1.24; framework region;

KW complementarity determining region; CDR: anti-HM1.24 antibody; myeloma;

XX humanised antibody.

XX Synthetic.

XX Mus sp.

ATTORNEY/AGENT INFORMATION:
NAME: NO. 6072035ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-246A-14

alignment_scores:
Quality: 493.50 Length: 123
Ratio: 4.446 Gaps: 1
Percent Similarity: 90.244 Percent Identity: 77.236

alignment_block:
US-08-487-283A-12_COPY_58_423 x US-08-485-246A-14 ..
Align seg 1/1 to: US-08-485-246A-14 from: 1 to: 142

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1 CAAGTCCAACTGGTGCATCCGCGCCGAGGTCAGAGCCAGGCGCTC 50
|||||
20 GlnValGlnLeuValGlnSerGlyAlaGluValLysProGlyAla 36
51 AGTCAAGAGTCTCTTAAGCTAGCGGCTATATTTTTCAATTATGGA 100
|||||
36 rAllyValSerGlyAlaSerGlyThrPheSerMetGlyTrpL 53
101 TTCATGGGCTGCTGAGCGCCGCGGAGGCGCTGGAATGATGGGAG 150
|||||
53 euGlnTrpValArgGlnAlaProGlyHisGlyLeuGlnTrpValGlyGlu 69
151 ATCTTACCGGCGCTGTGTAGCACCGCAATATACCAAAATTTTAAAGCCG 200
|||||
70 IleSerProGlyThrPheThrThrAsnTyraSngLulysPheLysAla 86
201 TTTTACTATGACGCGTGCACACTTGCAGTACATATACATGAGCTCT 250
|||||
86 gAlaTrpPheThrAlaAspThrSerThrAsnThrAlaTyraMetGluLeu 103
251 CCAGCTCGATCGAGGACGACGCGCTCATATATGCGCGCTATTTT 300
|||||
103 erSerLeuArgSerGlnAspThrAlaValTyrcysAlaArgPheSer 119
301 TTTGGTCTAGCCCAATTGG...TATTTGATGTTGGGTCAGGAAC 347
|||||
120 HisPheSerGlySerAsnTyraSptyrPheAspTyrTrpGlyGlnGly 136
348 CCTGTCTACTGTCTCGAGC 366
|||||
136 rLeuValThrValSerSer 142
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seq_name: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:US-08-428-257A-78

seq_documentation_block:
Sequence 78, Application US/08428257A
Patent No. 5885808
GENERAL INFORMATION:
APPLICANT: Spooner, Robert A.
APPLICANT: Epenetos, A.A.
TITLE OF INVENTION: Compounds to target cells
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jules E. Goldberg
STREET: 261 Madison Avenue
CITY: New York
STATE: NY

COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (ERO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,257A
FILING DATE: 07/05/95
CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-428-257A-78

alignment_scores:
Quality: 493.00 Length: 123
Ratio: 4.441 Gaps: 2
Percent Similarity: 90.244 Percent Identity: 78.862

alignment_block:
US-08-487-283A-12_COPY_58_423 x US-08-428-257A-78 ..
Align seg 1/1 to: US-08-428-257A-78 from: 1 to: 118

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1 CAAGTCCAACTGGTGCATCCGCGCCGAGGTCAGAGCCAGGCGCTC 50
|||||
1 GlnValGlnLeuValGlnSerGlyAlaGluValLysProGlyAla 17
51 AGTCAAGAGTCTCTTAAGCTAGCGGCTATATTTTTCAATTATGGA 100
|||||
17 rAllyValSerGlyAlaSerGlyThrPheSerMetGlyTrpL 34
101 TTCATGGGCTGCTGAGCGCCGCGGAGGCGCTGGAATGATGGGAG 150
|||||
34 leuGlnTrpValArgGlnAlaProGlyLysGlyLeuGlnTrpValGlyGlu 50
151 ATCTTACCGGCGCTGTGTAGCACCGCAATATACCAAAATTTTAAAGCCG 200
|||||
51 IleLeuProGlySerAsnAspThrArgTyraSngLulysPheLysGly 67
201 TTTTACTATGACGCGTGCACACTTGCAGTACATATACATGAGCTCT 250
|||||
67 gValThrValThrAlaGspThrSerThrAsnThrAlaTyraMetGluLeu 84
251 CCAGCTCGATCGAGGACGACGCGCTCATATATGCGCGCT...TAT 297
|||||
84 erSerLeuArgSerGlnAspThrAlaValTyrcysAlaArgSerTy 100
298 TTTTGGTCTAGCCCAATTGGTATTTGATGTTGGGTCAGGAAC 347
|||||
101 AspPheAla.....TrpPheAlaTyTrpGlyGlnGlyTh 112
348 CCTGTCTACTGTCTCGAGC 366
|||||
112 rLeuValThrValSerSer 118
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seq_name: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:US-07-987-264-60

seq_documentation_block:
Sequence 60, Application US/07987264
Patent No. 6204366
GENERAL INFORMATION:
APPLICANT: VERHOEYEN, MARTINE ELISA
TITLE OF INVENTION: SPECIFIC BINDING AGENTS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN

```

STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/987,264
FILING DATE: 08-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9019553.8
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB PCT/GB91/01511
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 200332/P309505A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-987-264-60

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alignment_scores:
Quality: 493.00      Length: 123
Ratio: 4.441        Gaps: 2
Percent Similarity: 90.244      Percent Identity: 78.862

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alignment_block:

US-08-487-283A-12_COPY_58_423 x US-07-987-264-60 ..

Align seg 1/1 to: US-07-987-264-60 from: 1 to: 118

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1 CAAGTCCAAGTGTGCAATCCGCGCGAGTCAAGAGCCAGGGGCTC 50
|||||
1 GlnValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyAlaIse 17
51 AGTCAAAAGTGTCTGTAAGCTAGCGGCTATATTTTCTAATTAATGGA 100
|||||
17 rValLysValSerCysLysAlaSerGlyTyrThrPheSerAlaTyrTrpI 34
101 TTCATGGGTCGTGACGGCCCCCGGCGAGGCGCTGATGATGGTGTAG 150
|||||
34 LeuItrPvalAlaGlnAlaProGlyLysGlyLeuGluItrPvalGlyGlu 50
151 ATCTTACCGGGCTCTGTAGACCGCAATATACGAAATTTTAAAGACCG 200
|||||
51 IleLeuProGlySerAsnAsnSerArgLysAsnGluLysPheLysGlyArg 67
201 TGTACTATGACGGCTGACACTTGACTAGTACATATACATGAGCTCT 250
|||||
67 gValItrPvalAlaThrArgAspTrnSerThrAsnThrAlaTyrMetGluLeu 84
251 CCACCGTCGGTTCGAGACACAGCGGCTATATATTCGCGCGCT...TAT 297
|||||
84 erSerLeuArgSerGlnAspThrAlaValTyrTyrCysAlaArgSerTyr 100
298 TTTTGTGGTCTACGCCGAATGTGATTTTGTGATGTTGGGGTCAAGAAC 347

```

```

|||||
101 AspPheAla.....TrrPheAlaTyrTrpLysGlnGlyTh 112
348 CCGTGTCACTGTCTCGAGC 366
|||||
112 rLeuValThrValSerSer 118

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seq_name: /cgn2_6/ptodata/2/laa/5B.COMB.pep:US-08-476-176B-18

seq_documentation_block:

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Sequence 18, Application US/08476176B
Patent No. 5958708
GENERAL INFORMATION:
Applicant: Hardman, No. 5958708man
Applicant: Kolbinger, Frank
Applicant: Saldanha, Jose
TITLE OF INVENTION: Reshaped monoclonal antibodies against an
NUMBER OF SEQUENCES: 55.
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5958708artis Patent Department
STREET: 59 Route 10
CITY: East Hanover
STATE: New Jersey
COUNTRY: USA
ZIP: 07936-1080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,176B
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/127,721
FILING DATE: 27-SEPTEMBER-1993
APPLICATION NUMBER: US 07/952,802
FILING DATE: 25-SEPTEMBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5958708ak, Henry P.
REGISTRATION NUMBER: 33,200
REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 277-5110
TELEFAX: (908) 277-4306
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 142 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-476-176B-18

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alignment_scores:
Quality: 492.50      Length: 123
Ratio: 4.477        Gaps: 1
Percent Similarity: 89.431      Percent Identity: 78.049

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alignment_block:

US-08-487-283A-12_COPY_58_423 x US-08-476-176B-18 ..

Align seg 1/1 to: US-08-476-176B-18 from: 1 to: 142

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1 CAAGTCCAAGTGTGCAATCCGCGCGAGTCAAGAGCCAGGGGCTC 50
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20 GlnValGlnLeuValGlnSerGlyAlaGluValLysLysProGlyAlaIse 36
51 AGTCAAAAGTGTCTGTAAGCTAGCGGCTATATTTTCTAATTAATGGA 100
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36 rValLysValSerCysLysAlaSerGlyTyrTrnPheSerMetLysTrpL 53

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101 TTCAATGGGTGGTGCAGCCCCCGGCGAGGCGCTGGAATGATGGGTGAG 150
53 euglutrprvalarglnalaspthrserlaserthrvalatymetglsu 69
151 ATCTACCGGCTGTGTGACGACGCAATATACGAAATTTTAAAGACCG 200
70 lleserprogllythrphethrthrasnlyrasnglulysphenysalaar 86
201 TGTACTATGACGCGTGCAGCTTCGACTGATGACTATACATGAGCTCT 250
86 galathrphethrthralaaspthrserlaserthrvalatymetglsu 103
251 CCAGCCTGCGATCGAGACGACGCGCGCTATATTATTCGCGCGTTATTT 300
103 erSerleuargSerGlnasprthrAlaValIYrYrCYsalaarGpneser 119
301 TTTGGTTTCAGCCGCAATTG...TATTTGATNGTTGGGGGCAAGAAC 347
120 HispheneserGlySerasnlyrasnlyrphenasptryrtrpelyngllyth 136
348 CCTGCTACACTGTCTCGAGC 366
136 rleuvalthrvalserSer 142
seq_name: /cgn2_6/prodata/2/1aa/6A_COMB.pep:US-08-127-721A-18
seq_documentation_block:
; Sequence 18, Application US/08127721A
; Patent No. 6066718
; GENERAL INFORMATION:
; APPLICANT: Hardman, No. 6066718man
; APPLICANT: Kolbinger, Frank
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
; TITLE OF INVENTION: Immunoglobulin isotype
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6066718artis Patent and Trademark Department
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936-1080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/127,721A
; FILING DATE: 27-SEPTEMBER-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952,802
; FILING DATE: 25-SEPTEMBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6066718ak, Henry P.
; REGISTRATION NUMBER: 33,200
; REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 142 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-127-721A-18
alignment_scores:

Quality: 492.50 Length: 123
Ratio: 4.477 Gaps: 1
Percent Similarity: 89.431 Percent Identity: 78.049
Alignment_block:
US-08-487-283A-12_COPY_58_423 x US-08-127-721A-18 ..
Align seg 1/1 to: US-08-127-721A-18 from: 1 to: 142
1 CAACTCCAACTGTGTCATCCGCGCGCGAGGTCAAGAACCGAGGCGCTC 50
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20 GlnvalGlnleuvalGlnserGlyAlaGlnvallyslsprogllyAla 36
51 AGTCAAACTGCTCTGTAAGCTAGCGGCTATATTTTCTAATTAFTGA 100
36 rAllyslvalserGlyslsAlaserGlyrYrthrphenesermetYrtrPL 53
101 TTCAATGGGTGGTGCAGCCCCCGGCGAGGCGCTGGAATGATGGGTGAG 150
53 euglutrprvalarglnalaspthrserlaserthrvalatymetglsu 69
151 ATCTACCGGCTGTGTGACGACGCAATATACGAAATTTTAAAGACCG 200
70 lleserprogllythrphethrthrasnlyrasnglulysphenysalaar 86
201 TGTACTATGACGCGTGCAGCTTCGACTGATGACTATACATGAGCTCT 250
86 galathrphethrthralaaspthrserlaserthrvalatymetglsu 103
251 CCAGCCTGCGATCGAGACGACGCGCGCTATATTATTCGCGCGTTATTT 300
103 erSerleuargSerGlnasprthrAlaValIYrYrCYsalaarGpneser 119
301 TTTGGTTTCAGCCGCAATTG...TATTTGATNGTTGGGGGCAAGAAC 347
120 HispheneserGlySerasnlyrasnlyrphenasptryrtrpelyngllyth 136
348 CCTGCTACACTGTCTCGAGC 366
136 rleuvalthrvalserSer 142
seq_name: /cgn2_6/prodata/2/1aa/6A_COMB.pep:US-08-485-246A-18
seq_documentation_block:
; Sequence 18, Application US/08485246A
; Patent No. 6072035
; GENERAL INFORMATION:
; APPLICANT: Hardman, No. 6072035man
; APPLICANT: Kolbinger, Frank
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
; TITLE OF INVENTION: Immunoglobulin isotype
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6072035artis Patent Department
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936-1080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/485,246A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/127,721
; FILING DATE: 27-SEPTEMBER-1993
; APPLICATION NUMBER: US 07/952,802


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; FILING DATE: 25-SEPTEMBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6072035ak, Henry P.
; REGISTRATION NUMBER: 33,200
; REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 142 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-485-246A-18

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alignment_scores:
  Quality: 492.50      Length: 123
  Ratio: 4.477         Gaps: 1
  Percent Similarity: 89.431   Percent Identity: 78.049

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alignment_block:

US-08-487-283A-12_COPY_58_423 x US-08-485-246A-18 ..

Align seg 1/1 to: US-08-485-246A-18 from: 1 to: 142

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1 CAAGTCCACGCTGTCATCCGGCCGAGCGACAGACCCAGGGCCCTC 50
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20 GlnValGlnLeuValGlnSerGlyAlaGluValLysProGlyAlaSe 36
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51 AGTCAAGTGTCTGTAAAGCTAGCGGCTATATTTTCTAATTAATGA 100
  ||||||||||||||||||||||||||||||||||||||||||||
36 rValLysValSerGlyAlaSerGlyTyrThrPheSerMetLysTrpL 53
  ||||||||||||||||||||||||||||||||||||||||||||
101 TTCATGGGTCGTCAGGCCCGCCGAGGGCCCTGAATGATGGGTGAG 150
  ||||||||||||||||||||||||||||||||||||||||||||
53 euGluTrpValArgGlnAlaProGlyGlnArgLeuGluTrpMetGlyGlu 69
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151 ATCTACCGGGCTCGTAGCAGCGAATATCCGAAATTTTAAAGACCG 200
  ||||||||||||||||||||||||||||||||||||||||||||
70 IleSerProGlyThrPheThrThrAsnTyrAsnGluLysPheLysAlaAr 86
  ||||||||||||||||||||||||||||||||||||||||||||
201 TGTACTATGACGGGTGACACTTCGACTAGTACATATACATGAGCTCT 250
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86 gAlaThrPheThrAlaAspThrSerAlaSerThrAlaTyrMetGluLeuS 103
  ||||||||||||||||||||||||||||||||||||||||||||
251 CCAGCCTGCGATCGAGAGACAGCGCGCTATATTATTCGCGCGTTATTT 300
  ||||||||||||||||||||||||||||||||||||||||||||
103 erSerLeuArgSerGluAspThrAlaValTyrTyrCysAlaArgPheSer 119
  ||||||||||||||||||||||||||||||||||||||||||||
301 TTTGGTCTACGCCGAATTGG...TATTTGATGTTGGGCTAGCAAGAAC 347
  ||||||||||||||||||||||||||||||||||||||||||||
120 HisPheSerGlySerAsnTyrAspThrPheAspTyrTrpGlyGlnGlyThr 136
  ||||||||||||||||||||||||||||||||||||||||||||
348 CCGTGTCACTGTCTCGAGC 366
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136 rLeuValrPheValSerSer 142

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seq_name: /cgn2.6/ptodata/2/iaa/5A_COMB pep: US-07-946-421-28

seq_documentation_block:

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; Sequence 28, Application US/07946421
; Patent No. 5558864
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Kettleborough, Catherine A.
; APPLICANT: Saidanba, Jose
; TITLE OF INVENTION: Humanized and Chimeric Monoclonal
; TITLE OF INVENTION: Antibodies
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.

```

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; STREET: 2200 Clarendon Boulevard, Suite 1400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,421
; FILING DATE: 06-NOV-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP92/00480
; FILING DATE: 04-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 911933892
; FILING DATE: 06-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hamlet-King, Diana
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: Merck 1430
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; TELEX: 64191
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-07-946-421-28

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alignment_scores:
  Quality: 478.50      Length: 122
  Ratio: 4.350         Gaps: 1
  Percent Similarity: 90.164   Percent Identity: 76.230

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alignment_block:

US-08-487-283A-12_COPY_58_423 x US-07-946-421-28 ..

Align seg 1/1 to: US-07-946-421-28 from: 1 to: 140

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51 AGTCAAGTGTCTGTAAAGCTAGCGGCTATATTTTCTAATTAATGA 100
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36 rValLysValSerGlyAlaSerGlyTyrThrPheSerSerHisTrpM 53
  ||||||||||||||||||||||||||||||||||||||||||||
101 TTCATGGGTCGTCAGGCCCGCCGAGGGCCCTGAATGATGGGTGAG 150
  ||||||||||||||||||||||||||||||||||||||||||||
53 ethIstrPValArgGlnAlaProGlyGlnGlyLeuGluTrpValGlyGlu 69
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151 ATCTTACCGGGCTCTGTAGCAGCCGAAATATACGAAATTTTAAAGCCG 200
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70 PheAsnProSerAsnGlyArgThrAsnTyrAsnGluLysPheLysSerAr 86
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201 TGTACTATGACGGGTGACACTTCGACTAGTACATATACATGAGCTCT 250
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86 gValThrMetThrLeuAspThrSerThrAsnThrAlaTyrMetGluLeuS 103
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251 CCAGCCTGCGATCGAGAGACAGCGCGCTATATTATTCGCGCGTTATTT 300
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301 TTTGGTCTACGCCGAATTGGTATTTGATGTTGGGCTAGCAAGACCT 350
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120 TyrAspTyrAspGlyArg...TyrPheAspTyrTrpLysGlnGlyThrLe 135

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351 GGTCACTGTCTGAGC 366
 135 uValthrValSerSer 140

seq_name: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:US-09-199-149-12

seq_documentation_block:

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; Sequence 12, Application US/09199149
; Patent No. 6160099
; GENERAL INFORMATION:
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Taylor, Alexander H.
; APPLICANT: Trulll Jr., Stephen H.
; APPLICANT: Johnson, Kyung O.
; TITLE OF INVENTION: Humanized Monoclonal Antibodies
; FILE REFERENCE: P50860
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 12
; LENGTH: 128
; TYPE: PRT
; ORGANISM: murine B9
US-09-199-149-12
  
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alignment_scores:

Quality:	478.00	Length:	123
Ratio:	4.385	Gaps:	2
Percent Similarity:	88.618	Percent Identity:	77.236

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51 AGTCAAGTGTCTGTAAAGCTAATGCTATATTTTCTAATTATGGA 100
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22 rValLysValSerCysLysAlaSerGlyTyrThrPheSerSerTyrTri 39
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101 TTCAAAGGCGCTCAGAGCCCGGCGAGGCGCTGGAATGATGGGTGAG 150
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39 leuLutrpValLysGlnAlaProGlyGlnLysLeuGluTyrPheGly 55
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151 ATCTTACCGGGCTCTGTAGACACCGAATATACGAAATTTTAAAGCCG 200
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56 lleuLeuProArgSerGlyAsnThrAsnTyrAsnGlnLysPheLysGly 72
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201 TGTACTATGACCGCTGACACTTCGACTAGTACAGTATACATGAGGCTCT 250
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72 salAthrPheThrAlaAspThrSerThrAlaTyrMetClnLeuS 89
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251 CCAGCTCGGATCGAGAGACAGCGCGCTATATTATTC...GCGGCTTAT 297
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89 erSerLeuArgSerGluAspThrAlaValTyrTyrCysSerSerArgGly 105
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298 TTTTGTGTTCTAGCCCGAATGTGATTTTGGGTTCAGAGAAC 347
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106 ValArgGlySer.....MetAspTyrTriPheLysGlnGlyTh 117
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348 CCTGTCACTGTCTGAGC 366
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117 rLeuValThrValSerSer 123
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seq_documentation_block:
  
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; Sequence 5, Application US/09199149

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; Patent No. 6160099
; GENERAL INFORMATION:
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Taylor, Alexander H.
; APPLICANT: Trulll Jr., Stephen H.
; APPLICANT: Johnson, Kyung O.
; TITLE OF INVENTION: Humanized Monoclonal Antibodies
; FILE REFERENCE: P50860
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 5
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Humanized B9
US-09-199-149-5
  
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alignment_scores:

Quality:	478.00	Length:	123
Ratio:	4.385	Gaps:	2
Percent Similarity:	88.618	Percent Identity:	77.236

alignment_block:

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Align seg 1/1 to: US-09-199-149-5 from: 1 to: 118

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51 AGTCAAGTGTCTGTAAAGCTAATGCTAATTTTCTAATTATGGA 100
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17 rValLysValSerCysLysAlaSerGlyTyrThrPheSerSerTyrTri 34
  ||||||||||||||||||||||||||||||||||||||||||||
101 TTCAAAGGCGCTCAGAGCCCGGCGAGGCGCTGGAATGATGGGTGAG 150
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34 leuLutrpValLysGlnAlaProGlyGlnLysLeuGluTyrPheGly 50
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151 ATCTTACCGGGCTCTGTAGACACCGAATATACGAAATTTTAAAGCCG 200
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51 lleuLeuProArgSerGlyAsnThrAsnTyrAsnGlnLysPheLysGly 67
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201 TGTACTATGACCGCTGACACTTCGACTAGTACAGTATACATGAGGCTCT 250
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67 salAthrPheThrAlaAspThrSerThrAlaTyrMetClnLeuS 84
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251 CCAGCTCGGATCGAGAGACAGCGCGCTATATTATTC...GCGGCTTAT 297
  ||||||||||||||||||||||||||||||||||||||||||||
84 erSerLeuArgSerGluAspThrAlaValTyrTyrCysSerSerArgGly 100
  ||||||||||||||||||||||||||||||||||||||||||||
298 TTTTGTGTTCTAGCCCGAATGTGATTTTGGGTTCAGAGAAC 347
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101 ValArgGlySer.....MetAspTyrTriPheLysGlnGlyTh 112
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348 CCTGTCACTGTCTGAGC 366
  ||||||||||||||||||||||||||||||||||||||||||||
112 rLeuValThrValSerSer 118
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seq_name: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:US-08-202-047-9
seq_documentation_block:
; Sequence 9, Application US/08202047
; Patent No. 5800815
; GENERAL INFORMATION:
; APPLICANT: CHESNUT, Robert W.
; APPLICANT: POLLEY, Margaret J.
; APPLICANT: PAULSON, James C.
; APPLICANT: JONES, S. Tarran
; APPLICANT: SALDANHA, Jose W.
  
```

```

? APPLICANT: BENDIG, Mary M.
? TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
? NUMBER OF SEQUENCES: 45
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Townsend and Townsend Kourie and Crew
? STREET: One Market Plaza, Stewart Tower, Suite 2000
? CITY: San Francisco
? STATE: California
? COUNTRY: USA
? ZIP: 94105
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
?
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/202,047
? FILING DATE: 25-FEB-1994
? CLASSIFICATION: 424
? ATTORNEY/AGENT INFORMATION:
? NAME: Smith, William M.
? REGISTRATION NUMBER: 30,223
? REFERENCE/DOCKET NUMBER: 14137-77
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415-326-2400
? TELEFAX: 415-326-2422
? INFORMATION FOR SEQ ID NO: 9:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 139 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
?
US-08-202-047-9

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alignment_scores:

Quality	473.00	Length:	124
Ratio:	4.339	Gaps:	2
Percent Similarity:	87.903	Percent Identity:	75.806

alignment_block:

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Align seg 1/1 to: US-08-202-047-9 from: 1 to: 139

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51 AGTCAAGTCTCTGTAAAGCTAGCGGCTATTTCTCTAATTAATGGA 100
  |||||||
36 rValLysValSerCysLysAlaSerGlyTyrThrPheThrAsnIyrValM 53
  |||||||
101 TTCAATGGGTCGTCAGGCCCGCGGCGAGGGCTGAATGATGGGTGAG 150
  |||||||
53 ethStrpValArgGlnAlaProGlyGlnArgLeuGluTrpMetGlyPhe 69
  |||||||
151 ATCTTACGGGGCTCTGTAGCACCAGAAATATACCGAAATTTTAAAGCCG 200
  |||||||
70 IleAsnProSerAsnAspGlyProLysTyrAsnGluArgPheLysAsnAr 86
  |||||||
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86 gValThrIleThrSerAspThrSerAlaSerThrAlaIyrMetGluLeuS 103
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251 CCACCTCGCATCGAGAGACAGCGCGCTATATTGCGCGGCTATATT 300
  |||||||
103 erSerLeuArgSerGlnAspThrAlaValIyrTyrCysAlaArg..... 117
  |||||||
301 TTTCGTTCTTACCCG.....AATTGATTTTGTGTTGGGGTCAACG 344
  |||||||
118 .....AlaArgProGlyPheAspIrrPyrPheAspValIrrPglYglnd1 132

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345 AACCTGTCACATGTCGAGC 366
  |||||||
132 yThrLeuValThrValSerSer 139

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seq name: /cogn2.6/ptodata/2/1aa/6A.COMB.pep:US-08-964-690-9

seq documentation_block:

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? Sequence 9, Application US/08964690
? Patent No. 6033667
?
? GENERAL INFORMATION:
? APPLICANT: CHESNOT, Robert W.
? APPLICANT: POLLEY, Margaret J.
? APPLICANT: PAULSON, James C.
? APPLICANT: JONES, S. Tarian
? APPLICANT: SALDANHA, Jose W.
?
? APPLICANT: BENDIG, Mary M.
? TITLE OF INVENTION: Antibodies to P-Selectin and Their Uses
? NUMBER OF SEQUENCES: 45
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Townsend and Townsend Kourie and Crew
? STREET: One Market Plaza, Stewart Tower, Suite 2000
? CITY: San Francisco
? STATE: California
? COUNTRY: USA
? ZIP: 94105
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
?
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/964,690
? FILING DATE:
?
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/08/202,047
? FILING DATE: 25-FEB-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Smith, William M.
? REGISTRATION NUMBER: 30,223
? REFERENCE/DOCKET NUMBER: 14137-77
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 415-326-2422
? TELEFAX: 415-326-2400
? INFORMATION FOR SEQ ID NO: 9:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 139 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
?
US-08-964-690-9

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alignment_scores:

Quality	473.00	Length:	124
Ratio:	4.339	Gaps:	2
Percent Similarity:	87.903	Percent Identity:	75.806

alignment_block:

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US-08-487-283A-12_COPY_58_423 x US-08-964-690-9 ..
Align seg 1/1 to: US-08-964-690-9 from: 1 to: 139

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1 CAAGTCCAACTGTCGATCCGGCGCGAGTCAAGAGCCAGGGGCTC 50
  |||||||
20 GlnValGlnLeuValGlnSerGlyAlaGluValLysProGlyAlaSe 36
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51 AGTCAAGTCTCTGTAAAGCTAGCGGCTATATTCTCTAATTAATGGA 100
  |||||||
36 rValLysValSerCysLysAlaSerGlyTyrThrPheThrAsnIyrValM 53
  |||||||
101 TTCAATGGGTCGTCAGGCCCGCGGCGAGGGCTGAATGATGGGTGAG 150
  |||||||

```

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53 eH1StrpValArgInAlaProGlyGlnArgLeuGluTrpMetGlyPhe 69
151 ATCTTACCGCGGCTCTGTAGACACCGCAATATACGAAATTTTAAAGCCG 200
70 IleasnProSerAsnaspGlyProGlyTyrAsnGlnArgPheGlyAsnAr 86
201 TGTACTATGACGCGTGTACGACTGTACATGATATACATGAGACTCT 250
86 gValThrIleThrSerAspThrSerAlaSerThrAlaTyrMeGluLeuS 103
251 CCAGCCTGGCATCGAGACACGCGCTCTATATTGCGCGCTTATTATT 300
103 eSerLeuArgSerGluAspThrAlaValTyrTyrCysAlaArg..... 117
301 TTGGTCTACAGCCG.....AATTGCTATTGATGTTGGGCTCAAG 344
118 .....AlaArgProGlyPheAspTyrTyrPheAspValTrpGlyGln 132
345 AACCGTGCCTGCTCTGAGC 366
132 yThrLeuValThrValSerSer 139

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seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-09-199-149-3

seq_documentation_block:

```

; Sequence 3, Application US/09199149
; Patent No. 6160099
; GENERAL INFORMATION:
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Taylor, Alexander H.
; APPLICANT: Trull Jr., Stephen H.
; APPLICANT: Johanson, Kyung O.
; TITLE OF INVENTION: Humanized Monoclonal Antibodies
; FILE REFERENCE: P50860
; CURRENT APPLICATION NUMBER: US/09/199,149
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Kabat VH subgroup I
; US-09-199-149-3

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alignment_scores:

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Quality: 472.50      Length: 126
Ratio: 4.375         Gaps: 2
Percent Similarity: 85.714      Percent Identity: 76.190

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alignment_block:

US-08-487-283A-12_COPY_58_423 x US-09-199-149-3 ..

Align seg 1/1 to: US-09-199-149-3 from: 1 to: 125

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1 CAATGTCACACTGTGCAATCGCGCGCGAGTCAAGACGAGCGGCTC 50
1 |||||
1 GlnValGlnLeuValGlnSerGlyAlaGluValTyrLysProGlyLase 17
51 ACTCAAGTGTCTGTAAAGCTAGCGCGCTATATTTTCTAATTATTGA 100
1 |||||
1 rValTyrValSerCysLysAlaSerGlyTyrThrPheThrSerTyrAla 34
101 TTCATGGTGGTGTGAGCCCGCGGAGGCTGTGAATGAGATGGTGAG 150
1 |||||
34 leSerTrpAlaArgGlnAlaProGlyGlnGlyLeuGluTrpMetGlyTyr 50
151 ATCTTACCGCGGCTCTGTAGACACCGCAATATACGAAATTTTAAAGCCG 200
1 |||||
51 IleasnProGly...GlyAspThrAsnTyrAlaGlnLysPheGlnGlyAr 66
201 TGTACTATGACGCGTGTACGACTGTACATGATATACATGAGACTCT 250
1 |||||

```

```

66 gValThrIleThrAlaAspThrSerThrSerThrAlaTyrMeGluLeuS 83
251 CCAGCCTCGCATCGAGACACGCGCTCTATATTATTCGCGGCT..... 294
83 eSerLeuArgSerGluAspThrAlaValTyrTyrCysAlaArgProGly 99
295 .....TATTTTGGTGTACAGCCGCAATGCTATTTTGAATGTTGGG 338
100 TyrGlyTyrGlyGlyGlyCysTyrGlyTyrTrpTyrTrpGlyValTrpG 116
116 yGlnGlyThrLeuValThrValSerSer 125

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seq_name: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-476-176B-12

seq_documentation_block:

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; Sequence 12, Application US/08476176B
; Patent No. 5958708
; GENERAL INFORMATION:
; APPLICANT: Hardman, No. 5958708man
; APPLICANT: Kolbinger, Frank
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Reshaped monoclonal antibodies against an
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: No. 5958708artis Patent Department
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936-1080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,176B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/127,721
; FILING DATE: 27-SEPTEMBER-1993
; APPLICATION NUMBER: US 07/952,802
; FILING DATE: 25-SEPTEMBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5958708ak, Henry P.
; REGISTRATION NUMBER: 33,200
; REFERENCE/DOCKET NUMBER: 4-19276/A/P2/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 277-5110
; TELEFAX: (908) 277-4306
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 142 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-476-176B-12

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alignment_scores:

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Quality: 476.50      Length: 123
Ratio: 4.372         Gaps: 1
Percent Similarity: 88.618      Percent Identity: 73.984

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alignment_block:

US-08-487-283A-12_COPY_58_423 x US-08-476-176B-12 ..

Align seg 1/1 to: US-08-476-176B-12 from: 1 to: 142

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|||||
20 GlnValGlnLeuValGlnSerGlyAlaGlnValLysLysProGlyAlaSe 36
|||||
51 AGTCAAGTGTCCCTGAAGCTAGCGGCTATATTTTCTAATTATTTGA 100
|||||
36 rValLysValSerCysLysAlaSerGlyTyrThrPheSerMetTyrTrpL 53
|||||
101 TTCATGGGTGCTCAGGCCCCGGGCGAGGCTCGAATGGATGGGTGAG 150
|||||
53 euGluTrpValLysGlnArgProGlyHisGlyLeuGluTrpValGlyGlu 69
|||||
151 ATCTTACCGGGCTCTGTAGCACCGCAATATACGAAATTTTAAAGACCG 200
|||||
70 IleSerProGlyThrPheThrThrAsnTyrAsnGlnLysPheLysAlaLys 86
|||||
201 TGTACTATGACGCGTGTGACTTGTGACTAGTACATATACATGAGCTCT 250
|||||
86 sAlaThrPheThrAlaAspThrSerThrAsnThrAlaTyrMetGlnLeuS 103
|||||
251 CCAGCTGTGCGATCGAGACACAGGCGGCTATATTATTTGCGCGGTATTTT 300
|||||
103 erSerLeuThrSerGlnAspThrAlaValTyrCysAlaArgPheSer 119
|||||
301 TTTGGTTCTACCCGCAATTGG...TATTTGATGTTTGGGGTCAAGAAGC 347
|||||
120 HisPheSerGlySerAsnTyrAspTyrPheAspTyrTrpGlyGlnGlyTh 136
|||||
348 CCTGTCTACTGTCTCGAGC 366
|||||
136 rLeuValThrValSerSer 142
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Items Description

?

HIGHLIGHT set on as ''

HIGHLIGHT set on as ''

? begin 5,73,155,399,357

10nov00 09:22:02 User208760 Session D1713.2
 \$0.00 0.055 DialUnits File410
 \$0.00 Estimated cost File410
 \$0.01 TYMNET
 \$0.01 Estimated cost this search
 \$0.46 Estimated total session cost 0.169 DialUnits

SYSTEM:OS - DIALOG OneSearch

File 5:Biosis Previews(R) 1969-2000/Nov W2

(c) 2000 BIOSIS

File 73:EMBASE 1974-2000/Oct W3

(c) 2000 Elsevier Science B.V.

*File 73: Update codes are currently undergoing readjustment.

For details type Help News73.

File 155:MEDLINE(R) 1966-2000/Dec W4

(c) format only 2000 Dialog Corporation

*File 155: For changes to the file and check tags information
 please see Help News155.

File 399:CA SEARCH(R) 1967-2000/UD=13320

(c) 2000 American Chemical Society

*File 399: Use is subject to the terms of your user/customer agreement.

RANK charge added; see HELP RATES 399.

File 357:Derwent Biotechnology Abs 1982-2000/Nov B2

(c) 2000 Derwent Publ Ltd

Set Items Description

? s 5g1? and (c5 or c5a or complement)

89 5G1?

19902 C5

8617 C5A

237256 COMPLEMENT

S1 6 5G1? AND (C5 OR C5A OR COMPLEMENT)

? rd s1

...completed examining records

S2 2 RD S1 (unique items)

? t s2/3/all

2/3/1 (Item 1 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

(c) 2000 BIOSIS. All rts. reserv.

10974348 BIOSIS NO.: 199799595493

Inhibition of **complement** activity by humanized anti-C5 antibody
 and single-chain Fv.

AUTHOR: Thomas Thomas C(a); Rollins Scott A; Rother Russell P; Giannoni
 Michelle A; Hartman Sandra L; Elliott Eileen A; Nye Steven H; Matis Louis
 A; Squinto Stephen P; Evans Mark J

AUTHOR ADDRESS: (a)Alexion Pharmaceuticals, 25 Science Park, New Haven, CT
 06511**USA

JOURNAL: Molecular Immunology 33 (17-18):p1389-1401 1996 (1997)
ISSN: 0161-5890
RECORD TYPE: Abstract
LANGUAGE: English

2/3/2 (Item 1 from file: 357)
DIALOG(R) File 357:Derwent Biotechnology Abs
(c) 2000 Derwent Publ Ltd. All rts. reserv.

0190050 DBA Accession No.: 96-00821 PATENT
Treating glomerulonephritis with antibody against **complement-C5**
component - antiinflammatory monoclonal antibody production from
hybridoma cell culture, and Fv single chain antibody engineering
AUTHOR: Evans M J; Matis L; Mueller E E; Nye S H; Rollins S; Rother R
P; Springhorn J P; Squinto S P; Thomas T C; Wang Y; Wilkins J A
CORPORATE SOURCE: New Haven, CT, USA.
PATENT ASSIGNEE: Alexion-Pharm. 1995
PATENT NUMBER: WO 9529697 PATENT DATE: 951109 WPI ACCESSION NO.:
95-392923 (9550)
PRIORITY APPLIC. NO.: US 236208 APPLIC. DATE: 940502
NATIONAL APPLIC. NO.: WO 95US5688 APPLIC. DATE: 950501
LANGUAGE: English
? s (c5)(20n)(c5a)(20n)(antibod?)

>>>Operator "(5C)" in invalid position
? s (antibod?)(20n)(c5)(20n)(c5a)

>>>Operator "(5C)" in invalid position
? ds

Set	Items	Description
S1	6	5G1? AND (C5 OR C5A OR COMPLEMENT)
S2	2	RD S1 (unique items)
? s antibod?(10n)(c5 or c5a or complement)		
	1604233	ANTIBOD?
	19902	C5
	8617	C5A
	237256	COMPLEMENT
S3	52782	ANTIBOD?(10N)(C5 OR C5A OR COMPLEMENT)
? s antibod?(10n) c5 (10n) c5a		
	1604233	ANTIBOD?
	19902	C5
	8617	C5A
S4	106	ANTIBOD?(10N) C5 (10N) C5A
? rd s4		

...examined 50 records (50)
...examined 50 records (100)
...completed examining records
S5 52 RD S4 (unique items)
? t s5/7/all

s (c5) (20n) (c5a) (20n) (antibod?)

>>>Operator "(5C)" in invalid position
? s (antibod?) (20n) (c5) (20n) (c5a)

>>>Operator "(5C)" in invalid position
? ds

Set	Items	Description
S1	6	5G1? AND (C5 OR C5A OR COMPLEMENT)
S2	2	RD S1 (unique items)

? s antibod?(10n) (c5 or c5a or complement)

	1604233	ANTIBOD?
	19902	C5
	8617	C5A
	237256	COMPLEMENT
S3	52782	ANTIBOD?(10N) (C5 OR C5A OR COMPLEMENT)

? s antibod?(10n) c5 (10n) c5a

	1604233	ANTIBOD?
	19902	C5
	8617	C5A
S4	106	ANTIBOD?(10N) C5 (10N) C5A

? rd s4

...examined 50 records (50)
...examined 50 records (100)
...completed examining records
S5 52 RD S4 (unique items)
? t s5/7/all

File 73:EMBASE 1974-2000/Oct W3
 (c) 2000 Elsevier Science B.V.
 *File 73: Update codes are currently undergoing readjustment.
 For details type Help News73.
 File 155:MEDLINE(R) 1966-2000/Dec W4
 (c) format only 2000 Dialog Corporation
 *File 155: For changes to the file and check tags information
 please see Help News155.
 File 399:CA SEARCH(R) 1967-2000/UD=13320
 (c) 2000 American Chemical Society
 *File 399: Use is subject to the terms of your user/customer agreement.
 RANK charge added; see HELP RATES 399.
 File 357:Derwent Biotechnology Abs 1982-2000/Nov B2
 (c) 2000 Derwent Publ Ltd

Set	Items	Description
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? set hi ;set hi		

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$0.13 Estimated cost File5
    $0.20      0.024 DialUnits File73
$0.20 Estimated cost File73
    $0.08      0.024 DialUnits File155
$0.08 Estimated cost File155
    $0.30      0.024 DialUnits File399
$0.30 Estimated cost File399
    $0.28      0.024 DialUnits File357
$0.28 Estimated cost File357
    OneSearch, 5 files, 0.119 DialUnits FileOS
$0.05 TYMNET
$1.04 Estimated cost this search
$1.04 Estimated total session cost    0.119 DialUnits
  
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File 410:Chronolog(R) 1981-2000 Sep/Oct
 (c) 2000 The Dialog Corporation plc

Set	Items	Description
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HILIGHT set on as ''		
HILIGHT set on as ''		
? begin 5,73,155,399,357		

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10nov00 09:55:45 User208760 Session D1713.5
    $0.00      0.059 DialUnits File410
$0.00 Estimated cost File410
$0.02 TYMNET
$0.02 Estimated cost this search
$1.06 Estimated total session cost    0.178 DialUnits
  
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SYSTEM:OS - DIALOG OneSearch
 File 5:Biosis Previews(R) 1969-2000/Nov W2
 (c) 2000 BIOSIS
 File 73:EMBASE 1974-2000/Oct W3

(c) 2000 Elsevier Science B.V.
 *File 73: Update codes are currently undergoing readjustment.
 For details type Help News73.
 File 155:MEDLINE(R) 1966-2000/Dec W4
 (c) format only 2000 Dialog Corporation
 *File 155: For changes to the file and check tags information
 please see Help News155.
 File 399:CA SEARCH(R) 1967-2000/UD=13320
 (c) 2000 American Chemical Society
 *File 399: Use is subject to the terms of your user/customer agreement.
 RANK charge added; see HELP RATES 399.
 File 357:Derwent Biotechnology Abs 1982-2000/Nov B2
 (c) 2000 Derwent Publ Ltd

Set	Items	Description
---	-----	-----
? s	c5 (10n)	(alpha(w)chain) (10n) antibod?
	19902	C5
	1597067	ALPHA
	867947	CHAIN
	1604233	ANTIBOD?
S1	4	C5 (10N) (ALPHA(W)CHAIN) (10N) ANTIBOD?
? rd	s1	
...completed examining records		
	S2	2 RD S1 (unique items)
? t	s/7/all	
>>>Item list not allowed with accession number		
? t	s2/7/all	

2/7/1 (Item 1 from file: 5)
 DIALOG(R)File 5:Biosis Previews(R)
 (c) 2000 BIOSIS. All rts. reserv.

08377954 BIOSIS NO.: 000094108458
 FORMATION AND STRUCTURE OF THE C5B-7 COMPLEX OF THE LYTIC PATHWAY OF
 COMPLEMENT
 AUTHOR: DISCIPIO R G
 AUTHOR ADDRESS: DEP. IMMUNOLOGY IMM18, RESEARCH INSTITUTE SCRIPPS CLINIC,
 10666 N. TORREY PINES RD., LA JOLLA, CALIF. 92037.
 JOURNAL: J BIOL CHEM 267 (24). 1992. 17087-17094.
 FULL JOURNAL NAME: Journal of Biological Chemistry
 CODEN: JBCHA
 RECORD TYPE: Abstract
 LANGUAGE: ENGLISH

ABSTRACT: The formation and structure of the complement cytolytic intermediary complex, C5b-7, were studied with the aim of determining the interactive regions of C5, C6, and C7. The structure of human complement component C5 was elucidated by the application of limited proteolysis which generated well characterized major polypeptide fragments of this molecule. Plasmin, thrombin, and kallikrein cleave C5b with greater facility than C5. The most useful cleavage of C5b was effected by plasmin because the fragmentation pattern was similar to the processing the C3b by factors H, I, and kallikrein. Plasmin hydrolyzes peptide bonds within the .alpha.'-chain of C5b, resulting in a four-chain fragment, C5c (Mr = 142,000), and a single chain fragment, C5d (Mr = 43,000). Circular dichroism spectroscopic analyses indicated that C5d is substantially richer in .alpha.-helical content than is C5c (27 versus 9%). Polyclonal **antibodies** directed against C5c blocked the interaction of C5b-6 with C7, whereas **antibodies** directed against C5d inhibited the binding of C5 with C3b. Chemical cross-linking using a cleavable radioiodinated photoreactive reagent revealed that both C6 and C7

associate preferentially with the .alpha.'-chain of C5b. The reversible interactions of C5 with C6, C7, and major polypeptide fragments derived from these were investigated with solid phase binding assays. The results indicate that the carboxyl-terminal domains of C6 and C7, which have cysteine-rich modules homologous to those found in factors H and I, have the capacity to link specifically with C5.

2/7/2 (Item 1 from file: 357)
DIALOG(R)File 357:Derwent Biotechnology Abs
(c) 2000 Derwent Publ Ltd. All rts. reserv.

0190050 DBA Accession No.: 96-00821 PATENT
Treating glomerulonephritis with antibody against complement-C5 component
- antiinflammatory monoclonal antibody production from hybridoma cell
culture, and Fv single chain antibody engineering
AUTHOR: Evans M J; Matis L; Mueller E E; Nye S H; Rollins S; Rother R
P; Springhorn J P; Squinto S P; Thomas T C; Wang Y; Wilkins J A
CORPORATE SOURCE: New Haven, CT, USA.
PATENT ASSIGNEE: Alexion-Pharm. 1995
PATENT NUMBER: WO 9529697 PATENT DATE: 951109 WPI ACCESSION NO.:
95-392923 (9550)
PRIORITY APPLIC. NO.: US 236208 APPLIC. DATE: 940502
NATIONAL APPLIC. NO.: WO 95US5688 APPLIC. DATE: 950501
LANGUAGE: English
ABSTRACT: A new method for therapy of glomerulonephritis involves
introduction of an antibody (Ab) that binds to complement-C5 into the
bloodstream, to reduce the cell-lysing ability of complement present in
the blood. The Ab reduces conversion of complement-C5 to complement-C5a
and -C5b. The Ab may bind to C5b, and does not inhibit formation of
complement-C3b. The Ab may inhibit binding of C5 to complement-C3 or
complement-C4, by binding with a 5G46k, 5G27k, 5G325aa, 5G200aa or
KSSKC peptide fragment. A complete blockade of complement hemolytic
activity may occur. A monoclonal Ab (MAb) against human complement-
C5 **alpha-chain** or a peptide fragment, produced by
hybridoma 5G1.1 (ATCC HB 11625) is new. DNA encoding an Fv single chain
antibody with specified variable region light chain and heavy
chain sequences (including complementarity determining region-1, -2 and
-3) and an optional human constant domain is claimed, and may be
inserted in a vector for expression in a recombinant host cell. The MAb
eliminates glomerular inflammation and enlargement, and may also be
used in therapy of inflammatory joint disease or immunological or blood
disorders. (181pp)
? begin 652,653,654

10nov00 09:57:51 User208760 Session D1713.6
\$1.12 0.199 DialUnits File5
\$1.65 1 Type(s) in Format 7
\$1.65 1 Types
\$2.77 Estimated cost File5
\$1.76 0.207 DialUnits File73
\$1.76 Estimated cost File73
\$0.66 0.205 DialUnits File155
\$0.66 Estimated cost File155
\$2.75 0.219 DialUnits File399
\$2.75 Estimated cost File399
\$0.63 0.053 DialUnits File357
\$2.20 1 Type(s) in Format 7
\$2.20 1 Types
\$2.83 Estimated cost File357
OneSearch, 5 files, 0.883 DialUnits FileOS
\$0.15 TYMNET
\$10.92 Estimated cost this search
\$11.98 Estimated total session cost 1.061 DialUnits

SYSTEM:OS - DIALOG OneSearch

File 652:US Patents Fulltext 1971-1979

(c) format only 2000 The Dialog Corp.

*File 652: Reassignment data current through 7/25/2000 recordings.
Due to recent processing problems, the SORT command is not working.

File 653:US Patents Fulltext 1980-1989

(c) format only 2000 The Dialog Corp.

*File 653: Reassignment data current through 7/25/2000 recordings.
Due to recent processing problems, the SORT command is not working.

File 654:US Pat.Full. 1990-2000/Nov 07

(c) format only 2000 The Dialog Corp.

*File 654: Reassignment data current through 7/25/2000 recordings.
Due to recent processing problems, the SORT command is not working.

Set Items Description

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? s c5 (10n) (alpha(w)chain) (10n) antibod?

19913 C5

310045 ALPHA

351863 CHAIN

45267 ANTIBOD?

S1 0 C5 (10N) (ALPHA(W)CHAIN) (10N) ANTIBOD?

5/7/52 (Item 2 from file: 357)
DIALOG(R)File 357:Derwent Biotechnology Abs
(c) 2000 Derwent Publ Ltd. All rts. reserv.

0117029 DBA Accession No.: 91-04671 PATENT
Sensitive assay of complement-C5a peptide or des-Arg derivative - new
monoclonal antibody, anti-idiotypic monoclonal antibody and hybridoma
PATENT ASSIGNEE: Goetze O 1991
PATENT NUMBER: EP 411306 PATENT DATE: 910206 WPI ACCESSION NO.: 91-038259
(9106)

PRIORITY APPLIC. NO.: DE 3924924 APPLIC. DATE: 890727

NATIONAL APPLIC. NO.: EP 90111920 APPLIC. DATE: 900622

LANGUAGE: German

ABSTRACT: A method for the detection and/or quantitative determination of the complement peptides C5a and/or C5a-des-Arg (C5a') in biological fluid comprises immobilized antibodies (Ab 1) which bind C5a and C5a', and second detectable antibodies (Ab 2) which bind to C5a and/or C5a' bound to the first **antibodies**. The following are claimed: (1) cell lines producing monoclonal **antibodies** (MAbs) which bind to the receptor-binding sites in C5a and C5a' but not with the corresponding amino acid sequence in native C5; (2) MAbs produced by these cell lines; (3) anti-idiotypic (AIAb) against MAb produced by the specified cell lines; and (4) the cell line CNCM I-188 which produces AIAb F23/14. Ab 1 and Ab 2 are MAbs produced in mice or humans, and are MAb C17/5 (produced by the cell line CNCM I-887) and MAb G25/2 (produced by the cell line CNCM I-889), respectively. Compositions containing the MAbs can be used to treat and prevent diseases associated with elevated C5a levels in the blood or other disorders related to intra- or extra-vascular complement activation. AIAb can be used to block reaction of C5a with its receptors. (27pp)

03412845 EMBASE No: 1987165422

Rapid and simple measurement of human C5a-des-Arg level in plasma or serum using monoclonal antibodies

Takeda J.; Kinoshita T.; Takata Y.; et al.

Department of Bacteriology, Osaka University Medical School, Suita, Osaka 565 Japan

Journal of Immunological Methods (J. IMMUNOL. METHODS) (Netherlands) 1987, 101/2 (265-270)

CODEN: JIMMB

DOCUMENT TYPE: Journal

LANGUAGE: ENGLISH

A new sandwich immunoassay method for measuring human C5a-des-Arg was developed using monoclonal antibody specifically reactive with C5a-des-Arg. Monoclonal antibodies were obtained from a panel of hybridomas produced by fusion of mouse myeloma cells, P3 x 63-AG8,653, with spleen cells from a CBF1(C57BL/6 x BALB/c) mouse immunized with purified C5a. The reactivities of these monoclonal **antibodies** against C5a, C5a-des-Arg and C5 were tested by solid-phase radioimmunoassay. One of the **antibodies** reacted with C5a-des-Arg, but not with C5a and C5. By use of this **antibody** for capturing **antibody** in sandwich immunoassay, a rapid and simple method was developed for measuring C5a-des-Arg without previous removal of C5. The sensitivity of this assay system was approximately 1 ng/ml

5/7/35 (Item 4 from file: 73)
DIALOG(R)File 73:EMBASE
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07290420 EMBASE No: 1998173819
Immunotherapy for autoimmune and inflammatory renal diseases
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Current Opinion in Nephrology and Hypertension (CURR. OPIN. NEPHROL.
HYPERTENS.) (United Kingdom) 1998, 7/3 (311-315)
CODEN: CNHYE ISSN: 1062-4821
DOCUMENT TYPE: Journal; Article
LANGUAGE: ENGLISH SUMMARY LANGUAGE: ENGLISH
NUMBER OF REFERENCES: 46

New treatments for autoimmune renal disease are required, and a developing knowledge of its underlying immunopathogenesis has identified sites where immunotherapy is likely to be effective. Experience with intravenous immunoglobulin and lymphocyte depletion by monoclonal antibodies in systemic vasculitis and systemic lupus erythematosus is awaiting confirmation by randomized trials. Treatments at or near clinical testing include monoclonal antibody blockade of leucocyte-endothelial interactions and CD40 mediated B-cell activation, and immunoablation with autologous stem- cell transplantation for more severe multisystem autoimmune disease.

06268778 BIOSIS NO.: 000086102961

DETECTION OF NATIVE HUMAN COMPLEMENT COMPONENTS C3 AND C5 AND THEIR
PRIMARY ACTIVATION PEPTIDES C3a AND C5a ANAPHYLATOXIC PEPTIDES BY
ELISA WITH MONOCLONAL ANTIBODIES

AUTHOR: KLOS A; IHRIG V; MESSNER M; GRABBE J; BITTER-SUERMAN D

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MAINZ, WEST GERMANY.

JOURNAL: J IMMUNOL METHODS 111 (2). 1988. 241-252.

FULL JOURNAL NAME: Journal of Immunological Methods

CODEN: JIMMB

RECORD TYPE: Abstract

LANGUAGE: ENGLISH

ABSTRACT: Monoclonal antibodies (mAbs) were raised against human C3a, C3b, C5a, and C5b after immunization of BALB/c mice with the native components C3 and C5. Using different combinations of these mAbs we have developed four sensitive sandwich-enzyme-linked immunosorbent assays (ELISAs) for the detection of native C3 or C5 in samples with low concentrations of these proteins, e.g., in cell culture supernatants or synovial fluids and cerebrospinal fluids (CSF) and for the detection of the anaphylatoxic peptides (AT-peptides) C3a or C5a in human EDTA-plasma. The C3- and C5-ELISAs were found to be specific for the uncleaved complement proteins. Two different anti-C3a or anti-C5a mAbs were combined for the C3a- and C5a-eLISA. Before assaying a sample in the C3a- or C5a-ELISA a precipitation step to eliminate uncleaved C3 and C5 was necessary. The sensitivity and specificity of the four ELISAs were treated with purified antigens and EDTA-plasma or Cobra venom factor-activated EGTA-plasma samples as a source of C3a and C5a. The detection limits were 1 ng/ml for C3, 1 ng/ml for C3a, 2 ng/ml for C5, and 100 pg/ml for C5a. Plasma samples from patients undergoing cardiopulmonary bypass (CPB) surgery were used as a source of pathological material.

10225205 BIOSIS NO.: 199698680123

In vitro and in vivo inhibition of complement activity by a single-chain Fv fragment recognizing human C5.

AUTHOR: Evans Mark J(a); Rollins Scott A; Wolff Dennis W; Rother Russell P; Norin Allen J; Therrien Denise M; Grijalva Galo A; Mueller John P; Nye Steven H; Squinto Stephen P; Wilkins James A

AUTHOR ADDRESS: (a)Dep. Molecular Dev., Alexion Pharmaceuticals, 25 Science Park, New Haven, CT 06511**USA

JOURNAL: Molecular Immunology 32 (16):p1183-1195 1995

ISSN: 0161-5890

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Complement activation has been implicated in the pathogenesis of several human diseases. Recently, a monoclonal **antibody** (N19-8) that recognizes the human complement protein C5 has been shown to effectively block the cleavage of C5 into C5a and C5b, thereby blocking terminal complement activation. In this study, a recombinant N19-8 scFv **antibody** fragment was constructed from the N19-8 variable regions, and produced in both mammalian and bacterial cells. The N19-8 scFv bound human C5 and was as potent as the N19-8 monoclonal antibody at inhibiting human C5b-9-mediated hemolysis of chicken erythrocytes. In contrast, the N19-8 scFv only partially retained the ability of the N19-8 monoclonal antibody to inhibit C5a generation. To investigate the ability of the N19-8 scFv to inhibit complement-mediated tissue damage, complement-dependent myocardial injury was induced in isolated mouse hearts by perfusion with Krebs-Henseleit buffer containing 6% human plasma. The perfused hearts sustained extensive deposition of human C3 and C5b-9, resulting in increased coronary artery perfusion pressure, end-diastolic pressure, and a decrease in heart rate until the hearts ceased beating approximately 10 min after the addition of plasma. Hearts treated with human plasma supplemented with either the N19-8 monoclonal antibody or the N19-8 scFv did not show any detectable changes in cardiac performance for at least 1 hr following the addition of plasma. Hearts treated with human plasma alone showed extensive deposition of C3 and C5b-9, while hearts treated with human plasma containing the N19-8 scFv showed extensive deposition of C3, but no detectable deposition of C5b-9. Administration of a 100 mg bolus dose of N19-8 scFv to rhesus monkeys inhibited the serum hemolytic activity by at least 50% for up to 2 hr. Pharmacokinetic analysis of N19-8 scFv serum levels suggested a two-compartment model with a T-1/2-alpha of 27 min. Together, these data suggest the recombinant N19-8 scFv is a potent inhibitor of the terminal complement cascade and may have potential in vivo applications where short duration inhibition of terminal complement activity is desirable.

5/7/13 (Item 13 from file: 5)

DIALOG(R)File 5:Biosis Previews(R)

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10061787 BIOSIS NO.: 199598516705

Anti-C5 monoclonal antibody therapy prevents collagen-induced arthritis and ameliorates established disease.

AUTHOR: Wang Yi(a); Rollins Scott A(a); Madri Joseph A; Matis Louis A(a)

AUTHOR ADDRESS: (a)Immunobiol. Program, Alexion Pharm. Inc., New Haven, CT 06511**USA

JOURNAL: Proceedings of the National Academy of Sciences of the United

ABSTRACT: Activated components of the complement system are potent mediators of inflammation that may play an important role in numerous disease states. For example, they have been implicated in the pathogenesis of inflammatory joint diseases including rheumatoid arthritis (RA). To target complement activation in immune-mediated joint inflammation, we have utilized monoclonal **antibodies** (mAbs) that inhibit the complement cascade at C5, blocking the generation of the major chemotactic and proinflammatory factors C5a and C5b-9. In this study, we demonstrate the efficacy of a mAb specific for murine C5 in the treatment of collagen-induced arthritis, an animal model for RA. We show that systemic administration of the anti-C5 mAb effectively inhibits terminal complement activation in vivo and prevents the onset of arthritis in immunized animals. Most important, anti-C5 mAb treatment is also highly effective in ameliorating established disease. These results demonstrate a critical role for activated terminal complement components not only in the induction but also in the progression of collagen-induced arthritis and suggest that C5 may be an attractive therapeutic target in RA.

5/7/14 (Item 14 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

5/7/9 (Item 9 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10514607 BIOSIS NO.: 199699135752

Amelioration of lupus-like autoimmune disease in NZB/W F-1 mice after treatment with a blocking monoclonal antibody specific for complement component C5.

AUTHOR: Wang Yi(a); Hu Qile; Madri Joseph A; Rollins Scott A; Chodera Amy; Matis Louis A

AUTHOR ADDRESS: (a)Immunobiol. Program, Alexion Pharmaceuticals, Inc., New Haven, CT 06511**USA

JOURNAL: Proceedings of the National Academy of Sciences of the United States of America 93 (16):p8563-8568 1996

ISSN: 0027-8424

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: New Zealand black times New Zealand white (NZB/W) F-1 mice spontaneously develop an autoimmune syndrome with notable similarities to human systemic lupus erythematosus. Female NZB/W F-1 mice produce high titers of antinuclear antibodies and invariably succumb to severe glomerulonephritis by 12 months of age. Although the development of the immune-complex nephritis is accompanied by abundant local and systemic complement activation, the role of proinflammatory complement components in disease progression has not been established. In this study we have examined the contribution of activated terminal complement proteins to the pathogenesis of the lupus-like autoimmune disease. Female NZB/W F-1 mice were treated with a monoclonal **antibody** (mAb) specific for the C5 component of complement that blocks the cleavage of C5 and thus prevents the generation of the potent proinflammatory factors C5a and C5b-9. Continuous therapy with anti-C5 mAb for 6 months resulted in significant amelioration of the course of glomerulonephritis and in markedly increased survival. These findings demonstrate an important role for the terminal complement cascade in the progression of renal disease in NZB//W F-1 mice, and suggest that mAb-mediated C5 inhibition may be a useful approach to the therapy of immune-complex glomerulonephritis in humans.

5/7/10 (Item 10 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10419584 BIOSIS NO.: 199699040729

Proteolytic inactivation of the leukocyte C5a receptor by proteinases derived from *Porphyromonas gingivalis*.

AUTHOR: Jagels Mark A(a); Travis James; Potempa Jan; Pike Robert; Hugli Tony E

AUTHOR ADDRESS: (a)IMM-18, Dep. Immunol., The Scripps Res. Inst., La Jolla, CA 92037**USA

5/7/4 (Item 4 from file: 5)
DIALOG(R)File 5:BIOSIS Previews(R)
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11517221 BIOSIS NO.: 199800298553

Myocardial infarction and apoptosis after myocardial ischemia and
reperfusion: Role of the terminal complement components and inhibition by
anti-C5 therapy.

AUTHOR: Vakeva Antti P; Agah Azin; Rollins Scott A; Matis Louis A; Li Lan;
Stahl Gregory L(a)

AUTHOR ADDRESS: (a)Cent. Exp. Ther. and Reperfusion Injury, Dep. Anesth.,
Brigham and Women's Hosp., Harv. Med. Sch**USA

JOURNAL: Circulation 97 (22):p2259-2267 June 9, 1998

ISSN: 0009-7322

DOCUMENT TYPE: Article

RECORD TYPE: Abstract

LANGUAGE: English

ABSTRACT: Background-Myocardial ischemia and reperfusion (MI/R)-induced
tissue injury involves necrosis and apoptosis. However, the precise
contribution of apoptosis to cell death, as well as the mechanism of
apoptosis induction, has not been delineated. In this study, we sought to
define the contribution of the activated terminal complement components
to apoptosis and necrosis in a rat model of MI/R injury. Methods and
Results-Monoclonal **antibodies** (mAbs; 18A and 16C) raised against
the rat C5 complement component bound to purified rat C5
(ELISA). 18A effectively blocked C5b-9-mediated cell lysis and C5a
-induced chemotaxis of rat polymorphonuclear leukocytes (PMNs), whereas
16C had no complement inhibitor activity. A single dose (20 mg/kg IV) of
18A blocked >80% of serum hemolytic activity for >4 hours. Administration
of 18A before myocardial ischemia (30 minutes) and reperfusion (4 hours)
significantly reduced (91%) left ventricular free wall PMN infiltration
compared with 16C treatment. Treatment with 18A 1 hour before ischemia or
5 minutes before reperfusion significantly reduced infarct size compared
with 16C treatment. A significant reduction in infarct size (42%) was
also observed in 18A-treated rats after 30 minutes of ischemia and 7 days
of reperfusion. DNA ladders and DNA labeling (eg, TUNEL assay)
demonstrated a dramatic reduction in MI/R-induced apoptosis in
18A-treated compared with 16C-treated rats. Conclusions-Anti-C5 therapy
in the setting of MI/R significantly inhibits cell apoptosis, necrosis,
and PMN infiltration in the rat despite C3 deposition. We conclude that
the terminal complement components C5a and C5b-9 are key mediators of
tissue injury in MI/R.

5/7/6 (Item 6 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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11340383 BIOSIS NO.: 199800121715
Controlling the complement system in inflammation.
AUTHOR: Kirschfink Michael(a)
AUTHOR ADDRESS: (a)Inst. Immunol., Univ. Heidelberg, Im Neuenheimer Feld
305, 69120 Heidelberg**Germany
JOURNAL: Immunopharmacology 38 (1-2):p51-62 Dec., 1997
ISSN: 0162-3109
DOCUMENT TYPE: Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Inappropriate or excessive activation of the complement system can lead to harmful, potentially life-threatening consequences due to severe inflammatory tissue destruction. These consequences are clinically manifested in various disorders, including septic shock, multiple organ failure and hyperacute graft rejection. Genetic complement deficiencies or complement depletion have been proven to be beneficial in reducing tissue injury in a number of animal models of severe complement-dependent inflammation. It is therefore believed that therapeutic inhibition of complement is likely to arrest the process of certain diseases. Attempts to efficiently inhibit complement include the application of endogenous soluble complement inhibitors (C1-inhibitor, recombinant soluble complement receptor 1-rsCR1), the administration of **antibodies**, either blocking key proteins of the cascade reaction (e.g. C3, C5), neutralizing the action of the complement-derived anaphylatoxin **C5a**, or interfering with complement receptor 3 (CR3, CD 18/11b)-mediated adhesion of inflammatory cells to the vascular endothelium. In addition, incorporation of membrane-bound complement regulators (DAF-CD55, MCP-CD46, CD59) has become possible by transfection of the correspondent cDNA into xenogeneic cells. Thereby, protection against complement-mediated inflammatory tissue damage could be achieved in various animal models of sepsis, myocardial as well as intestinal ischemia/reperfusion injury, adult respiratory distress syndrome, nephritis and graft rejection. Supported by results from first clinical trials, complement inhibition appears to be a suitable therapeutic approach to control inflammation. Current strategies to specifically inhibit complement in inflammation have been discussed at a recent meeting on the 'Immune Consequences of Trauma, Shock and Sepsis', held from March 4-8, 1997, in Munich, Germany. The Congress (chairman: E. Faist, Munich, Germany), which was held in close cooperation with various national and international shock and trauma societies, was attended by about 2000 delegates from 40 countries. The major objective of the meeting was to provide an overview on the most state-of-the-art methods to prevent multiple organ dysfunction syndrome (MODS)/multiple organ failure (MOF) following the systemic inflammatory response (SIRS) to severe trauma. One of the largest symposia held within the Congress was devoted to current aspects of controlling complement in inflammation (for abstracts see: Shock 1997, 7 Suppl., 71-75). After providing the audience with information on the scientific background by addressing the clinical relevance of complement activation (G.O. Till, Ann Arbor, MI, USA) and discussing recent developments in modern complement diagnosis (J. Kohl, Hannover, Germany), B.P. Morgan (Cardiff, UK) introduced the symposium's special issue by giving an overview on complement regulatory molecules. Selected topics included overviews on the application of C1 inhibitor (C.E. Hack, Amsterdam, NL), sCRI (U.S. Ryan, Needham, MA, USA),

antibodies to C5 (Y. Wang, New Haven CT, USA) and to the anaphylatoxin C5a (M. Oppermann, Gottingen, Germany), and a report on complement inhibition in cardiopulmonary bypass (T.E. Mollnes, Bodo, Norway). The growing interest of clinicians in complement-directed anti-inflammatory therapy, and the fact that only some of the various aspects of therapeutic complement inhibition could be addressed on the meeting, has motivated the author to expand a Congress report into a short comprehensive review on recent strategies to control complement in inflammation.

5/7/7 (Item 7 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10974348 BIOSIS NO.: 199799595493
Inhibition of complement activity by humanized anti-C5 antibody and
single-chain Fv.
AUTHOR: Thomas Thomas C(a); Rollins Scott A; Rother Russell P; Giannoni
Michelle A; Hartman Sandra L; Elliott Eileen A; Nye Steven H; Matis Louis
A; Squinto Stephen P; Evans Mark J
AUTHOR ADDRESS: (a)Alexion Pharmaceuticals, 25 Science Park, New Haven, CT
06511**USA
JOURNAL: Molecular Immunology 33 (17-18):p1389-1401 1996 (1997)
ISSN: 0161-5890
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Activation of the complement system contributes significantly to the pathogenesis of numerous acute and chronic diseases. Recently, a monoclonal **antibody** (5G1.1) that recognizes the human complement protein **C5**, has been shown to effectively block **C5** cleavage, thereby preventing the generation of the pro-inflammatory complement components **C5a** and **C5b-9**. Humanized 5G1.1 **antibody**, Fab and scFv molecules have been produced by grafting the complementarity determining regions of 5G1.1 on to human framework regions. Competitive ELISA analysis indicated that no framework changes were required in the humanized variable regions for retention of high affinity binding to **C5**, even at framework positions predicted by computer modeling to influence CDR canonical structure. The humanized Fab and scFv molecules blocked complement-mediated lysis of chicken erythrocytes and porcine aortic endothelial cells in a dose-dependent fashion, with complete complement inhibition occurring at a three-fold molar excess, relative to the human **C5** concentration. In contrast to a previously characterized anti-**C5** scFv molecule, the humanized h5G1.1 scFv also effectively blocked **C5a** generation. Finally, an intact humanized h5G1.1 **antibody** blocked human complement lytic activity at concentrations identical to the original murine monoclonal antibody. These results demonstrate that humanized h5G1.1 and its recombinant derivatives retain both the affinity and blocking functions of the murine 5G1.1 antibody, and suggest that these molecules may serve as potent inhibitors of complement-mediated pathology in human inflammatory diseases.

5/7/8 (Item 8 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10825740 BIOSIS NO.: 199799446885
Monoclonal **antibody** to **C5** inhibits **C5a** and **C5b-9**
generation without inhibition of C3 cleavage and significantly limits
myocardial ischemia and reperfusion induced tissue damage.
AUTHOR: Vakeva A(a); Rollins S A; Matis L A; Stahl G L
AUTHOR ADDRESS: (a)Brigham Women's Hosp., Boston, MA**USA
JOURNAL: Journal of the American College of Cardiology 29 (2 SUPPL. A):p
267A 1997
CONFERENCE/MEETING: 46th Annual Scientific Session of the American College
of Cardiology Anaheim, California, USA March 16-19, 1997
ISSN: 0735-1097
RECORD TYPE: Citation

LANGUAGE: English

5/7/9 (Item 9 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
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10514607 BIOSIS NO.: 199699135752

Amelioration of lupus-like autoimmune disease in NZB/W F-1 mice after treatment with a blocking monoclonal antibody specific for complement component C5.

AUTHOR: Wang Yi(a); Hu Qile; Madri Joseph A; Rollins Scott A; Chodera Amy; Matis Louis A

AUTHOR ADDRESS: (a)Immunobiol. Program, Alexion Pharmaceuticals, Inc., New Haven, CT 06511**USA

JOURNAL: Proceedings of the National Academy of Sciences of the United States of America 93 (16):p8563-8568 1996

ISSN: 0027-8424

DOCUMENT TYPE: Article

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